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OM protein - protein search, using sw model

Run on: February 13, 2003, 13:50:31 ; Search time 28.0159 Seconds
(without alignments)
1678.958 Million cell updates/sec

Title: US-09-885-478-28

Sequence: 1 MDLFASTLIPGPNASNTSDG.....IRAVNAQTADERTESKGT 353

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
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21: /SID2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SID2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query length	ID	Description
1	1824	100.0	353	19 AAW61370	Human 11CB splice
2	1824	100.0	353	20 AAY16570	Amino acid sequenc
3	1824	100.0	353	21 AAB13442	Truncated human MC
4	1824	100.0	353	22 AAY90258	Human 11CBY protei
5	1824	100.0	353	22 AAE07328	Human melanin-conc
6	1824	100.0	353	22 AAE04747	Human 11CBY protei
7	1824	100.0	353	22 AAY97668	Human MCH-R3 prote
8	1824	100.0	353	22 AAB85895	Human short form M
9	1824	100.0	353	23 AAY75893	Human melanin-conc
10	1824	100.0	353	23 AAY75859	Human melanin conc

11	1824	100.0	417	22 AAE07329	Human melanin-conc
12	1824	100.0	417	22 AAY97669	Human MCH-R2 prote
13	1824	100.0	422	21 AAB12779	Human SLC-1 protei
14	1824	100.0	422	21 AAB13436	Human MCH1 recepto
15	1824	100.0	422	22 AAE07330	Human melanin-conc
16	1824	100.0	422	22 AAB81123	Human melanin conc
17	1824	100.0	422	22 AAB96871	Human SLC-1. Homo
18	1824	100.0	422	22 AAY97670	Human MCH-R3 prote
19	1824	100.0	422	22 AAB85894	Human long form MC
20	1824	100.0	422	23 AAY75541	Human melanin conc
21	1824	100.0	422	23 AAY75853	Human melanin conc
22	1824	100.0	422	23 AAB04941	Human SLC-1 protei
23	1824	100.0	422	23 AAG80611	Human SLC-1 protei
24	1824	100.0	709	22 AAB56396	TSNR-GS-alpha fusi
25	1819	99.7	353	22 AAB56307	Non-endogenous hum
26	1819	99.7	422	21 AAB13440	Mutant human MCH1
27	1819	99.7	422	21 AAB13441	Mutant human MCH1
28	1819	99.7	422	23 AAY75857	Human melanin conc
29	1819	99.7	422	23 AAY75858	Human melanin conc
30	1818	99.7	353	22 AAB56297	Non-endogenous hum
31	1818	99.7	353	22 AAB56305	Non-endogenous hum
32	1817	99.6	353	22 AAB56306	Non-endogenous hum
33	1814	99.5	353	22 AAB56301	Non-endogenous hum
34	1814	99.5	353	22 AAB56303	Non-endogenous hum
35	1814	99.5	353	22 AAB58897	Human short form/m
36	1814	99.5	422	22 AAB58898	Human long form/mo
37	1814	99.5	604	22 AAB85906	Human short form/m
38	1814	99.5	673	22 AAB85907	Human long form/mo
39	1813	99.4	353	22 AAB56300	Non-endogenous hum
40	1812	99.3	353	22 AAB56298	Non-endogenous hum
41	1811	99.3	353	22 AAB56302	Non-endogenous hum
42	1811	99.3	353	22 AAB56304	Non-endogenous hum
43	1808	99.1	353	21 AAY72284	Human GPCR protein
44	1781	97.6	353	23 AAY76892	Dog melanin-concen
45	1763	96.7	353	21 AAB12778	Rat SLC-1 protein

ALIGNMENTS

RESULT 1
AAW61370
ID AAW61370 standard; Protein; 353 AA.
XX
AC AAW61370;
XX
DT 25-SEP-1998 (first entry)
XX
DE Human 11CB splice variant peptide.
XX
KW Human; 11CB splice variant; 7-transmembrane receptor family; asthma;
KW HIV; cancer; diabetes; eating disorder; Parkinson's disease;
KW heart failure; angina pectoris; myocardial infarction; osteoporosis;
KW benign prostatic hypertrophy; psychotic disorder; neurological disorder;
KW severe mental retardation; dyskinesias.
XX
OS Homo sapiens.
XX
PN EP848060-A2.
XX
PD 17-JUN-1998.
XX
PF 01-DEC-1997; 97EP-0309647.
XX
PR 11-DEC-1996; 96US-0032763.
XX
PA (SMIRK) SMITHKLINE BEECHAM CORP.
XX
PI Bergsma DJ, Ellis CE;
XX
DR WPI: 1998-314475/28.
XX
DR N-PSDB; AAY28115.
XX

PT Human 11cb splice variant polypeptide - used for treatment of e.g.
 PT bacterial, protozoal, fungal and viral infections e.g. caused by
 PT human immunodeficiency virus
 PS Claim 11; Page 23-24; 31pp; English.
 CC The human 11CB splice variant protein is related to the 11CB splice
 CC variant encoded by mouse cDNA and is also structurally related to other
 CC member of the 7-transmembrane receptor family. Polypeptides or agonists
 CC of the 11CB splice variant can be used to treat infections, such as
 CC bacterial, fungal, protozoal and viral infections, particularly infection
 CC caused by human immunodeficiency virus-1 or -2; pain; cancers; diabetes;
 CC obesity; anorexia; bulimia; asthma; Parkinson's disease; both acute and
 CC congestive heart failure; hypotension; hypertension; urinary retention;
 CC osteoporosis; angina pectoris; myocardial infarction; ulcers; allergies;
 CC benign prostatic hypertrophy and psychotic and neurological disorders or
 CC severe mental retardation, and dyskinesias.
 CC
 SQ Sequence 353 AA;
 Query Match 100.0%; Score 1824; DB 19; Length 353;
 Best Local Similarity 100.0%; Pred. No. 1.6e-203;
 Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDLEASLPTGPNASNTSDGPDNLTSA GSPRTGISYINIMPSVFGTICLLGIIGNST 60
 DB 1 MDLEASLPTGPNASNTSDGPDNLTSA GSPRTGISYINIMPSVFGTICLLGIIGNST 60
 QY 61 VIEFAVKKSKLHMCNNVPDIFINLSVVDLLFLGMPFHOLMGNGVHFGETKCTLT 120
 DB 61 VIEFAVKKSKLHMCNNVPDIFINLSVVDLLFLGMPFHOLMGNGVHFGETKCTLT 120
 QY 121 AMDANSQFTSYITLAMAIDRYLATVHPISSTKRRKPSVATVICLMAISFISTPWL 180
 DB 121 AMDANSQFTSYITLAMAIDRYLATVHPISSTKRRKPSVATVICLMAISFISTPWL 180
 QY 181 YARLIPFGAGVGCIRLPNDTLYWFTLYQFFLAFLPVTAAVYRIILQRMSSVA 240
 DB 181 YARLIPFGAGVGCIRLPNDTLYWFTLYQFFLAFLPVTAAVYRIILQRMSSVA 240
 QY 241 PASQSRIRLRTKRVTRTAICLVFVCMAPIYVQLTQLSIRPLTITVYLYNAISIG 300
 DB 241 PASQSRIRLRTKRVTRTAICLVFVCMAPIYVQLTQLSIRPLTITVYLYNAISIG 300
 QY 301 YANSCINPFYIVLCETFRKRLVSVKPAAGOLRAVSNAGTADERTESKGT 353
 DB 301 YANSCINPFYIVLCETFRKRLVSVKPAAGOLRAVSNAGTADERTESKGT 353
 RESULT 2
 AAY16570
 ID AAY16570 standard; Protein: 353 AA.
 XX
 AC AAY16570;
 XX
 DT 10-AUG-1999 (first entry)
 XX
 DE Amino acid sequence of the human 11cb splice variant.
 XX
 KW Human 11cb splice variant; antibacterial; gene therapy; vaccine; HIV-1;
 KW HIV-2; pain; cancer; diabetes; obesity; anorexia; bulimia; asthma;
 KW Parkinson's disease; heart failure; hypotension; hypertension;
 KW urinary retention; osteoporosis; angina pectoris; myocardial infarction;
 KW ulcer; allergy; benign prostatic hypertrophy; psychotic disorder;
 KW neurological disorder; anxiety; schizophrenia; manic depression;
 KW delirium; dementia; severe mental retardation; dyskinesia;
 KW Huntington's disease; Gilles de la Tourette's syndrome;
 KW bacterial adhesion.
 XX
 OS Homo sapiens.
 XX
 PN MO9928492-A1.
 XX

PD 10-JUN-1999.
 XX
 XX 02-DEC-1998; 98WO-US25497.
 PF
 XX 15-APR-1998; 98US-0060504.
 PR 03-DEC-1997; 97US-0984288.
 PR 05-FEB-1998; 98US-0073747.
 XX
 PA (SMK) SKITHLINE BECHAM CORP.
 XX
 PI Ames RS, Bergsma D, Chambers JK, Ellis CE, Foley JJ;
 PI Sarau HM;
 DR WPI: 1999-371132/31.
 DR N-PSDB; AAX60230.
 XX
 PT New human 11cb splice variant polypeptide and polynucleotide
 XX
 XX
 PS Claim 11; Fig 1B; 56pp; English.
 CC The present sequence represents a human 11cb splice variant polypeptide.
 CC 11cb splice variant polypeptides and polynucleotides are useful for
 CC diagnosing diseases due to an infection of an organism with the 11cb
 CC splice variant gene. They can diagnose the stage and type of infection.
 CC 11cb splice variant polypeptides are also useful for screening for
 CC compounds which affect activity of the protein. These can be used in
 CC treatment to inhibit (antagonist i.e. antibacterial drugs) or enhance
 CC (agonist) 11cb splice variant activity. In addition to direct
 CC administration of 11cb splice variant polypeptides to treat conditions
 CC associated with a lack of 11cb splice variant polypeptide, or direct
 CC administration of antisense sequences to prevent expression, 11cb splice
 CC variant polypeptides (administered directly, in a vector i.e. gene
 CC therapy, and as a vaccine) and antibodies induce an immune response to
 CC immunize and prevent disease. Diseases diagnosed, prevented or treated
 CC include HIV-1 or -2 infection, pain, cancer, diabetes, obesity, feeding
 CC and drinking abnormalities e.g. anorexia, bulimia; asthma; Parkinson's
 CC disease; acute and congestive heart failure; hypotension; hypertension;
 CC urinary retention; osteoporosis; angina pectoris; myocardial infarction;
 CC ulcers; allergies; benign prostatic hypertrophy and psychotic and
 CC neurological disorders, including anxiety, schizophrenia, manic
 CC depression, delirium, dementia or severe mental retardation, and
 CC dyskinesias, such as Huntington's disease or Gilles de la Tourette's
 CC syndrome. 11cb splice variant polypeptides, polynucleotides and their
 CC (ant)agonists can prevent adhesion of bacteria to matrix proteins, and
 CC are useful for use on wounds and body implants to prevent bacterial
 CC infection.
 CC
 SQ Sequence 353 AA;
 Query Match 100.0%; Score 1824; DB 20; Length 353;
 Best Local Similarity 100.0%; Pred. No. 1.6e-203;
 Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDLEASLPTGPNASNTSDGPDNLTSA GSPRTGISYINIMPSVFGTICLLGIIGNST 60
 DB 1 MDLEASLPTGPNASNTSDGPDNLTSA GSPRTGISYINIMPSVFGTICLLGIIGNST 60
 QY 61 VIEFAVKKSKLHMCNNVPDIFINLSVVDLLFLGMPFHOLMGNGVHFGETKCTLT 120
 DB 61 VIEFAVKKSKLHMCNNVPDIFINLSVVDLLFLGMPFHOLMGNGVHFGETKCTLT 120
 QY 121 AMDANSQFTSYITLAMAIDRYLATVHPISSTKRRKPSVATVICLMAISFISTPWL 180
 DB 121 AMDANSQFTSYITLAMAIDRYLATVHPISSTKRRKPSVATVICLMAISFISTPWL 180
 QY 181 YARLIPFGAGVGCIRLPNDTLYWFTLYQFFLAFLPVTAAVYRIILQRMSSVA 240
 DB 181 YARLIPFGAGVGCIRLPNDTLYWFTLYQFFLAFLPVTAAVYRIILQRMSSVA 240
 QY 241 PASQSRIRLRTKRVTRTAICLVFVCMAPIYVQLTQLSIRPLTITVYLYNAISIG 300
 DB 241 PASQSRIRLRTKRVTRTAICLVFVCMAPIYVQLTQLSIRPLTITVYLYNAISIG 300

QY 301 YANSCINPEYIVLCETFRKRLVSVKPAAGOLRAVSNAGTADERTESKGT 353
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 301 YANSCINPEYIVLCETFRKRLVSVKPAAGOLRAVSNAGTADERTESKGT 353

RESULT 3
 AAB13442
 ID AAB13442 standard; Protein: 353 AA.

XX AAB13442:

DT 17-NOV-2000 (first entry)

DE Truncated human MCH1 receptor encoded by plasmid B0120.

XX Human; MCH1 receptor; melanin concentrating hormone; neuroregulator;
 KW G-protein coupled; feeding; water balance; energy metabolism; arousal;
 KW attention; memory; cognitive function; psychiatric disorder; stress;
 KW sexual activity; hormone disorder; hypertension; diabetes;
 KW cardiovascular; gastrointestinal; electrolyte balance; respiratory;
 KW asthma; reproductive function; immune; endocrine; musculoskeletal;
 KW Alzheimer's disease; sensory modulation; transmission;
 KW motor coordination; Parkinson's disease; olfaction; urinary; depression;
 KW seizure; pain; schizophrenia; morphine tolerance; opiate addiction;
 KW migraine.

OS Homo sapiens.

PN W0200039279-A2.

PD 06-JUL-2000.

PF 30-DEC-1999; 99WO-US31169.

PR 31-DEC-1998; 98US-0224426.

PA (SYNA-) SYNAPTIC PHARM CORP.

PI Salon JA, Laz TM, Nagorny R, Wilson AE;

DR WPI: 2000-548644/50.

PT Novel nucleic acid encoding human melanin concentrating hormone
 receptor useful for treating cardiovascular disorders, hypertension and
 diabetes, whose mutant form is activated by melanin concentrating
 hormone

PS Claim 10; Fig 15; 173pp; English.

XX Neuroregulators modulate communication in the nervous system. Melanin
 CC concentrating hormone 1 (MCH) is one such neuroregulator. MCH may serve
 CC as an integrative neuropeptide, involved in stress response, feeding
 CC regulation and sexual activity. Also, MCH is thought to participate in
 CC water balance regulation, energy metabolism, general arousal/attention
 CC state, memory and cognitive functions and psychiatric disorders. The
 CC present sequence is the truncated human MCH1 receptor encoded by plasmid
 CC B0120. The present sequence is a G-protein coupled receptor. MCH1
 CC receptor may be used in the therapy for a variety of disorders: steroid
 CC or pituitary hormone disorder, epinephrine release disorder,
 CC gastrointestinal disorder, cardiovascular disorder, electrolyte balance
 CC disorder, hypertension, diabetes, respiratory disorder, asthma,
 CC reproductive function disorder, immune disorder, endocrine disorder,
 CC musculoskeletal disorder, neuroendocrine disorder, cognitive disorder,
 CC memory disorder e.g. Alzheimer's disease, sensory modulation and
 CC transmission disorder, motor coordination disorder, sensory integration
 CC disorder, dopaminergic function disorder e.g. Parkinson's disease,
 CC olfaction disorder, sympathetic innervation disorder, depression, stress,
 CC fluid-imbalance disorder, urinary disorder e.g. urinary incontinence,
 CC seizure, pain, psychotic behaviour e.g. schizophrenia, morphine
 CC tolerance, opiate addiction or migraine.

XX Sequence 353 AA;

Query Match 100.0%; Score 1824; DB 21; Length 353;
 Best Local Similarity 100.0%; Pred. No. 1.6e-203;
 Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLEASILPTGPNNASNTSDGPDNLTSGSPPRGSIYINIMPSVGTICLGIIONST 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 MDLEASILPTGPNNASNTSDGPDNLTSGSPPRGSIYINIMPSVGTICLGIIONST 60
 QY 61 VIFAVVKKSKLHMCONNPDIIFIINLSYVDLLEFLGMPFMIHQLMGNGVMHGEFMCTLIT 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 VIFAVVKKSKLHMCONNPDIIFIINLSYVDLLEFLGMPFMIHQLMGNGVMHGEFMCTLIT 120
 QY 121 AMDANSOFTSYIITANADRYLATVHPISSTKPKRSVATVLCMLALSISITPWL 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 AMDANSOFTSYIITANADRYLATVHPISSTKPKRSVATVLCMLALSISITPWL 180
 QY 181 YARLIIPPGGAVGCGIRLPNDTDLVFTLYQFLAALPVPVITAAVRLQMTSSVA 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 181 YARLIIPPGGAVGCGIRLPNDTDLVFTLYQFLAALPVPVITAAVRLQMTSSVA 240
 QY 241 PASQSRIRLRTKRYTFRALAIQVFEVQMAPYVYLQTLQISRPITLFEVLYNAAISLG 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 241 PASQSRIRLRTKRYTFRALAIQVFEVQMAPYVYLQTLQISRPITLFEVLYNAAISLG 300
 QY 301 YANSCINPEYIVLCETFRKRLVSVKPAAGOLRAVSNAGTADERTESKGT 353
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 301 YANSCINPEYIVLCETFRKRLVSVKPAAGOLRAVSNAGTADERTESKGT 353

RESULT 4
 AAY90258
 ID AAY90258 standard; Protein: 353 AA.

AC AAY90258:

DT 19-SEP-2000 (first entry)

DE Human 11cby protein.

XX Human; 11cby; diagnosis; therapy; infection; cancer; diabetes; obesity;
 KW anorexia; bulimia; asthma; Parkinson's disease; congestive heart failure;
 KW hypotension; hypertension; urinary retention; osteoporosis; delirium;
 KW angina pectoris; myocardial infarction; ulcer; allergy; manic depression;
 KW benign prostatic hyperplasia; psychotic disorder; neurological disorder;
 KW anxiety; schizophrenia; dementia; severe mental retardation; dyskinesia;
 KW Huntington's disease; Gilles de la Tourette's syndrome;
 KW genetic counselling.

OS Homo sapiens.

PN W0200037113-A1.

PD 29-JUN-2000.

PF 22-DEC-1999; 99WO-US30622.

PR 22-DEC-1998; 98US-0218467.

PA (SMIK) SMITHKLINE BEECHAM CORP.

PI Sathe G, Ellis CE, Halsey W, Bergsma D;

DR WPI: 2000-452132/39.

DR N-PSDB; AAA30875.

XX Novel 11cby polynucleotides for diagnosis, prevention and treatment of
 PT cancer, diabetes; psychotic and neurological disorders, microbial
 PT infections and for genetic counselling
 PS Disclosure; Page 41-42; 45pp; English.

CC This sequence represents the human 11cby protein sequence of the
 CC invention. 11cby polynucleotides are useful as diagnostic reagents for

CC detecting the presence or absence of a variation in a 11cby allele in
 CC an individual. Assaying for the presence or absence of a 11cby
 CC polynucleotide mutation by isolating DNA from the individuals is useful
 CC for screening an individual for an increased risk of developing a
 CC disease or for diagnosing a disease. 11cby polynucleotides may contain
 CC polymorphic markers, and are therefore useful for genetic association
 CC studies searching for a disease susceptibility gene and/or therapeutic
 CC response gene. Diseases treated include bacterial, fungal, protozoan and
 CC viral infections, particularly infection caused by human immunodeficiency
 CC virus (HIV)-1 or HIV-2, cancers, diabetes, obesity, feeding and drinking
 CC abnormalities, such as anorexia and bulimia, asthma, Parkinson's disease,
 CC acute and congestive heart failure, hypotension, hypertension, urinary
 CC retention, osteoporosis, angina pectoris, myocardial infarction, ulcers,
 CC allergies, benign prostatic hypertrophy, psychotic and neurological
 CC disorders, including anxiety, schizophrenia, manic depression, delirium,
 CC Huntington's disease or Gilles de la Tourette's syndrome. The methods for
 CC detecting a mutation in the 11cby gene, can therefore be further extended
 CC to include genetic counselling for an individual with respect to the
 CC individual's potential for developing one of the above diseases.

XX Sequence 353 AA;

Query Match 100.0%; Score 1824; DB 21; Length 353;

Best Local Similarity 100.0%; Pred. No. 1.6e-203;

Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLEASLPTGPNASNTSDGPDNLTSAGSPRTGSIYINIMPSVGTICLLGIIGNST 60

DB 1 MDLEASLPTGPNASNTSDGPDNLTSAGSPRTGSIYINIMPSVGTICLLGIIGNST 60

QY 61 VIFAVVKKSKLHMCNNVPDIFIIINLSVVDLFLGMPFMIHOLMGNGVHGETMCTLIT 120

DB 61 VIFAVVKKSKLHMCNNVPDIFIIINLSVVDLFLGMPFMIHOLMGNGVHGETMCTLIT 120

QY 121 AMDANSQFTSTYILTAAMIDRYLATVHPISSTKRKPSVATLVICLLMAISFISTPWWL 180

DB 121 AMDANSQFTSTYILTAAMIDRYLATVHPISSTKRKPSVATLVICLLMAISFISTPWWL 180

QY 181 VARLIPFGAVGCGIRLPNPDLYWFTLYQFPLAFALPFVYITAAVYRILOKMTSSVA 240

DB 181 VARLIPFGAVGCGIRLPNPDLYWFTLYQFPLAFALPFVYITAAVYRILOKMTSSVA 240

QY 241 PASORSIRLRTKRVTRTAIAICLVFVCWAPYYVLQTLQLSISRPTLFFVLYNNAISLG 300

DB 241 PASORSIRLRTKRVTRTAIAICLVFVCWAPYYVLQTLQLSISRPTLFFVLYNNAISLG 300

QY 301 YANSCLPFVYIVLCETFRKRLVLSVKPAAGQLRAVSNQOTADEERTESKGT 353

DB 301 YANSCLPFVYIVLCETFRKRLVLSVKPAAGQLRAVSNQOTADEERTESKGT 353

RESULT 5

AAE07328 ID AAE07328 standard; Protein; 353 AA.

XX AAE07328;

XX 06-NOV-2001 (first entry)

DE Human melanin-concentrating hormone receptor variant #1.

XX Human; melanin-concentrating hormone; MCH analogue; signal transduction;

KW appetite; therapy; anorexia; acquired immune deficiency syndrome; AIDS;

KM wasting; cachexia; frail elderly; weight maintenance; cancer; anorectic;

XX pain reduction; stress reduction; sexual dysfunction; variant.

OS Homo sapiens.

XX Synthetic.

XX WO200157070-A1.

XX 09-AUG-2001.

XX 01-FEB-2001; 2001WO-US03293.

XX 03-FEB-2000; 2000US-0179967.

XX (MERI) MERCK & CO INC.

XX Bednarek M;

XX WPI; 2001-483416/52.

DR N-PSDB; AAD13652.

PT Novel peptide encoding a melanin-concentrating hormone analog useful

XX for increasing weight or appetite

XX Example 2; Page 33-34; 66pp; English.

CC The present invention relates to truncated melanin-concentrating hormone

CC (MCH) analogues active at the MCH receptor. The truncated MCH analogues

CC are optionally modified peptide derivatives of mammalian MCH. The MCH

CC analogues can bind to the MCH receptor and bring about signal

CC transduction. The MCH agonists can be used to facilitate a weight gain,

CC maintenance of weight and/or an appetite increase. The MCH agonists can

CC also be used to treat disorders such as anorexia, acquired immune

CC deficiency syndrome (AIDS), wasting, cachexia and frail elderly. The MCH

CC antagonists can be used to facilitate weight loss, appetite decrease,

CC weight maintenance, cancer treatment, pain reduction, stress reduction

CC and/or treatment of sexual dysfunction. The present sequence is a human

XX MCH receptor variant.

SQ Sequence 353 AA;

Query Match 100.0%; Score 1824; DB 22; Length 353;

Best Local Similarity 100.0%; Pred. No. 1.6e-203; Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLEASLPTGPNASNTSDGPDNLTSAGSPRTGSIYINIMPSVGTICLLGIIGNST 60

DB 1 MDLEASLPTGPNASNTSDGPDNLTSAGSPRTGSIYINIMPSVGTICLLGIIGNST 60

QY 61 VIFAVVKKSKLHMCNNVPDIFIIINLSVVDLFLGMPFMIHOLMGNGVHGETMCTLIT 120

DB 61 VIFAVVKKSKLHMCNNVPDIFIIINLSVVDLFLGMPFMIHOLMGNGVHGETMCTLIT 120

QY 121 AMDANSQFTSTYILTAAMIDRYLATVHPISSTKRKPSVATLVICLLMAISFISTPWWL 180

DB 121 AMDANSQFTSTYILTAAMIDRYLATVHPISSTKRKPSVATLVICLLMAISFISTPWWL 180

QY 181 VARLIPFGAVGCGIRLPNPDLYWFTLYQFPLAFALPFVYITAAVYRILOKMTSSVA 240

DB 181 VARLIPFGAVGCGIRLPNPDLYWFTLYQFPLAFALPFVYITAAVYRILOKMTSSVA 240

QY 241 PASORSIRLRTKRVTRTAIAICLVFVCWAPYYVLQTLQLSISRPTLFFVLYNNAISLG 300

DB 241 PASORSIRLRTKRVTRTAIAICLVFVCWAPYYVLQTLQLSISRPTLFFVLYNNAISLG 300

QY 301 YANSCLPFVYIVLCETFRKRLVLSVKPAAGQLRAVSNQOTADEERTESKGT 353

DB 301 YANSCLPFVYIVLCETFRKRLVLSVKPAAGQLRAVSNQOTADEERTESKGT 353

RESULT 6

AAE04747 ID AAE04747 standard; Protein; 353 AA.

XX AAE04747;

XX 10-SEP-2001 (first entry)

DE Human 11cby protein.

XX 11cby; stroke; pain; neuropathy; analgesic; cerebroprotective; vaccine;

KW gene therapy; G-protein coupled receptor superfamily; MCH receptor;

KW melanin-concentrating hormone; human.
 OS Homo sapiens.
 XX
 XX WO200143759-A2.
 PN
 XX
 XX 21-JUN-2001.
 PD
 XX
 XX 12-DEC-2000; 2000WO-BE12703.
 PF
 XX 16-DEC-1999; 99GB-0029772.
 PR
 XX (SMK) SMITHKLINE BEECHAM PLC.
 PA
 XX Campbell CA, Haddingham SJ, Harrison DC, Hervieu GJ;
 PI
 DR WPI; 2001-398072/42.
 DR N-PSDB; AAD09345.
 XX
 XX
 PT Use of a compound selected from 11CBY polypeptide, a compound which
 PT activates or inhibits the polypeptide, or a polynucleotide encoding the
 PT polypeptide, for treating stroke, pain or neuropathies
 PS
 PS Claim 6; Page 31; 40pp; English.
 XX
 CC The present invention relates to use of 11CBY polypeptides and
 CC polynucleotides for the manufacture of medicament for treating stroke,
 CC pain or neuropathies. The 11CBY polypeptides and polynucleotides are
 CC useful for identifying compounds which may be agonists, antagonists or
 CC inhibitors which are potentially useful in therapy. The polypeptide
 CC is useful for inducing an immunological response in a mammal, for
 CC identifying interacting proteins or other molecules, as immunogens to
 CC produce antibodies, in vaccine formulation, and in a method for the
 CC structure-based design of its agonist, antagonist or inhibitor. The
 CC 11CBY polypeptide and polynucleotide are also useful to configure
 CC screening methods for detecting the effect of added components on the
 CC production of mRNA and polypeptide in cells. The present sequence is
 CC human 11CBY protein. 11CBY polypeptide is a member of G-protein coupled
 CC receptor superfamily and is believed to be a physiological melanin-
 CC concentrating hormone (MCH) receptor.
 XX
 XX Sequence 353 AA;
 SQ
 Query Match 100.0%; Score 1824; DB 22; Length 353;
 Best Local Similarity 100.0%; Pred. No. 1.6e-203;
 Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDEASLLPTGPNASNTSDGPDNLTSAGSPRTGSISYINIMPSVEGTICLLGIIGNST 60
 DB 1 MDEASLLPTGPNASNTSDGPDNLTSAGSPRTGSISYINIMPSVEGTICLLGIIGNST 60
 QY 61 VIRAIVVKKSKLHMCNNVPDIFITINLSVVDLFLGMPFMHQLMGNGVMHGEIMCTLIT 120
 DB 61 VIRAIVVKKSKLHMCNNVPDIFITINLSVVDLFLGMPFMHQLMGNGVMHGEIMCTLIT 120
 QY 121 AMDANSOFTSTYIITAMADRYLATVHPISSTKFRKPSVATLVICLLMAISFISITTPVWL 180
 DB 121 AMDANSOFTSTYIITAMADRYLATVHPISSTKFRKPSVATLVICLLMAISFISITTPVWL 180
 QY 181 YARLIPEPGAVGCGIRLPNPDIDLWFTLYQFLAFLAPFVITAAVYRILQMTSSVA 240
 DB 181 YARLIPEPGAVGCGIRLPNPDIDLWFTLYQFLAFLAPFVITAAVYRILQMTSSVA 240
 QY 241 PASORSIRLRTKRYTRAIACLVFPCWAPYVYLQTLQSLSPRTLTFVYLYNAAISLG 300
 DB 241 PASORSIRLRTKRYTRAIACLVFPCWAPYVYLQTLQSLSPRTLTFVYLYNAAISLG 300
 QY 301 YANSCLNPFYIYLCETFRKRLVLSVPAAGQLRAVSNQTADEERTESKGT 353
 DB 301 YANSCLNPFYIYLCETFRKRLVLSVPAAGQLRAVSNQTADEERTESKGT 353

AAV97668
 ID AAV97668 standard; protein; 353 AA.
 XX
 XX AAV97668;
 AC
 XX
 XX 08-MAY-2001 (first entry)
 DT
 XX
 XX Human MCH-R1 protein sequence.
 DE
 XX
 XX Human; melanin-concentrating hormone receptor; MCH-R1; MCH-R2; MCH-R3;
 KW weight loss; weight gain; cancer; pain; diabetes; stress; therapy;
 KW sexual dysfunction.
 XX
 XX Homo sapiens.
 OS
 XX
 XX WO200105947-A1.
 PN
 XX
 XX 25-JAN-2001.
 PD
 XX
 XX 10-JUL-2000; 2000WO-US18733.
 PF
 XX 14-JUL-1999; 99US-0143706.
 PR
 XX (MERI) MERCK & CO INC.
 PA
 XX
 XX Howard AD;
 PI
 DR WPI; 2001-159528/16.
 DR N-PSDB; AAA91187.
 XX
 XX Melanin-concentrating hormone receptor polypeptides for increasing or
 PT decreasing appetite, reducing stress and to screen for compounds that
 PT bind to the receptor -
 PS
 PS Disclosure; Page 20-21; 43pp; English.
 XX
 CC This sequence is a melanin-concentrating hormone (MCH) receptor
 CC protein of the invention, designated MCH-R1. MCH receptor fragments and
 CC polypeptides are useful in assays to screen for compounds that bind to
 CC the MCH receptor and modulate the activity of the receptor. MCH Receptor
 CC activity is modulated to achieve weight loss, weight gain, to treat
 CC cancer (e.g. colon or breast), reduce pain, treat diabetes, reduce stress
 CC or treat sexual dysfunction. Nucleic acid coding for the MCH receptor can
 CC be used to cause an increase in appetite and to create a test system
 CC (e.g. a transgenic animal) for screening for compounds affecting MCH
 CC receptor expression. Inhibition of MCH receptor nucleic acid activity is
 CC useful to inhibit appetite or stress.
 CC
 XX
 XX Sequence 353 AA;
 SQ
 Query Match 100.0%; Score 1824; DB 22; Length 353;
 Best Local Similarity 100.0%; Pred. No. 1.6e-203;
 Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDEASLLPTGPNASNTSDGPDNLTSAGSPRTGSISYINIMPSVEGTICLLGIIGNST 60
 DB 1 MDEASLLPTGPNASNTSDGPDNLTSAGSPRTGSISYINIMPSVEGTICLLGIIGNST 60
 QY 61 VIRAIVVKKSKLHMCNNVPDIFITINLSVVDLFLGMPFMHQLMGNGVMHGEIMCTLIT 120
 DB 61 VIRAIVVKKSKLHMCNNVPDIFITINLSVVDLFLGMPFMHQLMGNGVMHGEIMCTLIT 120
 QY 121 AMDANSOFTSTYIITAMADRYLATVHPISSTKFRKPSVATLVICLLMAISFISITTPVWL 180
 DB 121 AMDANSOFTSTYIITAMADRYLATVHPISSTKFRKPSVATLVICLLMAISFISITTPVWL 180
 QY 181 YARLIPEPGAVGCGIRLPNPDIDLWFTLYQFLAFLAPFVITAAVYRILQMTSSVA 240
 DB 181 YARLIPEPGAVGCGIRLPNPDIDLWFTLYQFLAFLAPFVITAAVYRILQMTSSVA 240
 QY 241 PASORSIRLRTKRYTRAIACLVFPCWAPYVYLQTLQSLSPRTLTFVYLYNAAISLG 300
 DB 241 PASORSIRLRTKRYTRAIACLVFPCWAPYVYLQTLQSLSPRTLTFVYLYNAAISLG 300

QY 301 YANSCINPFVYIVLCETFRKRLVLSVKPPAOGOLRAVSNAGTADERTESKGT 353
 |||
 Db 301 YANSCINPFVYIVLCETFRKRLVLSVKPPAOGOLRAVSNAGTADERTESKGT 353

RESULT 8

AAB85895
 ID AAB85895 standard; Protein; 353 AA.

AC AAB85895;

DT 30-NOV-2001 (first entry)

DE Human short form MCH1R sequence.

KM Melanin concentrating hormone receptor; MCHR; MCH; chimeric; fusion;
 fluorescent polypeptide; orexigenic; anabolic; food intake; MCH1R.

OS Homo sapiens.

PN WO200168706-A1.

PD 20-SEP-2001.

PF 14-MAR-2001; 2001WO-US08071.

PR 15-MAR-2000; 2000US-0189698.

PA (MERI) MERCK & CO INC.

PI Marsh DJ;

DR WPI: 2001-565791/63.

DR N-PSDB; AAK47298.

PT Fusion proteins comprising melanin concentrating hormone receptor
 peptides and fluorescent proteins, useful for identifying appetite
 stimulants -

PS Claim 1; Page 13; 71pp; English.

XX The invention provides melanin concentrating hormone (MCH) receptor
 CC (MCHR) chimeric and fusion proteins. The MCHR chimeric proteins comprise
 CC MCHR polypeptide regions from different species. The MCHR fusion protein
 CC comprise MCHR polypeptide region and a fluorescent polypeptide region
 CC joined directly or via a linker, to the carboxy side of the MCHR
 CC polypeptide region. The MCHR fusion proteins can be expressed by standard
 CC recombinant methodology. MCH action promotes feeding (orexigenic) and up
 CC regulation of MCH activity stimulates food intake. The present sequence
 CC represents a human short form MCH1R protein sequence.

SO Sequence 353 AA;

Query Match 100.0%; Score 1824; DB 22; Length 353;
 Best Local Similarity 100.0%; Pred. No. 1.6e-203;

Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLEASLPTGPNASNTSDGPDNLTSAGSPRTGSISYINIMPSVFGTICLLGIGNST 60
 |||

Db 1 MDLEASLPTGPNASNTSDGPDNLTSAGSPRTGSISYINIMPSVFGTICLLGIGNST 60

QY 61 VIFAVVKKSKLHMCNNVPDIFIINLSYVDLLFLGMPFMIHQLMGNGVMHFGETMCLIT 120
 |||

Db 61 VIFAVVKKSKLHMCNNVPDIFIINLSYVDLLFLGMPFMIHQLMGNGVMHFGETMCLIT 120

QY 121 AMDANSQFTSTYITLTAADIRYATVHPISSTFRKPSVATLVICLIMALSFTSTPPWL 180
 |||

Db 121 AMDANSQFTSTYITLTAADIRYATVHPISSTFRKPSVATLVICLIMALSFTSTPPWL 180

QY 181 YARLIPFGGAVGCGIRLPNDPDLVWFYLLQFPLAFALPEFVYTTAAYVRILQRMSSVA 240
 |||

Db 181 YARLIPFGGAVGCGIRLPNDPDLVWFYLLQFPLAFALPEFVYTTAAYVRILQRMSSVA 240

QY 241 PASORSIRLRKRVTRPAIACLVFVCWAPYVVLDTOLSTSRPTLFFVLYNNAISIG 300
 |||
 Db 241 PASORSIRLRKRVTRPAIACLVFVCWAPYVVLDTOLSTSRPTLFFVLYNNAISIG 300

QY 301 YANSCINPFVYIVLCETFRKRLVLSVKPPAOGOLRAVSNAGTADERTESKGT 353
 |||
 Db 301 YANSCINPFVYIVLCETFRKRLVLSVKPPAOGOLRAVSNAGTADERTESKGT 353

RESULT 9

AAU76893
 ID AAU76893 standard; Protein; 353 AA.

AC AAU76893;

DT 05-JUN-2002 (first entry)

DE Human melanin-concentrating hormone (MCH) receptor.

KM Dog; melanin-concentrating hormone; MCH; receptor; weight loss; cancer;
 weight gain; colon; breast; pain; stress; sexual dysfunction; anorexia;
 bulimia; cancer cachexia; wasting; chemotherapy; radiation therapy;
 immobilisation; dialysis; cytostatic; anorectic; analgesic; endocrine;
 immunomodulatory; human.

OS Homo sapiens.

PN WO200208290-A1.

PD 31-JAN-2002.

PF 17-JUL-2001; 2001WO-US22458.

PR 21-JUL-2000; 2000US-219669P.

PA (MERI) MERCK & CO INC.

PI Tan CP;

DR WPI: 2002-257333/30.

DR N-PSDB; AAK10702.

PT New dog MCH receptor polypeptides and nucleic acids, useful for
 achieving weight loss or gain, treating cancer (e.g. colon or breast),
 reducing pain or stress, or treating sexual dysfunction -

PS Example 1; Fig 1; 36pp; English.

XX The invention relates to a dog melanin-concentrating hormone (MCH)
 CC receptor and the polynucleotide encoding the polypeptide. The sequences
 CC are useful for achieving weight loss or gain, treating cancer (e.g. of
 CC the colon or breast), reducing pain or stress, or treating sexual
 CC dysfunction. They are also useful for treating a patient having a disease
 CC or disorder, or under going a treatment accompanied by weight loss.
 CC Examples of diseases or disorders accompanied by weight loss include
 CC anorexia, bulimia, cancer cachexia, and wasting in frail elderly.
 CC Examples of treatments accompanied by weight loss include chemotherapy,
 CC radiation therapy, temporary or permanent immobilisation, and dialysis.
 CC The nucleic acid is useful as a hybridisation probe or a PCR primer used
 CC to identify the presence of dog MCH nucleic acid, to identify or clone a
 CC nucleic acid encoding a receptor related to the MCH receptor from a
 CC different source, or for the recombinant expression of a dog MCH receptor
 CC polypeptide. This sequence represents the human MCH receptor.

SO Sequence 353 AA;

Query Match 100.0%; Score 1824; DB 23; Length 353;
 Best Local Similarity 100.0%; Pred. No. 1.6e-203;

Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLEASLPTGPNASNTSDGPDNLTSAGSPRTGSISYINIMPSVFGTICLLGIGNST 60
 |||

```
Db      1 MDLEASLLPTGPNASNTSDGPDNLTSGSPPTGSIYINIMPSYFGTICLLGIIGNST 60
QY      61 VIFAIVKSKSLHMCNNVPDIFIINLSVVDLFLFGMPFMIHQLMGVWHEGFTMCLIT 120
Db      61 VIFAIVKSKSLHMCNNVPDIFIINLSVVDLFLFGMPFMIHQLMGVWHEGFTMCLIT 120
QY      121 AMDANSOFTSYIILTMAIDRYLATVHPISSTFKRPSVATLVICLLMAFSISTPVM 180
Db      121 AMDANSOFTSYIILTMAIDRYLATVHPISSTFKRPSVATLVICLLMAFSISTPVM 180
QY      181 YARLIPPGGAVGCGIRLPNDPDLWFTLYQFPLALPFWVITAAVRILOQMTSSVA 240
Db      181 YARLIPPGGAVGCGIRLPNDPDLWFTLYQFPLALPFWVITAAVRILOQMTSSVA 240
QY      241 PASORSIRLRTKRTVTRTAICLVFVCMAPIYVLOLTQISIRPTLFYLYNNAISLG 300
Db      241 PASORSIRLRTKRTVTRTAICLVFVCMAPIYVLOLTQISIRPTLFYLYNNAISLG 300
QY      301 YANSCINPFYIYVLCETFRKRLVSVKPAAGOLRAVSNMQTADEERTESKGT 353
Db      301 YANSCINPFYIYVLCETFRKRLVSVKPAAGOLRAVSNMQTADEERTESKGT 353

RESULT 10
AAU75859
ID      AAU75859 standard; Protein; 353 AA.
XX
AC      AAU75859;
XX
DT      08-MAY-2002 (first entry)
XX
DE      Human melanin concentrating hormone receptor, MCH1, B0120 mutant.
XX
KW      Human; melanin concentrating hormone receptor; MCH1;
KW      steroid hormone disorder; pituitary hormone disorder; B0120;
KW      epinephrine release disorder; gastrointestinal disorder; mutleai;
KW      cardiovascular disorder; hypertension; diabetes; respiratory disorder;
KW      asthma; reproductive function disorder; immune disorder; mutant;
KW      musculoskeletal disorder; neuroendocrine disorder; cognitive disorder;
KW      memory disorder; motor coordination disorder; obesity; eating disorder;
KW      dopaminergic function disorder; pain; psychosis; opiate addiction;
KW      affective disorder; migraine; transgenic.
XX
OS      Homo sapiens.
XX
PN      Synthetic.
XX
PD      WO200202744-A2.
XX
PF      05-JUL-2001: 2001WO-US21350.
XX
PR      05-JUL-2000: 2000US-0610635.
XX
PA      (SYNA-) SYNAPTIC PHARM CORP.
XX
PI      Salon JA, Laz TM, Nagorny R, Wilson AE;
XX
DR      WPI: 2002-164532/21.
XX
PT      Purified human melanin concentrating hormone receptor protein and
PT      polynucleotides for screening modulator useful for treating memory
PT      disorder, sensory modulation and transmission disorder, motor
PT      coordination disorder -
XX
PS      Claim 10; Fig 15; 524pp; English.
XX
CC      The invention relates to a purified human melanin concentrating hormone
CC      (MCH) receptor protein and its encoding nucleic acid (or mutant
CC      activated by MCH or its analogue or homologue). Also included are
CC      expression vectors, probes, transformed insect cells, antisense
CC      oligonucleotides, anti-MCH1 antibodies, an agent capable of inhibiting
CC      the binding of the antibody to MCH1, a transgenic animal expressing the
```

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CC      protein, or a homologous knockout or antisense complementary to the MCH1
CC      nucleic acid, ant/agonists of MCH1, and methods of isolating chemical
CC      compounds which activate MCH1. The protein, nucleic acid, antibody,
CC      ant/agonists and compound are useful for diagnosing and treating a
CC      steroid or pituitary hormone disorder, an epinephrine release disorder, a
CC      gastrointestinal disorder, cardiovascular disorder, electrolyte balance
CC      disorder, hypertension, diabetes, respiratory disorder, asthma,
CC      reproductive function disorder, immune disorder, endocrine disorder,
CC      musculoskeletal disorder, neuroendocrine disorder, cognitive disorder,
CC      memory disorder, sensory modulation and transmission disorder, motor
CC      coordination disorder, sensory integration disorder, motor integration
CC      disorder, dopaminergic function disorder, sensory transmission disorder,
CC      infaction disorder, sympathetic innervation disorder, pain, psychotic
CC      behaviour, morphine tolerance, opiate addiction, affective disorder,
CC      stress-related disorder, fluid-balance disorder, seizure disorder or
CC      migraine, an eating disorder or obesity. The present sequence
CC      represents human MCH1 mutant encoded by plasmid B0120, where
CC      residues 1-70 of the wild-type MCH1 have been deleted and residue
CC      71 replaced by a new initiator methionine.
XX
SQ      Sequence 353 AA:
XX
Query Match 100.0%; Score 1824; DB 23; Length 353;
Best Local Similarity 100.0%; Pred. No. 1.6e-203;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 MDLEASLLPTGPNASNTSDGPDNLTSGSPPTGSIYINIMPSYFGTICLLGIIGNST 60
Db      1 MDLEASLLPTGPNASNTSDGPDNLTSGSPPTGSIYINIMPSYFGTICLLGIIGNST 60
QY      61 VIFAIVKSKSLHMCNNVPDIFIINLSVVDLFLFGMPFMIHQLMGVWHEGFTMCLIT 120
Db      61 VIFAIVKSKSLHMCNNVPDIFIINLSVVDLFLFGMPFMIHQLMGVWHEGFTMCLIT 120
QY      121 AMDANSOFTSYIILTMAIDRYLATVHPISSTFKRPSVATLVICLLMAFSISTPVM 180
Db      121 AMDANSOFTSYIILTMAIDRYLATVHPISSTFKRPSVATLVICLLMAFSISTPVM 180
QY      181 YARLIPPGGAVGCGIRLPNDPDLWFTLYQFPLALPFWVITAAVRILOQMTSSVA 240
Db      181 YARLIPPGGAVGCGIRLPNDPDLWFTLYQFPLALPFWVITAAVRILOQMTSSVA 240
QY      241 PASORSIRLRTKRTVTRTAICLVFVCMAPIYVLOLTQISIRPTLFYLYNNAISLG 300
Db      241 PASORSIRLRTKRTVTRTAICLVFVCMAPIYVLOLTQISIRPTLFYLYNNAISLG 300
QY      301 YANSCINPFYIYVLCETFRKRLVSVKPAAGOLRAVSNMQTADEERTESKGT 353
Db      301 YANSCINPFYIYVLCETFRKRLVSVKPAAGOLRAVSNMQTADEERTESKGT 353

RESULT 11
AAE07329
ID      AAE07329 standard; Protein; 417 AA.
XX
AC      AAE07329;
XX
DT      06-NOV-2001 (first entry)
XX
DE      Human melanin-concentrating hormone receptor variant #2.
XX
KW      Human; melanin-concentrating hormone; MCH analogue; signal transduction;
KW      appetite; therapy; anorexia; acquired immune deficiency syndrome; AIDS;
KW      wasting; cachexia; frail elderly; weight maintenance; cancer; anorectic;
KW      pain reduction; stress reduction; sexual dysfunction; variant.
XX
OS      Homo sapiens.
XX
PN      Synthetic.
XX
PD      WO200157070-A1.
XX
PT      09-AUG-2001.
XX
```


DT 22-NOV-2000 (first entry)
XX
DE Human SLC-1 protein sequence SEQ ID NO:11.
XX
KW SLC-1: MCH; melanin concentrating hormone; screening; eating;
KW appetite stimulator; appetite regulator; period pain; atonic bleeding;
KW caesarean section; milk congestion; antioleptic agent; drug;
KW foetal asphyxia; cervical rupture; premature birth; uterine rupture;
KW Prader-Willi syndrome; anorectic; gynaecological; abortifacient;
KW antoanaemia; anabolic; orphan G protein-couple receptor protein.
XX
OS Homo sapiens.
XX
PN WO200040725-A1.
XX
PD 13-JUL-2000.
XX
PF 27-DEC-1999; 99WO-JP07336.
XX
PR 28-DEC-1998; 98JP-0374454.
PR 28-APR-1999; 99JP-0122688.
PR 02-SEP-1999; 99JP-0249300.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Mori M, Shimomura Y, Takekawa S, Sugo T, Ishibashi Y, Kltada C;
PI Suzuki N.
XX
DR WPI: 2000-475832/41.
DR N-PSDB; AAA72918.
XX
PT Screening methods for compounds as SLC-1 (ant)agonists useful in the
PT treatment of eating disorders and as preventives and remedies for e.g.
PT atonic bleeding and Prader-Willi syndrome -
XX
PS Claim 6: Page 111-113; 123pp; Japanese.
XX
XX The present invention describes a method for screening components (I) or
CC their salts that can alter the binding properties of melanin-
CC concentrating hormone (MCH) or its derivative or salt to SLC-1 or its
CC salt. Compounds identified by (I) are useful as SLC-1 (ant)agonists in
CC eating disorders and as preventives and remedies for e.g. period pains,
CC uterine recovery failure, caesarean section, artificial interruption of
CC pregnancy, galactostosis, tonic uterine contraction, foetal asphyxia,
CC rupture of uterus, cervical rupture, premature birth and Prader-Willi
CC syndrome. The present sequence represents the human SLC-1 protein
CC sequence, which is used in an example from the present invention.
XX
SQ Sequence 422 AA;
Query Match 100.0%; Score 1824; DB 21; Length 422;
Best local Similarity 100.0%; Pred. No. 2e-203;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 301 YANSCINPFVYIVLCETFRKRLVLSVKPAQCOLRAVSNAGTADERTESKGT 353
DB 370 YANSCINPFVYIVLCETFRKRLVLSVKPAQCOLRAVSNAGTADERTESKGT 422
RESULT 14
AAB13436
ID AAB13436 standard; Protein; 422 AA.
XX
XX AAB13436;
AC
XX
DT 17-NOV-2000 (first entry)
DE
XX
DE Human MCH1 receptor.
XX
XX Human; MCH1 receptor; melanin concentrating hormone; neuroregulator;
KW G-protein coupled; PEXr-HR-T1231; feeding; water balance; Neuroregulator;
KW energy metabolism; arousal; attention; memory; cognitive function;
KW psychiatric disorder; stress; sexual activity; hormone disorder;
KW hypertension; diabetes; cardiovascular; gastrointestinal;
KW electrolyte balance; respiratory; asthma; reproductive function;
KW immune; endocrine; musculoskeletal; Alzheimer's disease;
KW sensory modulation; transmission; motor coordination;
KW Parkinson's disease; olfaction; urinary; depression; seizure; pain;
KW schizophrenia; morphine tolerance; opiate addiction; migraine.
XX
XX Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FH Region 110..135
FT /label=Transmembrane_region_1
FT 149..169
FT /label=Transmembrane_region_2
FT 193..208
FT /label=Transmembrane_region_3
FT 228..262
FT /label=Transmembrane_region_4
FT 274..301
FT /label=Transmembrane_region_5
FT 323..349
FT /label=Transmembrane_region_6
FT 358..383
FT /label=Transmembrane_region_7
XX
XX WO200039279-A2.
XX
XX 06-JUL-2000.
XX
XX 30-DEC-1999; 99WO-US31169.
XX
XX 31-DEC-1998; 98US-0224426.
XX
XX (SYNA-) SYNAPTIC PHARM CORP.
XX
XX Salon JA, Laz TM, Nagorny R, Wilson AE;
XX
XX WPI: 2000-548644/50.
XX
XX N-PSDB; AAA63240.
XX
XX Novel nucleic acid encoding human melanin concentrating hormone
PT receptor useful for treating cardiovascular disorders, hypertension and
PT diabetes, whose mutant form is activated by melanin concentrating
PT hormone -
XX
PS Claim 7; Fig 2; 173pp; English.
XX
XX Neuroregulators modulate communication in the nervous system. Melanin
CC concentrating hormone 1 (MCH1) is one such neuroregulator. MCH may serve
CC as an integrative neuropeptide, involved in stress response, feeding
CC regulation and sexual activity. Also, MCH is thought to participate in
CC water balance regulation, energy metabolism, general arousal/attention
CC state, memory and cognitive functions and psychiatric disorders. The

CC present sequence is the human MCH receptor. The present sequence is a
 CC G-protein coupled receptor and has 7 transmembrane regions. MCH receptor
 CC may be used in the therapy for a variety of disorders: steroid or
 CC pituitary hormone disorder, epinephrine release disorder,
 CC gastrointestinal disorder, cardiovascular disorder, electrolyte balance
 CC disorder, hypertension, diabetes, respiratory disorder, asthma,
 CC reproductive function disorder, immune disorder, endocrine disorder,
 CC musculoskeletal disorder, neuroendocrine disorder, cognitive disorder,
 CC memory disorder e.g. Alzheimer's disease, sensory modulation and
 CC transmission disorder, motor coordination disorder, sensory integration
 CC disorder, dopaminergic function disorder e.g. Parkinson's disease,
 CC olfaction disorder, sympathetic innervation disorder, depression, stress,
 CC fluid imbalance disorder, urinary disorder e.g. urinary incontinence,
 CC seizure, pain, psychotic behaviour e.g. schizophrenia, morphine
 CC tolerance, opiate addiction or migraine. The coding sequence for the
 CC present protein is also contained in plasmid pEX4-HR-TL231 (ATCC 203197).
 XX
 SQ Sequence 422 AA;
 Query Match 100.0%; Score 1824; DB 21; Length 422;
 Best Local Similarity 100.0%; Pred. No. 2e-203;
 Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDLEASILPTGPNASNTSDGPNLTSAGSPPTGSIYINIMPSVFGTICLLGIGNST 60
 DB 70 MDLEASILPTGPNASNTSDGPNLTSAGSPPTGSIYINIMPSVFGTICLLGIGNST 129
 QY 61 VIFAVYKSKLHMCNNVPDIFIINLSVVDLFLLGMPFMIHOLMGNGVHGEETCTLTIT 120
 DB 130 VIFAVYKSKLHMCNNVPDIFIINLSVVDLFLLGMPFMIHOLMGNGVHGEETCTLTIT 189
 QY 121 AMDANSQFTSTYITLTAADRYLATVHPISSTKFKPSVATLVICLMAISFISITPVWL 180
 DB 190 AMDANSQFTSTYITLTAADRYLATVHPISSTKFKPSVATLVICLMAISFISITPVWL 249
 QY 181 YARLIPEPGAVGCGIRLPNDTDLWFTLYOFLAFALPFAVITAAVRIIQRMSSVA 240
 DB 250 YARLIPEPGAVGCGIRLPNDTDLWFTLYOFLAFALPFAVITAAVRIIQRMSSVA 309
 QY 241 PASORSIRLRTKRVTRTAIAICLVFFVCWAPYYVQLTQLSISRPTLTFVLYNAAISLG 300
 DB 310 PASORSIRLRTKRVTRTAIAICLVFFVCWAPYYVQLTQLSISRPTLTFVLYNAAISLG 369
 QY 301 YANSCINPFYIYLCEFTFRKRLVSVKPAAGQLRAVSNAGTADERTESKGT 353
 DB 370 YANSCINPFYIYLCEFTFRKRLVSVKPAAGQLRAVSNAGTADERTESKGT 422
 RESULT 15
 AAEO7330
 ID AAEO7330 standard; Protein: 422 AA.
 XX
 AC AAEO7330;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human melanin-concentrating hormone receptor variant #3.
 XX
 KW Human; melanin-concentrating hormone; MCH analogue; signal transduction;
 KW appetite; therapy; anorexia; acquired immune deficiency syndrome; AIDS;
 KW wasting; cachexia; frail elderly; weight maintenance; cancer; anorectic;
 KW pain reduction; stress reduction; sexual dysfunction; variant.
 XX
 OS Homo sapiens.
 OS Synthetic.
 OS
 PN WO200157070-A1.
 XX
 PD 09-AUG-2001.
 XX
 PF 01-FEB-2001; 2001WO-US03293.
 XX
 PR 03-FEB-2000; 2000US-0179967.

XX
 PA (MERI) MERCK & CO INC.
 XX
 PI Bednarek M;
 XX
 DR WPI: 2001-483416/52.
 DR N-PSDB: AAD13654.
 PT Novel peptide encoding a melanin-concentrating hormone analog useful
 PT for increasing weight or appetite -
 XX
 PS Disclosure: Page 35-36; 66pp; English.
 XX
 CC The present invention relates to truncated melanin-concentrating hormone
 CC (MCH) analogues active at the MCH receptor. The truncated MCH analogues
 CC are optionally modified peptide derivatives of mammalian MCH. The MCH
 CC analogues can bind to the MCH receptor and bring about signal
 CC transduction. The MCH agonists can be used to facilitate a weight gain,
 CC maintenance of weight and/or an appetite increase. The MCH agonists can
 CC also be used to treat disorders such as anorexia, acquired immune
 CC deficiency syndrome (AIDS), wasting, cachexia and frail elderly. The MCH
 CC antagonists can be used to facilitate weight loss, appetite decrease,
 CC weight maintenance, cancer treatment, pain reduction, stress reduction
 CC and/or treatment of sexual dysfunction. The present sequence is a human
 CC MCH receptor variant.
 XX
 SQ Sequence 422 AA;
 Query Match 100.0%; Score 1824; DB 22; Length 422;
 Best Local Similarity 100.0%; Pred. No. 2e-203;
 Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 70 MDLEASILPTGPNASNTSDGPNLTSAGSPPTGSIYINIMPSVFGTICLLGIGNST 129
 QY 61 VIFAVYKSKLHMCNNVPDIFIINLSVVDLFLLGMPFMIHOLMGNGVHGEETCTLTIT 120
 DB 130 VIFAVYKSKLHMCNNVPDIFIINLSVVDLFLLGMPFMIHOLMGNGVHGEETCTLTIT 189
 QY 121 AMDANSQFTSTYITLTAADRYLATVHPISSTKFKPSVATLVICLMAISFISITPVWL 180
 DB 190 AMDANSQFTSTYITLTAADRYLATVHPISSTKFKPSVATLVICLMAISFISITPVWL 249
 QY 181 YARLIPEPGAVGCGIRLPNDTDLWFTLYOFLAFALPFAVITAAVRIIQRMSSVA 240
 DB 250 YARLIPEPGAVGCGIRLPNDTDLWFTLYOFLAFALPFAVITAAVRIIQRMSSVA 309
 QY 241 PASORSIRLRTKRVTRTAIAICLVFFVCWAPYYVQLTQLSISRPTLTFVLYNAAISLG 300
 DB 310 PASORSIRLRTKRVTRTAIAICLVFFVCWAPYYVQLTQLSISRPTLTFVLYNAAISLG 369
 QY 301 YANSCINPFYIYLCEFTFRKRLVSVKPAAGQLRAVSNAGTADERTESKGT 353
 DB 370 YANSCINPFYIYLCEFTFRKRLVSVKPAAGQLRAVSNAGTADERTESKGT 422

Search completed: February 13, 2003, 13:58:02
 Job time : 29.0159 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 13, 2003, 13:56:21 ; Search time 10.3216 Seconds
(without alignments)
1006.264 Million cell updates/sec

Title: US-09-885-478-28

Perfect score: 1824
Sequence: 1 MDLEASILPTGPNASNTSDG.....LRASNAQTADEERTESKGT 353

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%
Listing first 45 summaries

Database :

Issued Patents_AA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	1824	100.0	353	3	US-08-984-288-2
2	1824	100.0	353	4	US-09-218-467B-2
3	1824	100.0	422	4	US-09-224-426-2
4	1824	100.0	422	4	US-09-478-601-2
5	1824	100.0	422	4	US-09-478-602-2
6	1763	96.7	353	4	US-09-224-426-4
7	1763	96.7	353	4	US-09-478-601-4
8	1763	96.7	353	4	US-09-478-602-4
9	1687	92.5	400	3	US-08-602-809-2
10	1676	91.9	400	5	PCr-US95-16472-2
11	532.5	29.1	369	4	US-08-120-601B-9
12	530.5	29.1	369	1	US-07-816-283-6
13	530.5	29.1	369	1	US-08-417-103-6
14	530.5	29.1	369	1	US-08-417-103-16
15	529.5	29.0	369	1	US-07-816-283-8
16	529.5	29.0	369	1	US-08-417-103-8
17	524.5	28.8	369	2	US-08-411-859-3
18	524.5	28.8	369	4	US-08-387-707-9
19	524.5	28.8	369	4	US-08-405-271A-9
20	504.5	27.7	418	1	US-07-816-283-10
21	504.5	27.7	418	1	US-08-417-103-10
22	502	27.5	391	4	US-08-120-601B-8
23	496.5	27.2	391	1	US-07-816-283-2
24	496.5	27.2	391	1	US-07-816-283-4
25	496.5	27.2	391	1	US-08-417-103-2
26	496.5	27.2	391	1	US-08-417-103-4
27	496.5	27.2	391	1	US-08-417-103-14

28	494.5	27.1	384	3	US-09-071-434-3	Sequence 3, Appl1
29	494	27.1	389	4	US-08-430-286A-7	Sequence 7, Appl1
30	472	25.9	428	1	US-07-816-283-12	Sequence 12, Appl1
31	472	25.9	428	1	US-08-417-103-12	Sequence 12, Appl1
32	456	25.0	370	4	US-08-405-271A-21	Sequence 21, Appl1
33	449	24.6	400	4	US-08-188-275A-2	Sequence 2, Appl1
34	449	24.6	400	4	US-09-351-198-2	Sequence 2, Appl1
35	449	24.6	400	4	US-09-113-426-2	Sequence 20, Appl1
36	449	24.6	415	4	US-08-405-271A-20	Sequence 7, Appl1
37	447.5	24.5	372	4	US-08-120-601B-7	Sequence 4, Appl1
38	446.5	24.5	367	2	US-08-454-549-4	Sequence 4, Appl1
39	446.5	24.5	367	3	US-08-454-552-4	Sequence 3, Appl1
40	446.5	24.5	367	3	US-08-676-351-3	Sequence 4, Appl1
41	446.5	24.5	372	4	US-08-188-275A-4	Sequence 4, Appl1
42	446.5	24.5	372	4	US-09-351-198-4	Sequence 4, Appl1
43	446.5	24.5	372	4	US-09-113-426-4	Sequence 4, Appl1
44	446	24.5	372	4	US-08-430-286A-6	Sequence 6, Appl1
45	444	24.3	400	3	US-08-889-108-8	Sequence 8, Appl1

ALIGNMENTS

RESULT 1
US-08-984-288-2
; Sequence 2, Application US/08984288

; Patent No. 6033872

; GENERAL INFORMATION:

; APPLICANT: BERGMA, DERK

; TITLE OF INVENTION: NOVEL HUMAN 11CB SPLICE V

; TITLE OF INVENTION: ARIANT

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: RATNER & PRESTIA

; STREET: P.O. BOX 980

; CITY: VALLEY FORGE

; STATE: PA

; COUNTRY: USA

; ZIP: 19482

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FASTSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/984, 288

; FILING DATE: 03-DEC-1997

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/032,763

; FILING DATE: 11-DEC-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: PRESTIA, PAUL F

; REGISTRATION NUMBER: 23,031

; REFERENCE/DOCKET NUMBER: P50599

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 610-407-0700

; TELEFAX: 610-407-0701

; TELEX: 846169

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 353 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-984-288-2

Query Match 100.0%; Score 1824; DB 3; Length 353;
Best Local Similarity 100.0%; Pred. No. 3.2e-159;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MDLEASLLPTGPNASNTSDGPDNLTSAGSPRTGSIYINIMPVFGTICLLGIIGNST 60
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|
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Db 61 VIFAAYKKSKLHMCNNVPDIFIIINLSVVDLFLGMPFMIHOLMGVWHFGETMCTLLT 120
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Db 121 AMDANSQFTSTYILTMADIRLATVHPISSTKFRKPSVATLVICLLMALSFSITPVM 180
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|
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Db 181 YARLIPFGGAVGCGIRLPNDPDLXWFTLYOFLAFALPFVYITAAVYRIIQRMTSSVA 240
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|
Db 241 PASORSIRLRTRKRVRTAICLVFVCWAPYVVDLTQLSISRPLTFVYLYNNAISIG 300
QY 301 YANSCINPFIYIVLCETFRKRLVLSVKAPOGOLRAVSNAGTADERTESKGT 353
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|
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Db 301 YANSCINPFIYIVLCETFRKRLVLSVKAPOGOLRAVSNAGTADERTESKGT 353

RESULT 2
US-09-218-467B-2
; Sequence 2, Application US/09218467B
; Patent No. 6362326
; GENERAL INFORMATION:
; APPLICANT: SATHE, GANESH
; APPLICANT: ELLIS, CATHERINE
; APPLICANT: HALSEY, WENDY
; APPLICANT: BERGMA, DEBK
; TITLE OF INVENTION: 11cdy Genomic Sequence
; FILE REFERENCE: GP-50010
; CURRENT APPLICATION NUMBER: US/09/218,467B
; CURRENT FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 353
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-218-467B-2

Query Match 100.0%; Score 1824; DB 4; Length 353;
Best Local Similarity 100.0%; Pred. No. 3.2e-159;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 VIFAAYKKSKLHMCNNVPDIFIIINLSVVDLFLGMPFMIHOLMGVWHFGETMCTLLT 120
QY 121 AMDANSQFTSTYILTMADIRLATVHPISSTKFRKPSVATLVICLLMALSFSITPVM 180
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|
Db 121 AMDANSQFTSTYILTMADIRLATVHPISSTKFRKPSVATLVICLLMALSFSITPVM 180
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Db 181 YARLIPFGGAVGCGIRLPNDPDLXWFTLYOFLAFALPFVYITAAVYRIIQRMTSSVA 240
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|
|
|
Db 241 PASORSIRLRTRKRVRTAICLVFVCWAPYVVDLTQLSISRPLTFVYLYNNAISIG 300
QY 301 YANSCINPFIYIVLCETFRKRLVLSVKAPOGOLRAVSNAGTADERTESKGT 353
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Db 301 YANSCINPFIYIVLCETFRKRLVLSVKAPOGOLRAVSNAGTADERTESKGT 353
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RESULT 3
US-09-224-426-2
; Sequence 2, Application US/09224426
; Patent No. 6221613
; GENERAL INFORMATION:
; APPLICANT: Salton, John A
; APPLICANT: Laz, Thomas M.
; APPLICANT: Nagorny, Raisa
; APPLICANT: Wilson, Amy E.
; TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
; FILE REFERENCE: 57453/JPM/JHB
; CURRENT APPLICATION NUMBER: US/09/224,426
; CURRENT FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 2
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-224-426-2

Query Match 100.0%; Score 1824; DB 4; Length 422;
Best Local Similarity 100.0%; Pred. No. 3.9e-159;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|
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Db 130 VIFAAYKKSKLHMCNNVPDIFIIINLSVVDLFLGMPFMIHOLMGVWHFGETMCTLLT 189
QY 121 AMDANSQFTSTYILTMADIRLATVHPISSTKFRKPSVATLVICLLMALSFSITPVM 180
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Db 190 AMDANSQFTSTYILTMADIRLATVHPISSTKFRKPSVATLVICLLMALSFSITPVM 249
QY 181 YARLIPFGGAVGCGIRLPNDPDLXWFTLYOFLAFALPFVYITAAVYRIIQRMTSSVA 240
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Db 250 YARLIPFGGAVGCGIRLPNDPDLXWFTLYOFLAFALPFVYITAAVYRIIQRMTSSVA 309
QY 241 PASORSIRLRTRKRVRTAICLVFVCWAPYVVDLTQLSISRPLTFVYLYNNAISIG 300
|
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|
Db 310 PASORSIRLRTRKRVRTAICLVFVCWAPYVVDLTQLSISRPLTFVYLYNNAISIG 369
QY 301 YANSCINPFIYIVLCETFRKRLVLSVKAPOGOLRAVSNAGTADERTESKGT 353
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|
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Db 370 YANSCINPFIYIVLCETFRKRLVLSVKAPOGOLRAVSNAGTADERTESKGT 422

RESULT 4
US-09-478-601-2
; Sequence 2, Application US/09478601
; Patent No. 6221616
; GENERAL INFORMATION:
; APPLICANT: Salton, John A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Nagorny, Raisa
; APPLICANT: Wilson, Amy E.
; TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
; FILE REFERENCE: 57453z/JPM
; CURRENT APPLICATION NUMBER: US/09/478,601
; CURRENT FILING DATE: 2000-01-06
; EARLIER APPLICATION NUMBER: 09/224,426
; EARLIER FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 422
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TYPE: PRT
ORGANISM: Homo sapiens
US-09-478-601-2

Query Match 100.0%; Score 1824; DB 4; Length 422;
Best Local Similarity 100.0%; Pred. No. 3.9e-159;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 130 VIFAVVKKSKLHMCNNVPDIFIINLSYVDLFLGMPFMHQLMGNGVHGEFMTCLIT 189
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QY 181 YARLIPPGAVGCGIRLPNDTDLWFTLYQFLAFALPFPVITAAVRILOQMTSSVA 240
DB 250 YARLIPPGAVGCGIRLPNDTDLWFTLYQFLAFALPFPVITAAVRILOQMTSSVA 309
QY 241 PASORSIRLTRKRVTRTAIAICLVFVCWAPYVYLQTLQISRPITLFFVLYNAISLG 300
DB 310 PASORSIRLTRKRVTRTAIAICLVFVCWAPYVYLQTLQISRPITLFFVLYNAISLG 369
QY 301 YANSCINPFIYIVLCETFRKRLVSVKPAAGOLRAVSNQTADEERTESKGT 353
DB 370 YANSCINPFIYIVLCETFRKRLVSVKPAAGOLRAVSNQTADEERTESKGT 422
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RESULT 5

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US-09-478-602-2
; Sequence 2, Application US/09478602
; Patent No. 6291195
; GENERAL INFORMATION:
; APPLICANT: Salton, John A.
; APPLICANT: Negorny, Raisa
; APPLICANT: Wilson, Amy E.
; TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
; FILE REFERENCE: 57453/JPW
; CURRENT APPLICATION NUMBER: US/09/478,602
; EARLIER FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-478-602-2
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Query Match 100.0%; Score 1824; DB 4; Length 422;
Best Local Similarity 100.0%; Pred. No. 3.9e-159;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 70 MDLEASLLPTGPNASNTSDGPDNLTSAGSPPRGTSIYINIMPSVGTICLLIGNST 129
QY 61 VIFAVVKKSKLHMCNNVPDIFIINLSYVDLFLGMPFMHQLMGNGVHGEFMTCLIT 120
DB 130 VIFAVVKKSKLHMCNNVPDIFIINLSYVDLFLGMPFMHQLMGNGVHGEFMTCLIT 189
QY 121 AMDANSOFTSTYILTAADRYLATVHPISSTFKRPSVATLVICLMAISFISTPVL 180
DB 190 AMDANSOFTSTYILTAADRYLATVHPISSTFKRPSVATLVICLMAISFISTPVL 249
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QY 181 YARLIPPGAVGCGIRLPNDTDLWFTLYQFLAFALPFPVITAAVRILOQMTSSVA 240
DB 250 YARLIPPGAVGCGIRLPNDTDLWFTLYQFLAFALPFPVITAAVRILOQMTSSVA 309
QY 241 PASORSIRLTRKRVTRTAIAICLVFVCWAPYVYLQTLQISRPITLFFVLYNAISLG 300
DB 310 PASORSIRLTRKRVTRTAIAICLVFVCWAPYVYLQTLQISRPITLFFVLYNAISLG 369
QY 301 YANSCINPFIYIVLCETFRKRLVSVKPAAGOLRAVSNQTADEERTESKGT 353
DB 370 YANSCINPFIYIVLCETFRKRLVSVKPAAGOLRAVSNQTADEERTESKGT 422
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RESULT 6

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US-09-224-426-4
; Sequence 4, Application US/09224426
; Patent No. 6221613
; GENERAL INFORMATION:
; APPLICANT: Salton, John A.
; APPLICANT: Negorny, Raisa
; APPLICANT: Wilson, Amy E.
; TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
; FILE REFERENCE: 57453/JPW/JHB
; CURRENT APPLICATION NUMBER: US/09/224,426
; EARLIER FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin Ver. 2.0 - beta
; SEQ ID NO 4
; LENGTH: 353
; TYPE: PRT
; ORGANISM: rat
US-09-224-426-4
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Query Match 96.7%; Score 1763; DB 4; Length 353;
Best Local Similarity 96.0%; Pred. No. 1.2e-153;
Matches 339; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

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DB 1 MDLQTSLSLTGPNASNTSDGPDNLTSAGSPPRGTSIYINIMPSVGTICLLIGNST 60
QY 61 VIFAVVKKSKLHMCNNVPDIFIINLSYVDLFLGMPFMHQLMGNGVHGEFMTCLIT 120
DB 121 VIFAVVKKSKLHMCNNVPDIFIINLSYVDLFLGMPFMHQLMGNGVHGEFMTCLIT 180
QY 121 AMDANSOFTSTYILTAADRYLATVHPISSTFKRPSVATLVICLMAISFISTPVL 180
DB 121 AMDANSOFTSTYILTAADRYLATVHPISSTFKRPSVATLVICLMAISFISTPVL 180
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DB 181 YARLIPPGAVGCGIRLPNDTDLWFTLYQFLAFALPFPVITAAVRILOQMTSSVA 240
QY 241 PASORSIRLTRKRVTRTAIAICLVFVCWAPYVYLQTLQISRPITLFFVLYNAISLG 300
DB 241 PASORSIRLTRKRVTRTAIAICLVFVCWAPYVYLQTLQISRPITLFFVLYNAISLG 300
QY 301 YANSCINPFIYIVLCETFRKRLVSVKPAAGOLRAVSNQTADEERTESKGT 353
DB 301 YANSCINPFIYIVLCETFRKRLVSVKPAAGOLRAVSNQTADEERTESKGT 353
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RESULT 7

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US-09-478-601-4
; Sequence 4, Application US/09478601
; Patent No. 6221616
; GENERAL INFORMATION:
; APPLICANT: Salton, John A.
; APPLICANT: Negorny, Raisa
; APPLICANT: Wilson, Amy E.
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;; TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
;; TITLE OF INVENTION: Receptor (MCH1) And Uses Thereof
;; FILE REFERENCE: 57453\JPM
;; CURRENT APPLICATION NUMBER: US/09/478, 601
;; EARLIER APPLICATION NUMBER: 09/224, 426
;; EARLIER FILING DATE: 1998-12-31
;; NUMBER OF SEQ ID NOS: 15
;; SOFTWARE: Patentln Ver. 2.1
;; SEQ ID NO 4
;; LENGTH: 353
;; TYPE: PRT
;; ORGANISM: Rattus norvegicus
US-09-478-601-4

Query Match 96.7%; Score 1763; DB 4; Length 353;
Best Local Similarity 96.0%; Pred. No. 1.2e-153;
Matches 339; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 MDLEASLPTGPNASNTSDGPDNLTSGSPRTGSIYINIMPSVFGTICLLIGNST 60
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DB 61 VIFAVYKSKLHMCNNVPDIFIINLSVVDLFLGMPFMIHQLMGNGVHGFETMCTLIT 120
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DB 121 AMDANSOFTSTYILTMADIDRYLATVHPISSTFRKPSVATVLCILMAISFISTPWL 180
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DB 181 YARLIPFGGAVGCGIRLPNDPDLWFTLYQFELAFALPFVITAAVRIIQRMSSVA 240
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DB 241 PASQSRIRLTKRYTRTAIAICLVFVCWAPYVYLQLTQLSISRPTLFFVLYNAISLG 300
QY 301 YANSCINPFYIYLCETFRKRLVLSVKPAAGQLRAVSNQTADEERTESKGT 353
DB 301 YANSCINPFYIYLCETFRKRLVLSVKPAAGQLRAVSNQTADEERTESKGT 353

RESULT 8
US-09-478-602-4
;; Sequence 4, Application US/09478602
;; Patent No. 6291195
;; GENERAL INFORMATION:
;; APPLICANT: Salton, John A.
;; APPLICANT: Laz, Thomas M.
;; APPLICANT: Nagorny, Raisa
;; APPLICANT: Wilson, Amy E.
;; TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
;; TITLE OF INVENTION: Receptor (MCH1) And Uses Thereof
;; FILE REFERENCE: 57453\JPM
;; CURRENT APPLICATION NUMBER: US/09/478, 602
;; CURRENT FILING DATE: 2000-01-06
;; EARLIER APPLICATION NUMBER: 09/224, 426
;; EARLIER FILING DATE: 1998-12-31
;; NUMBER OF SEQ ID NOS: 15
;; SOFTWARE: Patentln Ver. 2.1
;; SEQ ID NO 4
;; LENGTH: 353
;; TYPE: PRT
;; ORGANISM: Rattus norvegicus
US-09-478-602-4

Query Match 96.7%; Score 1763; DB 4; Length 353;
Best Local Similarity 96.0%; Pred. No. 1.2e-153;
Matches 339; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
QY 1 MDLEASLPTGPNASNTSDGPDNLTSGSPRTGSIYINIMPSVFGTICLLIGNST 60

DB 1 MDLQTSLSLTPGNASNISDGDNLTLPGSPRTGSIYINIMPSVFGTICLLIGNST 60
QY 61 VIFAVYKSKLHMCNNVPDIFIINLSVVDLFLGMPFMIHQLMGNGVHGFETMCTLIT 120
DB 61 VIFAVYKSKLHMCNNVPDIFIINLSVVDLFLGMPFMIHQLMGNGVHGFETMCTLIT 120
QY 121 AMDANSOFTSTYILTMADIDRYLATVHPISSTFRKPSVATVLCILMAISFISTPWL 180
DB 121 AMDANSOFTSTYILTMADIDRYLATVHPISSTFRKPSVATVLCILMAISFISTPWL 180
QY 181 YARLIPFGGAVGCGIRLPNDPDLWFTLYQFELAFALPFVITAAVRIIQRMSSVA 240
DB 181 YARLIPFGGAVGCGIRLPNDPDLWFTLYQFELAFALPFVITAAVRIIQRMSSVA 240
QY 241 PASQSRIRLTKRYTRTAIAICLVFVCWAPYVYLQLTQLSISRPTLFFVLYNAISLG 300
DB 241 PASQSRIRLTKRYTRTAIAICLVFVCWAPYVYLQLTQLSISRPTLFFVLYNAISLG 300
QY 301 YANSCINPFYIYLCETFRKRLVLSVKPAAGQLRAVSNQTADEERTESKGT 353
DB 301 YANSCINPFYIYLCETFRKRLVLSVKPAAGQLRAVSNQTADEERTESKGT 353

RESULT 9
US-08-602-809-2
;; Sequence 2, Application US/08602809
;; Patent No. 6008012
;; GENERAL INFORMATION:
;; APPLICANT: BERGMA, DEBK
;; APPLICANT: ELLIS, CATHERINE
;; TITLE OF INVENTION: HUMAN SONATOSTATIN-LIKE R
;; TITLE OF INVENTION: RECEPTOR
;; NUMBER OF SEQUENCES: 3
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Ratner & Prestia
;; STREET: P.O. Box 980
;; CITY: Valley Forge
;; STATE: PA
;; COUNTRY: US
;; ZIP: 19482-0980
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FASTSEQ for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/602, 809
;; FILING DATE: 13-JUN-1997
;; CLASSIFICATION: 536
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US95/16472
;; FILING DATE: 15-DEC-1995
;; APPLICATION NUMBER: US 08/357, 675
;; FILING DATE: 16-DEC-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Prestia, Paul F.
;; REGISTRATION NUMBER: 23, 031
;; REFERENCE/DOCKET NUMBER: P50277
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 601-407-0700
;; TELEFAX: 610-407-0701
;; TELEX: 846169
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 402 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-602-809-2

Query Match 92.5%; Score 1687; DB 3; Length 402;

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Page 5

Best Local Similarity 99.1%; Pred. No. 1.2e-146;
Matches 327; Conservative 0; Mismatches 3; Indels 0; Gaps 0.

Qy	24	LTSGSPRGSGTSTYINIMPSVEGTCJLGIIGNSVIPEAVYKRSKLMCNVNDPIT	83
Db	73	LIRGSPRGSGTSTYINIMPSVEGTCJLGIIGNSVIPEAVYKRSKLMCNVNDPIT	133
Qy	84	NLSVVDLLFLGPMHIQMGNGVHMGEMTCLITAMDANSQFTSYIILTMAIDRYL	144
Db	133	NLSVVDLLFLGPMHIQMGNGVHMGEMTCLITAMDANSQFTSYIILTMAIDRYL	193
Qy	144	ATVHPISRRKRPKSPATVLCILMALSFISITPEVMYLARLPEPGAGAGCIRLPNDT	204
Db	193	ATVHPISRRKRPKSPATVLCILMALSFISITPEVMYLARLPEPGAGAGCIRLPNDT	253
Qy	204	DLTWFLYLQFFLAFALPEVVTITAAVRILOMRMTSSVAPASQNSIRLRTKRVTRIALICL	264
Db	253	DLTWFLYLQFFLAFALPEVVTITAAVRILOMRMTSSVAPASQNSIRLRTKRVTRIALICL	313
Qy	264	VFEVPCAPVYVIOIQLSISRPITLFFVINYAAISLCYANSCINPEVYIVLCETPRKRLV	324
Db	313	VFEVPCAPVYVIOIQLSISRPITLFFVINYAAISLCYANSCINPEVYIVLCETPRKRLV	373
Qy	324	LSYKPAAGQGLRAVNSAQTADEERESGCT	353
Db	373	LSYKPAAGQGLRAVNSAQTADEERESGCT	402

RESULT 10
PCT-US95-16472-2

1 Sequence 2, Application PC/US9516472
2 GENERAL INFORMATION:
3 APPLICANT: Bergsma, Dark J
4 APPLICANT: Ellis, Catherine E
5 TITLE OF INVENTION: Human Somatostatin Receptor
6 NUMBER OF SEQUENCES: 3
7 CORRESPONDENCE ADDRESS:
8 ADDRESSEE: Smithline Beecham Corporation/Corporate
9 ADDRESSEE: Intellectual Proper
10 STREET: P. O. Box 1539-UM2220
11 CITY: King of Prussia
12 STATE: Pennsylvania
13 COUNTRY: USA
14 ZIP: 19406-0939
15
16 COMPUTER READABLE FORM:
17 MEDIUM TYPE: Floppy disk
18 COMPUTER: IBM PC compatible
19 OPERATING SYSTEM: PC-DOS/MS-DOS
20 SOFTWARE: PatentIn Release #1.0, Version #1.25
21
22 CURRENT APPLICATION DATA:
23 APPLICATION NUMBER: PCT/US95/16472

Query Match	91.98;	Score 1676;	DB 5;	Length 400;
Best Local Similarity	99.18;	Pred. No. 1.3e-145;		
Matches 325; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

QY	24	LTSMGSPRSTISIVINIMSVGTCILGIGENSIVIVAVYKSLHMCNNVPDIEI	83
Db	73	LICRSPRSTISIVINIMSVGTCILGIGENSIVIVAVYKSLHMCNNVPDIEI	132
QY	84	NLSVVDLLELLGMPFMHQLMGNGVMHGETMCTLTAMDANSOTSTYTLTMAIDRYL	143
Db	133	NLSVVDLLELLGMPFMHQLMGNGVMHGETMCTLTAMDANSOTSTYTLTMAIDRYL	192
QY	144	ATVHPISSTKRKRSVATLVLCILMAHSFISITPVVYLARLIPPGGAVGCGIRLPMDF	203
Db	193	ATVHPISSTKRKRSVATLVLCILMAHSFISITPVVYLARLIPPGGAVGCGIRLPMDF	252
QY	204	DLVWTLTQFLFALRPVVITATVYRILQMSTSVAPASORSRLTKVTRATATCL	263
Db	253	DLVWTLTQFLFALRPVVITATVYRILQMSTSVAPASORSRLTKVTRATATCL	312
QY	264	VEFVCMARYVYVLOLTOLISIRPTLTFFYLYLNAASISLGVANSCUNPFIYIVLCETFRKRLV	323
Db	313	VEFVCMARYVYVLOLTOLISIRPTLTFFYLYLNAASISLGVANSCUNPFIYIVLCETFRKRLV	372
QY	324	LSVKPAAQGLRAVNSQTADEERTESK	351
Db	373	LSVKPAAQGLRAVNSQTADEERTESK	400

RESULT 11
US-08-120-601B-9

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: Sequence 9, Application US/08120601B
: Patent No. 6235496
: GENERAL INFORMATION:
: APPLICANT: Yu, lei
: TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND
: TITLE OF INVENTION: METHODS
: NUMBER OF SEQUENCES: 9
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Arnold, White & Durkee
: STREET: P. O. Box 4433
: CITY: Houston
: STATE: Texas
: COUNTRY: USA
: ZIP: 77210
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/120,601B
: FILING DATE: 13-SEP-1993
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Wilson, Mark B.
: REGISTRATION NUMBER: 37,259
: REFERENCE/DOCKET NUMBER: INDA:002
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 512/418-3000
: TELEFAX: 512/474-7577
: INFORMATION FOR SEQ ID NO: 9:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 369 amino acids
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: linear
US-08-120-601B-9

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Query Match          29.2%; Score 53.5; DB: 4; length 369;
Best Local Similarity 31.8%; Pcore NO. 4.4e-41;
Matches 114; Conservative 75; Mismatches 128; Indels 41; Gaps 8

QY      2 DLEASLPTGMSNMSDGEFNLTSAAGSPRGGISLTINIIMPSVFETGLGIGNSTY 61
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Db      20 DLSNLSLPS--NNSNNTPEPYDMS-----NAVLRTFYFVCGVSGITLV 64

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Page 6

Qy	62	IFWVWFKSLHMCNNVPDIFETINSVDLFLFLGMF-----MIHOLMGNVHFGSTM	115
Db	65	IYVILRYAKK---KTFNIIYIINIAIDELPMLGLPELMAQVALVH-----WPGKAI	114
Qy	116	CTLTITMADNSQSFSTYIILTMALIDRLTALVHPHSSTKRRKSVATVLCILMLSPFSI	175
Db	115	CRVYVMTVDGIGNQFTSIFCLTWSIDRLTALVHHPIKSKMRRTKIMNIVAWGVSILVI	174
Qy	176	TPWLTARILPPPGAGVCGIRLNPDPDLY--MPTLYQELFALPFIYVITRAAVRIQOR	234
Db	175	LPIMTIAGLRSMQWBSRSCITIMWBGESANTGTGIYAPILGEVLPHTLCGLCHIRIIRK	234
Qy	235	MESVAPAAQORSLRTKRYRTAIRTAICLFYPCVAPYVYLOLTOLUS--RPTLFYVLY	293
Db	235	VKSSGIRVQSSKRRKSEKRYTRMWSIYVAVIFICMLPEFTIENVSYSIAISTPALKGMF	294
Qy	294	NAALISGIYNSCLNFPYIVILCEFFKRRLVSYKPAAGQLRAVSNQADBERTESK	351
Db	295	DEVVILTYLNSCANPILTAFLSDNKK-----SFQVNLCLMVSGAEIGEDSSDK	344

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	Query Match	29.1%	Score 530.5	DB: 1	Length 369
	Best Local Similarity	31.8%	Pred. No. 6,7e-41		
	Matches 114	Conservative	75	Mismatches 128	Indels 41
					Gaps 8
Oy	2	DLEASLLPGRNMSDSDPDMLTNSGSPRRGISYINIIIMSEVETGILLIGINSY	61		
Db	20	DLSGVSST--MSNSTEPTDYDIS-----NAVLTFIVVCLIGIGLTLV	64		
Oy	62	IFAVYAKSKLIHMCNNVPDIFILNLSVDLLFLGNPF-----MIHLMGNSVWHFGETM	115		
Db	65	IYILIRAKKK--KTTNIIYILNLIADELGLGPFILAMQVALVH-----WPGKGI	114		

[illegible]

RESULT 13
 US-08-417-103-6
 Sequence 6, Application US/08417103
 Patent No. 5723299
 GENERAL INFORMATION:
 APPLICANT: Bell, Graeme I.
 APPLICANT: Yamada, Yutichiro
 APPLICANT: Seino, Susumu
 TITLE OF INVENTION: SOMATOSTATIN RECEPTORS
 NUMBER OF SEQUENCES: 16
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Arnold, White & Durkee
 STREET: P.O. Box 4433
 CITY: Houston
 STATE: Texas
 COUNTRY: United States of America
 ZIP: 77210
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/417,103
 FILING DATE: 05-APR-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/816,283
 FILING DATE: 01-DEC-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Wilson, Mark B.
 REGISTRATION NUMBER: 37,259
 REFERENCE/DOCKET NUMBER: ARCD:144
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (512) 418-3000
 TELEFAX: (512) 474-7577
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 369 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-417-103-6

	Query Match	29.1%	Score 530.5	DB 1	Length 369;
	Best Local Similarity	31.8%	Pred. No. 6,7e-41		
	Matches 114;	Conservative	75;	Mismatches 128;	Indels 41; Gaps 8;
QY	2	DLEASLLPTCPNANSTSDGPDMLTSAGSPRRGSTSYNIITMPSVETCLLTIGTISNY	61		
		: : : : : : : : : : : : : : : : : : : : : : : : :			
	20	DLSGSVST--NSNSTEPRYDLS-----NAVLRIIVYGLTGCGATLV	64		
Db		: : : : : : : : : : : : : : : : : : : : : : : : :			
QY	62	IFAVYKSKSLHMCNNVDIFILINLVSVDLFLFGMPF-----MIHDMGNVWHFEETM	115		
		: : : : : : : : : : : : : : : : : : : : : : : : :			
Db	65	IYVLRPAKK--KITNTIYIILNLIADELWGLGFPLAMVALVH-----WPGEKAL	114		
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Oy 116 CTTTADANDANSQFSTYITLMAADRLAVIHPSSKRPKPSVATVETOLMAAPSISI 175
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 115 CRVWTVGQINFQSTICFLVMSIDRLAVIHPHFKSKMRKPRATAKKTAAVGVSLVI 174
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy 176 TPVWLYARLIEPCGAVGCGIRLENPPTDLY-NETLEQOFELAPLPEVITTAAYVRIIQR 234
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 175 LPIMTYAGLRBNQMGRRSSCTINMPGEGSAWMTGHTIYTFILGFLVPLTIIICLCYLFIIK 234
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy 235 MTSSVAPASQSRIRLTKRVTRTALICLPEFVGVMAIYVULQLEIS-RPLITTFYLY 293
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 235 VKSSGIRGSSKRRKSEKKVTRMWSIYAAVFIQWLEFFIYFNWSSVMAASPIPALKGMF 294
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy 234 NAAISLGAVNSCLNDPEVYIVICEFTRKRLVSVKPAAGOLGRAVSNQATADEERTSEK 351
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 235 DFFVVLVIYANSCANPIYALFSLDNFK-----SFQNVLCIYKVSCTDGGESDK 344

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Thu Feb 20 11:32:52 2003

us-09-885-478-28.ra1

Page 8

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QY 176 TPVWMLARLPPPGVAGCGIRLNPDTDL-WEYLKQFLAFLPVTVAAYRLQR 234
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 175 LPIMTIATGRSNQWRSSCTINMPGEGAWYTFGIITAFILFVLPULLICLCFLTIIK 234
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 235 MTSSVAPASQSRIRLRTKRTAFIALCLFEFCMAVPYVLOLPJLSTIS-PRYLTFVLYL 293
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 235 VKSSGIRVSSSRKKSEKKVTRMWSIYVAFITCMLPEYITFNWSSVAISPTALGMF 294
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 294 NAAISLGAVNSCLNPFVYIVLCETFRRLVSVKPAACQLRAVNSMAOTADEERTESK 351
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 295 DFVYIILTYANSCANILVAFIJSDFKK-----SFQWYLCIVKYSTGDEGERSDK 344

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Job time : 11.3216 secs
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 13, 2003, 13:56:21 ; Search time 12.3392 Seconds
(without alignments)
1006.264 Million cell updates/sec

Title: us-09-885-478-2

perfect score: 2212
Sequence: 1 MSYGAMKKKGVGRAVGLGGSS.....LRVSNQATDEPTEKSKT 422

Scoring table: BLOSUM62
Gapop 10.0 , Gapect 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA: *
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
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6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	2212	100.0	422	4	US-09-224-426-2
2	2212	100.0	422	4	US-09-478-601-2
3	2212	100.0	422	4	US-09-478-602-2
4	1824	82.5	353	3	US-08-984-288-2
5	1824	82.5	353	4	US-09-218-467B-2
6	1763	79.7	353	4	US-09-224-426-4
7	1763	79.7	353	4	US-09-478-601-4
8	1763	79.7	353	4	US-09-478-602-4
9	1691	76.4	402	3	US-08-602-809-2
10	1680	75.9	400	5	PCRT-US95-16472-2
11	535	24.2	369	4	US-08-120-601B-9
12	533	24.1	369	1	US-07-816-283-8
13	533	24.1	369	1	US-08-417-103-8
14	531.5	24.0	369	1	US-07-816-283-6
15	531.5	24.0	369	1	US-08-417-103-6
16	531.5	24.0	369	1	US-08-417-103-16
17	527	23.8	369	2	US-08-411-859-3
18	527	23.8	369	4	US-08-387-707-9
19	527	23.8	369	4	US-08-405-271A-9
20	514	23.2	331	1	US-07-816-283-2
21	514	23.2	331	1	US-08-417-103-2
22	514	23.2	331	1	US-08-417-103-14
23	508	23.0	391	1	US-07-816-283-4
24	508	23.0	391	1	US-08-417-103-4
25	504.5	22.8	418	1	US-07-816-283-10
26	504.5	22.8	418	1	US-08-417-103-10
27	502	22.7	391	4	US-08-120-601B-8

28	496.5	22.4	389	4	US-08-430-286A-7	Sequence 7, Appl
29	494.5	22.4	384	3	US-09-071-434-3	Sequence 3, Appl
30	472	21.3	428	1	US-07-816-283-12	Sequence 12, Appl
31	472	21.3	428	1	US-08-417-103-12	Sequence 12, Appl
32	456.5	20.6	370	4	US-08-405-271A-21	Sequence 21, Appl
33	453	20.5	400	4	US-08-188-275A-2	Sequence 2, Appl
34	453	20.5	400	4	US-09-351-198-2	Sequence 2, Appl
35	453	20.5	400	4	US-09-113-426-2	Sequence 2, Appl
36	453	20.5	415	4	US-08-405-271A-20	Sequence 20, Appl
37	452.5	20.5	398	1	US-08-149-093A-5	Sequence 5, Appl
38	452.5	20.5	398	3	US-08-911-245-5	Sequence 5, Appl
39	452.5	20.5	398	3	US-08-889-108-2	Sequence 2, Appl
40	452.5	20.5	398	4	US-08-120-601B-2	Sequence 2, Appl
41	452.5	20.5	398	4	US-08-387-707-16	Sequence 16, Appl
42	452.5	20.5	398	4	US-09-310-473-5	Sequence 5, Appl
43	452.5	20.5	398	4	US-08-405-271A-16	Sequence 16, Appl
44	452.5	20.5	398	5	PCT-US94-10358-2	Sequence 2, Appl
45	451.5	20.4	391	2	US-08-454-549-3	Sequence 3, Appl

ALIGNMENTS

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RESULT 1
US-09-224-426-2
; Sequence 2, Application US/09224426
; Patent No. 6221613
; GENERAL INFORMATION:
; APPLICANT: Salton, John A
; APPLICANT: Laz, Thomas M
; APPLICANT: Negorony, Amy E.
; APPLICANT: Wilson, Amy E.
; TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
; TITLE OF INVENTION: Receptor (MCH1) And Uses Thereof
; FILE REFERENCE: 57453/jpm/jhb
; CURRENT APPLICATION NUMBER: US/09/224,426
; CURRENT FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 2
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-224-426-2
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Query Match 100.0%; Score 2212; DB 4; Length 422;
Best Local Similarity 100.0%; Pred. No. 9.5e-174;
Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MSYGAMKKKGVGRAVGLGGSSGOATEEDPLPDGCACAPGOGGRWRRLPOPAWEGSSARL	60
DB	1	MSYGAMKKKGVGRAVGLGGSSGOATEEDPLPDGCACAPGOGGRWRRLPOPAWEGSSARL	60
QY	61	WEQATGTGMDLEASILPTGPNASNTSDGPDNLTSAGSPPTGSIYINIMPSVETIC	120
DB	61	WEQATGTGMDLEASILPTGPNASNTSDGPDNLTSAGSPPTGSIYINIMPSVETIC	120
QY	121	ILGIIINSVIVPAVVKSKSLHMCNNVPDIFITINSVDLLEFLCAMPIMHQLGNGVWHR	180
DB	121	ILGIIINSVIVPAVVKSKSLHMCNNVPDIFITINSVDLLEFLCAMPIMHQLGNGVWHR	180
QY	181	GEFMCLITRAMDANSOFSTYITLTMAIDRLAYVHPSSTKFKBSVATLVICLMAIS	240
DB	181	GEFMCLITRAMDANSOFSTYITLTMAIDRLAYVHPSSTKFKBSVATLVICLMAIS	240
QY	241	FISITPVMYLARLIPPGGAVCGIRLPNPDLDLWFTLYOFFLAFLAPFVITAAVYR1	300
DB	241	FISITPVMYLARLIPPGGAVCGIRLPNPDLDLWFTLYOFFLAFLAPFVITAAVYR1	300
QY	301	LOMTSSVAPASORSIRLRTKRVRTATATACLVFVPCAPVYVLOLQISISPTLTFYV	360
DB	301	LOMTSSVAPASORSIRLRTKRVRTATATACLVFVPCAPVYVLOLQISISPTLTFYV	360

QY 361 LYNAAISLGANSCLNPFVYIVLCETFRKRLVLSVCKPAAGOLRAVSNMOTADEERTESK 420
Db 361 LYNAAISLGANSCLNPFVYIVLCETFRKRLVLSVCKPAAGOLRAVSNMOTADEERTESK 420
QY 421 GT 422
Db 421 GT 422

RESULT 2
US-09-478-601-2
; Sequence 2, Application US/09478601
; Patent No. 6221616
; GENERAL INFORMATION:
; APPLICANT: Salton, John A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Nagorny, Raisa
; APPLICANT: Wilson, Amy E.
; TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
; FILE REFERENCE: 574532JPW
; CURRENT APPLICATION NUMBER: US/09/478,601
; EARLIER FILING DATE: 2000-01-06
; EARLIER APPLICATION NUMBER: 09/224,426
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-478-601-2

Query Match 100.0%; Score 2212; DB 4; Length 422;
Best Local Similarity 100.0%; Pred. No. 9,5e-174;
Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSYGAMKKGVGRAVGLGGSGCOATEEDPLPDGCACAPGCGGRWRRLPOPAAVEGSSARL 60
Db 1 MSYGAMKKGVGRAVGLGGSGCOATEEDPLPDGCACAPGCGGRWRRLPOPAAVEGSSARL 60
QY 61 WEQATGTGMDLEASILPTGPNASNTSDGPDNLTSAGSPRRGSIYINIMPSVFGTIC 120
Db 61 WEQATGTGMDLEASILPTGPNASNTSDGPDNLTSAGSPRRGSIYINIMPSVFGTIC 120
QY 121 LGITIGNSVIFAYVKKSKLHCNNVPDIFILNSVYDILFLGMPFHOLMGNGVWHF 180
Db 121 LGITIGNSVIFAYVKKSKLHCNNVPDIFILNSVYDILFLGMPFHOLMGNGVWHF 180
QY 181 GETMCTLTITAMDANSOFTSYIILTAMADRYLATVHPISSTFRKPSVATVICTLMAIS 240
Db 181 GETMCTLTITAMDANSOFTSYIILTAMADRYLATVHPISSTFRKPSVATVICTLMAIS 240
QY 241 FISTPFWMLYARLIPPGAVGCGIRLPNPTDLYMFTLXOFFLAPALPFVYITAAVRI 300
Db 241 FISTPFWMLYARLIPPGAVGCGIRLPNPTDLYMFTLXOFFLAPALPFVYITAAVRI 300
QY 301 LQRMSSVAPASORSIRLRTKRVTRTAIAICLVFVCMAPYVLOLTOLISRPFLTFVY 360
Db 301 LQRMSSVAPASORSIRLRTKRVTRTAIAICLVFVCMAPYVLOLTOLISRPFLTFVY 360
QY 361 LYNAAISLGANSCLNPFVYIVLCETFRKRLVLSVCKPAAGOLRAVSNMOTADEERTESK 420
Db 361 LYNAAISLGANSCLNPFVYIVLCETFRKRLVLSVCKPAAGOLRAVSNMOTADEERTESK 420
QY 421 GT 422
Db 421 GT 422

RESULT 3
US-09-478-602-2
; Sequence 2, Application US/09478602

; Patent No. 6291195
; GENERAL INFORMATION:
; APPLICANT: Salton, John A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Nagorny, Raisa
; APPLICANT: Wilson, Amy E.
; TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
; FILE REFERENCE: 574532JPW
; CURRENT APPLICATION NUMBER: US/09/478,602
; EARLIER FILING DATE: 2000-01-06
; EARLIER APPLICATION NUMBER: 09/224,426
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-478-602-2

Query Match 100.0%; Score 2212; DB 4; Length 422;
Best Local Similarity 100.0%; Pred. No. 9,5e-174;
Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSYGAMKKGVGRAVGLGGSGCOATEEDPLPDGCACAPGCGGRWRRLPOPAAVEGSSARL 60
Db 1 MSYGAMKKGVGRAVGLGGSGCOATEEDPLPDGCACAPGCGGRWRRLPOPAAVEGSSARL 60
QY 61 WEQATGTGMDLEASILPTGPNASNTSDGPDNLTSAGSPRRGSIYINIMPSVFGTIC 120
Db 61 WEQATGTGMDLEASILPTGPNASNTSDGPDNLTSAGSPRRGSIYINIMPSVFGTIC 120
QY 121 LGITIGNSVIFAYVKKSKLHCNNVPDIFILNSVYDILFLGMPFHOLMGNGVWHF 180
Db 121 LGITIGNSVIFAYVKKSKLHCNNVPDIFILNSVYDILFLGMPFHOLMGNGVWHF 180
QY 181 GETMCTLTITAMDANSOFTSYIILTAMADRYLATVHPISSTFRKPSVATVICTLMAIS 240
Db 181 GETMCTLTITAMDANSOFTSYIILTAMADRYLATVHPISSTFRKPSVATVICTLMAIS 240
QY 241 FISTPFWMLYARLIPPGAVGCGIRLPNPTDLYMFTLXOFFLAPALPFVYITAAVRI 300
Db 241 FISTPFWMLYARLIPPGAVGCGIRLPNPTDLYMFTLXOFFLAPALPFVYITAAVRI 300
QY 301 LQRMSSVAPASORSIRLRTKRVTRTAIAICLVFVCMAPYVLOLTOLISRPFLTFVY 360
Db 301 LQRMSSVAPASORSIRLRTKRVTRTAIAICLVFVCMAPYVLOLTOLISRPFLTFVY 360
QY 361 LYNAAISLGANSCLNPFVYIVLCETFRKRLVLSVCKPAAGOLRAVSNMOTADEERTESK 420
Db 361 LYNAAISLGANSCLNPFVYIVLCETFRKRLVLSVCKPAAGOLRAVSNMOTADEERTESK 420
QY 421 GT 422
Db 421 GT 422

RESULT 4
US-08-984-288-2
; Sequence 2, Application US/08984288
; Patent No. 6033872
; GENERAL INFORMATION:
; APPLICANT: BERGSM, DEK
; APPLICANT: ELLIS, CATHERINE
; TITLE OF INVENTION: NOVEL HUMAN IICB SPLICE V
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESS: RATER & PRESTIA
; STREET: P. O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA


```

: COUNTRY: USA
: ZIP: 19482
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FASTSEQ for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/984,288
: FILING DATE: 03-DEC-1997
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 60/032,763
: FILING DATE: 11-DEC-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: PRESTIA, PAUL F
: REGISTRATION NUMBER: 23,031
: REFERENCE/DOCKET NUMBER: P50599
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 610-407-0700
: TELEFAX: 610-407-0701
: TELEX: 846169
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 353 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-984-288-2

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Query Match      82.5%; Score 1824; DB 3; Length 353;
Best Local Similarity 100.0%; Pred. No. 4.9e-142;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 70 MDLPSLLPTGPNASNTSDGPDNLTSAGSPPTGTSISYINIMPSVFGTICLLGIIGNST 129
DB 1 MDLPSLLPTGPNASNTSDGPDNLTSAGSPPTGTSISYINIMPSVFGTICLLGIIGNST 60
QY 130 VIFAVVKKSKLHMCNNVPODIFIINLSVVDLFLGMPMHQLMGNGVWHGEMCTCLIT 189
DB 61 VIFAVVKKSKLHMCNNVPODIFIINLSVVDLFLGMPMHQLMGNGVWHGEMCTCLIT 120
QY 190 AMDANSOFTSTYILITAMADRYLATVHPISSTKFRKPSVATLVICLLMAISFISITPVWL 249
DB 121 AMDANSOFTSTYILITAMADRYLATVHPISSTKFRKPSVATLVICLLMAISFISITPVWL 180
QY 250 YARLIPEPGGAVGCGIRLPNPDLDLYWFTLYOFLAFALPFWVITAAYVRILOMTSSVA 309
DB 181 YARLIPEPGGAVGCGIRLPNPDLDLYWFTLYOFLAFALPFWVITAAYVRILOMTSSVA 240
QY 310 PASORSIRLRTKRYTRTAIAICLVFVCWAPYVYVQLTQLSISRTLTFFVLYNAATISLG 369
DB 241 PASORSIRLRTKRYTRTAIAICLVFVCWAPYVYVQLTQLSISRTLTFFVLYNAATISLG 300
QY 370 YANGLNPFYIIVLCETFRRLVLSVKPAQGLRAVSNQAOTADEERTESKGT 422
DB 301 YANGLNPFYIIVLCETFRRLVLSVKPAQGLRAVSNQAOTADEERTESKGT 353

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RESULT 5
US-09-218-467B-2
: Sequence 2, Application US/09218467B
: Patent No. 6362326
: GENERAL INFORMATION:
: APPLICANT: SATHE, GANESH
: APPLICANT: ELLIS, CATHERINE
: APPLICANT: HALSEY, WENDY
: APPLICANT: BERGMA, DEBK
: TITLE OF INVENTION: 11cby Genomic Sequence
: FILE REFERENCE: GP-50010
: CURRENT APPLICATION NUMBER: US/09/218,467B
: CURRENT FILING DATE: 2001-06-22

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: NUMBER OF SEQ ID NOS: 8
: SOFTWARE: FASTSEQ for Windows Version 3.0
: SEQ ID NO 2
: LENGTH: 353
: TYPE: PRT
: ORGANISM: HOMO SAPIENS
US-09-218-467B-2

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Query Match      82.5%; Score 1824; DB 4; Length 353;
Best Local Similarity 100.0%; Pred. No. 4.9e-142;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 70 MDLPSLLPTGPNASNTSDGPDNLTSAGSPPTGTSISYINIMPSVFGTICLLGIIGNST 129
DB 1 MDLPSLLPTGPNASNTSDGPDNLTSAGSPPTGTSISYINIMPSVFGTICLLGIIGNST 60
QY 130 VIFAVVKKSKLHMCNNVPODIFIINLSVVDLFLGMPMHQLMGNGVWHGEMCTCLIT 189
DB 61 VIFAVVKKSKLHMCNNVPODIFIINLSVVDLFLGMPMHQLMGNGVWHGEMCTCLIT 120
QY 190 AMDANSOFTSTYILITAMADRYLATVHPISSTKFRKPSVATLVICLLMAISFISITPVWL 249
DB 121 AMDANSOFTSTYILITAMADRYLATVHPISSTKFRKPSVATLVICLLMAISFISITPVWL 180
QY 250 YARLIPEPGGAVGCGIRLPNPDLDLYWFTLYOFLAFALPFWVITAAYVRILOMTSSVA 309
DB 181 YARLIPEPGGAVGCGIRLPNPDLDLYWFTLYOFLAFALPFWVITAAYVRILOMTSSVA 240
QY 310 PASORSIRLRTKRYTRTAIAICLVFVCWAPYVYVQLTQLSISRTLTFFVLYNAATISLG 369
DB 241 PASORSIRLRTKRYTRTAIAICLVFVCWAPYVYVQLTQLSISRTLTFFVLYNAATISLG 300
QY 370 YANGLNPFYIIVLCETFRRLVLSVKPAQGLRAVSNQAOTADEERTESKGT 422
DB 301 YANGLNPFYIIVLCETFRRLVLSVKPAQGLRAVSNQAOTADEERTESKGT 353

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RESULT 6
US-09-224-426-4
: Sequence 4, Application US/09224426
: Patent No. 6221613
: GENERAL INFORMATION:
: APPLICANT: Sajon, John A
: APPLICANT: Iaz, Thomas M.
: APPLICANT: Wilson, Amy E.
: APPLICANT: Magorjny, Ralsia
: TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
: FILE REFERENCE: 57453/JPW/JHB
: CURRENT APPLICATION NUMBER: US/09/224,426
: CURRENT FILING DATE: 1998-12-31
: NUMBER OF SEQ ID NOS: 15
: SOFTWARE: PatentIn Ver. 2.0 - beta
: SEQ ID NO 4
: LENGTH: 353
: TYPE: PRT
: ORGANISM: rat
US-09-224-426-4

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Query Match      79.7%; Score 1763; DB 4; Length 353;
Best Local Similarity 96.0%; Pred. No. 4.9e-137;
Matches 339; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

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DB 1 MDLPSLLPTGPNASNTSDGPDNLTSAGSPPTGTSISYINIMPSVFGTICLLGIIGNST 60
QY 130 VIFAVVKKSKLHMCNNVPODIFIINLSVVDLFLGMPMHQLMGNGVWHGEMCTCLIT 189
DB 61 VIFAVVKKSKLHMCNNVPODIFIINLSVVDLFLGMPMHQLMGNGVWHGEMCTCLIT 120
QY 190 AMDANSOFTSTYILITAMADRYLATVHPISSTKFRKPSVATLVICLLMAISFISITPVWL 249

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Thu Feb 20 11:32:10 2003

us-09-885-478-2.1.ai

Page 4

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Db      121 AMDANSOFTSYLTAMTIDRYLATVHPISSTKFRKPSMATVLCILMALSFISITPPVL 180
Qy      250 YARLIPFGAGVGGCIRLPNDPDLWFLYLXOFELAFALPFPVITAAYVRILOMTSSVA 309
        181 YARLIPFGAGVGGCIRLPNDPDLWFLYLXOFELAFALPFPVITAAYVRILOMTSSVA 240
Qy      310 PASORSIRLRTKRTVTRTAICLVFVCWAPYVYVLOLQLSISRPFTLFVLYNAAISLG 369
        241 PASORSIRLRTKRTVTRTAICLVFVCWAPYVYVLOLQLSISRPFTLFVLYNAAISLG 300
Qy      370 YANSLNPFYIYVLCETFFRRRLVLSVKPAAGQLRTVSNMQTADERTESKGT 422
        301 YANSLNPFYIYVLCETFFRRRLVLSVKPAAGQLRTVSNMQTADERTESKGT 353

RESULT 7
US-09-478-601-4
; Sequence 4, Application US/09478601
; Patent No. 6221616
; GENERAL INFORMATION:
; APPLICANT: Salom, John A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Nagorny, Raisa
; APPLICANT: Wilson, Amy E.
; TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
; TITLE OF INVENTION: Receptor (MCH1) And Uses Thereof
; FILE REFERENCE: 574532,JPW
; CURRENT APPLICATION NUMBER: US/09/478,601
; CURRENT FILING DATE: 2000-01-06
; EARLIER APPLICATION NUMBER: 09/224,426
; EARLIER FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-478-601-4

Query Match          79.7%; Score 1763; DB 4; Length 353;
Best Local Similarity 96.0%; Pred. No. 4,9e-137;
Matches 339; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Qy      70 MDLEASLPTGPNASNTSDGPNLTSAGSPPTGSISYINIMPSVFGTICLGIIGNST 129
        1 MDLQTSILSTGPNASNISDQDNLTLPSPPTGSISYINIMPSVFGTICLGIIGNST 60
Db      130 VIFAVYKSKLHMCNNVDPDIFINLSVVDLFLGMPFMIHOLMGNGVWHFGTMCCTLT 189
        61 VIFAVYKSKLHMCNSVDPDIFINLSVVDLFLGMPFMIHOLMGNGVWHFGTMCCTLT 120
Qy      190 AMDANSOFTSYLTAMTIDRYLATVHPISSTKFRKPSMATVLCILMALSFISITPPVL 249
        121 AMDANSOFTSYLTAMTIDRYLATVHPISSTKFRKPSMATVLCILMALSFISITPPVL 180
Qy      250 YARLIPFGAGVGGCIRLPNDPDLWFLYLXOFELAFALPFPVITAAYVRILOMTSSVA 309
        181 YARLIPFGAGVGGCIRLPNDPDLWFLYLXOFELAFALPFPVITAAYVRILOMTSSVA 240
Qy      310 PASORSIRLRTKRTVTRTAICLVFVCWAPYVYVLOLQLSISRPFTLFVLYNAAISLG 369
        241 PASORSIRLRTKRTVTRTAICLVFVCWAPYVYVLOLQLSISRPFTLFVLYNAAISLG 300
Qy      370 YANSLNPFYIYVLCETFFRRRLVLSVKPAAGQLRTVSNMQTADERTESKGT 422
        301 YANSLNPFYIYVLCETFFRRRLVLSVKPAAGQLRTVSNMQTADERTESKGT 353

RESULT 8
US-09-478-602-4
; Sequence 4, Application US/09478602
; Patent No. 6291195
; GENERAL INFORMATION:
;
```

```

; APPLICANT: Salom, John A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Nagorny, Raisa
; APPLICANT: Wilson, Amy E.
; TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
; TITLE OF INVENTION: Receptor (MCH1) And Uses Thereof
; FILE REFERENCE: 574532,JPW
; CURRENT APPLICATION NUMBER: US/09/478,602
; CURRENT FILING DATE: 2000-01-06
; EARLIER APPLICATION NUMBER: 09/224,426
; EARLIER FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-478-602-4

Query Match          79.7%; Score 1763; DB 4; Length 353;
Best Local Similarity 96.0%; Pred. No. 4,9e-137;
Matches 339; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Qy      70 MDLEASLPTGPNASNTSDGPNLTSAGSPPTGSISYINIMPSVFGTICLGIIGNST 129
        1 MDLQTSILSTGPNASNISDQDNLTLPSPPTGSISYINIMPSVFGTICLGIIGNST 60
Db      130 VIFAVYKSKLHMCNNVDPDIFINLSVVDLFLGMPFMIHOLMGNGVWHFGTMCCTLT 189
        61 VIFAVYKSKLHMCNSVDPDIFINLSVVDLFLGMPFMIHOLMGNGVWHFGTMCCTLT 120
Qy      190 AMDANSOFTSYLTAMTIDRYLATVHPISSTKFRKPSMATVLCILMALSFISITPPVL 249
        121 AMDANSOFTSYLTAMTIDRYLATVHPISSTKFRKPSMATVLCILMALSFISITPPVL 180
Qy      250 YARLIPFGAGVGGCIRLPNDPDLWFLYLXOFELAFALPFPVITAAYVRILOMTSSVA 309
        181 YARLIPFGAGVGGCIRLPNDPDLWFLYLXOFELAFALPFPVITAAYVRILOMTSSVA 240
Qy      310 PASORSIRLRTKRTVTRTAICLVFVCWAPYVYVLOLQLSISRPFTLFVLYNAAISLG 369
        241 PASORSIRLRTKRTVTRTAICLVFVCWAPYVYVLOLQLSISRPFTLFVLYNAAISLG 300
Qy      370 YANSLNPFYIYVLCETFFRRRLVLSVKPAAGQLRTVSNMQTADERTESKGT 422
        301 YANSLNPFYIYVLCETFFRRRLVLSVKPAAGQLRTVSNMQTADERTESKGT 353

RESULT 9
US-08-602-809-2
; Sequence 2, Application US/08602809
; Patent No. 6066012
; GENERAL INFORMATION:
; APPLICANT: BERGMA, DEBK
; APPLICANT: ELLIS, CATHERINE
; TITLE OF INVENTION: HUMAN SOMATOSTATIN-LIKE R
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: US
; ZIP: 19482-0980
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,809
; FILING DATE: 13-JUN-1997
;
```

Thu Feb 20 11:32:10 2003

us-09-885-478-2.rai

Page 5

```

1 CLASSIFICATION: 536
2 PRIOR APPLICATION DATA:
3 APPLICATION NUMBER: PCT/US95/16472
4 FILING DATE: 15-DEC-1995
5 APPLICATION NUMBER: US 08/357,675
6 FILING DATE: 16-DEC-1994
7 ATTORNEY/AGENT INFORMATION:
8 NAME: Prestia, Paul F
9 REGISTRATION NUMBER: 23,031
10 REFERENCE/DOCKET NUMBER: P50277
11 TELECOMMUNICATION INFORMATION:
12 TELEPHONE: 601-407-0700
13 TELEFAX: 610-407-0701
14 TELEX: 846169
15 INFORMATION FOR SEQ ID NO: 2:
16 SEQUENCE CHARACTERISTICS:
17 LENGTH: 402 amino acids
18 TYPE: amino acid
19 STRANDEDNESS: single
20 TOPOLOGY: linear
21 MOLECULE TYPE: protein
22 US-08-602-809-2

```

```

Query Match      76.4%  Score 1691:  Db 3:  Length 402:
Best Local Similarity 82.9%  Fred. No. 4.5e131:
Matches 340:  Conservative 7:  Matches 15:  Indels 48:  Gaps 4:

QY 50 PAMVGS--SARLMEQATGTGWMDEASLLPTGPNASNTSDGPDN----- 92
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 4 PRTKGSGSGSHHQETGHEGRKD-----KISN-SEGRENQGRFGOMNGSLAE 52
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 93 -----LTSAGSPRTGSIYSYNIIMPVFGITCLGIIGNSTYF 132
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 53 HASRMSVLRAKPMNSQRLLLCPGSPPTGSIYNIIMPVFGITCLGIIGNSTYF 112
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 133 AVYKSKRLMNCNNVPDIFIIINLSYVDLFLGLMPEMIHOLMGNGVHFGETMCTLTITAND 192
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 113 AVYKSKRLMNCNNVPDIFIIINLSYVDLFLGLMPEMIHOLMGNGVHFGETMCTLTITAND 172
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 193 ANSQSTSYILTMAIDRYLAVHPISSTFKRPSVATLYICLLMALSFISTTPVVLXAR 252
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 173 ANSQSFSTYILTMAIDRYLATVHPISSTFKRPSVATLYICLLMALSFISTTPVVLXAR 232
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 253 LIPFGGAVGCGRLNPDPDLYWFLYOFELAFALPEVYTAAYRIIQRMTSSVAPAS 312
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 233 LIPEPGGAVGCGRLNPDPDLYWFLYOFELAFALPEVYTAAYRIIQRMTSSVAPAS 292
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 313 QRSIRLRTRKVTATATACLVFEVCNAPYVYLQTLQSLSPLTTFVYLYNAAISIGYAN 372
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 293 QRSIRLRTRKVTATATACLVFEVCNAPYVYLQTLQSLSPLTTFVYLYNAAISIGYAN 352
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 373 SCINPEVYIYLCTEPRKRLVLSYKPAAGGLRAVSNAQTADERTESKGT 422
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 353 SCINPEVYIYLCTEPRKRLVLSYKPAAGGLRAVSNAQTADERTESKGT 402
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 10
PCT-US95-16472-2
: Sequence 2, Application PC/TUS9516472
: GENERAL INFORMATION:
: APPLICANT: Bergsma, Derek J
: APPLICANT: Ellis, Catherine E
: TITLE OF INVENTION: Human Somatostatin Receptor
: NUMBER OF SEQUENCES: 3
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: SmithKline Beecham Corporation/Corporate
: ADDRESSEE: Intellectual Property
: STREET: P. O. Box 1539-UW220
: CITY: King of Prussia
: STATE: Pennsylvania
: COUNTRY: USA
: ZIP: 19406-0939
: COMPUTER READABLE FORM:
:

```

```

1      MEDIUM TYPE: Floppy disk
2      COMPUTER: IBM PC compatible
3      OPERATING SYSTEM: PC-DOS/MS-DOS
4      SOFTWARE: Patentln Release #1.0, Version #1.25
5      CURRENT APPLICATION DATA:
6      APPLICATION NUMBER: PCT/US95/16472
7      FILING DATE:
8      CLASSIFICATION:
9      ATTORNEY/AGENT INFORMATION:
10     NAME: Sulten, Jeffrey A
11     REGISTRATION NUMBER: 34,028
12     REFERENCE/DOCKET NUMBER: P50277
13     TELECOMMUNICATION INFORMATION:
14     TELEPHONE: 610 270 5024
15     TELEFAX: 610 270 5090
16     INFORMATION FOR SEQ ID NO: 2:
17     SEQUENCE CHARACTERISTICS:
18     LENGTH: 400 amino acids
19     TYPE: amino acid
20     STRANDEDNESS: single
21     TOPOLOGY: linear
22     MOLECULE TYPE: protein
23
24 PCT-US95-16472-2

```

```

Query Match          75.9%; Score 1680; DB 5; Length 400;
Best Local Similarity 82.8%; Pred. No. 3,6e-130;
Matches 338; Conservative 7; Mismatches 15; Indels 48; Gaps

QY 50 PAMVEGS--SARLEWQATGNGWMDLEASLLPTGPNASNTSDGPDN----- 92
   1: 111 111111 111111 111111 111111 111111 111111 111111
DB 4 PSKTDSSGSHGRHQHETHEGKRD-----KISN--SEGRENGGRGPHONGSLAE 52
   1: 111 111111 111111 111111 111111 111111 111111 111111
QY 93 -----LTSAGSPRTGSIYINIMPSYFGITCLGITGNSTYAF 132
   1: 111111 111111 111111 111111 111111 111111 111111 111111
DB 53 HASRMGVLRKAPMNSQORLLLCPGSPPRGSIYINIMPSYFGITCLGITGNSTYAF 112
   1: 111111 111111 111111 111111 111111 111111 111111 111111
QY 133 AAYKSKRIHMCNNVPDIEIINLSVVDLFLGLMPMIHOLMGVNHFGETMCTLTAMD 192
   1: 111111 111111 111111 111111 111111 111111 111111 111111
DB 113 AAYKSKRLHMCNNVPDIEIINLSVVDLFLGLMPMIHOLMGVNHFGETMCTLTAMD 172
   1: 111111 111111 111111 111111 111111 111111 111111 111111
QY 193 ANSGFTSYLLTMAIDRYLATVHPISSTKRRPSVATVICTLMAISFISTIPWLYAR 252
   1: 111111 111111 111111 111111 111111 111111 111111 111111
DB 173 ANSGFTSYLLTMAIDRYLATVHPISSTKRRPSVATVICTLMAISFISTIPWLYAR 232
   1: 111111 111111 111111 111111 111111 111111 111111 111111
QY 253 LIPEPGGAVCGCIRLPNDPFDLYWFTLYOFFLAFPFVYITAAVYIIQRMSSVAPAS 312
   1: 111111 111111 111111 111111 111111 111111 111111 111111
DB 233 LIPEPGGAVCGCIRLPNDPFDLYWFTLYOFFLAFPFVYITAAVYIIQRMSSVAPAS 292
   1: 111111 111111 111111 111111 111111 111111 111111 111111
QY 313 ORSRILRTKRYTRTAIICLVFEFCMAPIYVLOLTQLSISRPITLFEVYIYNAASISGYAN 372
   1: 111111 111111 111111 111111 111111 111111 111111 111111
DB 293 QRSRLRTKRYTRTAIICLVFEFCMAPIYVLOLTQLSISRPITLFEVYIYNAASISGYAN 352
   1: 111111 111111 111111 111111 111111 111111 111111 111111
QY 373 SCINPEVYIVLCETFRKRLVSVKPAAGOLRAVSNQTADEERTSEK 420
   1: 111111 111111 111111 111111 111111 111111 111111 111111
DB 353 SCINPEVYIVLCETFRKRLVSVKPAAGOLRAVSNQTADEERTSEK 400
   1: 111111 111111 111111 111111 111111 111111 111111 111111

RESULT 11
US-08-120-601B-9
: Sequence 9, Application US/08120601B
: Patent No. 6235496
: GENERAL INFORMATION:
: APPLICANT: Yu, Lei
: TITLE OF INVENTION: MD OPTIOD RECEPTORS: COMPOSITIONS AND
: TITLE OF INVENTION: METHODS
: NUMBER OF SEQUENCES: 9
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Arnold, White & Durkee
: STREET: P.O. Box 4433
: CITY: Houston
: STATE: Texas
: COUNTRY: USA
: ZIP: 77210

```

Page 6

Query Match	24.2%;	Score 535;	DB 4;	length 369;
Best Local Similarity	31.7%;	Pred. No. 2.3e-36;		
Matches 118;	Conservative 77;	Mismatches 131;	Indels 46;	Gaps 10;

RESULT 12

```

? ZIP : 7210
? COMPUTER READABLE FORM:
? MEDIUM TYPE: floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DO$
? SOFTWARE: Patentin Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/07/816,283
? FILING DATE: 19911231
? CLASSIFICATION: 435
? ATTORNEY/AGENT INFORMATION:
? NAME: McDaniel, C. Steven
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 713-787-1400
? TELEX: 713-789-2679
? FAX: 79-0924
? INFORMATION FOR SEQ ID NO.: 8:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 369 amino acids
? TYPE: AMINO ACID
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? US-07-816-283-8

Query Match          24.1%; Score 533; DB 1; Length 369;
Best Local Similarity 31.7%. Pred. No. 3,3e-36;
Matches 118; Conservative      ; Mismatches 131; Indels    46; Gaps     10;

QY   62 EQATGTC-NM---DLEASLFTGFPMASNISDGPDNLTSAGSPPTRGSIYSINIIMPSVF 116
       || |::| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| 
Db    6 EOLNGSOVWVSPPFDINGSLGPS--NGSNOTEPYDMTSS-----NAVLTETLY 50

QY   117 GTICLLIGNSVTVEFAVVKKSKLDHCNWNVDIPFIINLSVDDLFLGLMPF-----MH 170
        |:|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::| 
Db    51 FYVCVGCLGNLVIVILIRAKM---KTIINIILLALADELFMLGLPIAMGVAVH 107

QY   171 QLMNGVMHFGEFMCTLTITAMDANSQSFSITYILTAAIIDRLIATVPISPSTFRKPSTAT 230
        || |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::| 
Db    108 -----WFPGAIQRVMTADGINOFTSIFCLTVMSIDRYLAHVHPISKARKRPRTAK 160

QY   231 LVLCILMALSFISTPVLVIARLIIPPFGAAGCGIRLPNPDTDLX-WFTLYOFFLAIALP 289
         ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::| 
Db    161 MINVAWCVSVLLYPIMPITYAGRNRNQGRRESSCTINMGESGAWYGTFIIYAFIGLPLP 220

QY   290 FVYTIAAYVRILIQRMTSSVAAPASQRSIRLRKRKYRTRAINACIEFYEVCAPIYVLOQL 349
        .:||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::| 
Db    221 LTTICLCYEFTIIHKASSGIKVRSRRKSSEKRVASTVAVFPCWPPIRNVS V 280

QY   350 SIS-RPLLTFEYLVAANAILSGYANSCLNFYYIVLCEFFRKRIYLVSVKPAQAQLRAVNS 408
        ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::| 
Db    281 SVAISFPALKGMDFPVVILTYANGCANPDIIFYALSDFNKFK-----SFONVICLVAV 332

QY   409 AQTAEDEERTSRK 420
       ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::| 
Db    333 SGTEDEERSDSK 344


RESULT 13
US-08-417-103-8
Sequence 8, Application us/08417103
Patent No. 5733299
GENERAL INFORMATION:
APPLICANT: Bell, Graeme I.
APPLICANT: Yamada, Yutichiro
APPLICANT: Seino, Susumu
TITLE OF INVENTION: SOMATOSTATIC RECEPTORS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: United States of America
```

```

;
; ZIP: 77210
;
; COMPUTER READABLE FORM:
;
; MEDIUM TYPE: Floppy disk
;
; COMPUTER: IBM PC compatible
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
;
; SOFTWARE: Patentin Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
;
; APPLICATION NUMBER: US/08/417,103
;
; FILING DATE: 05-APR-1995
;
; CLASSIFICATION: 435
;
; PRIORITY APPLICATION DATA:
;
; APPLICATION NUMBER: US 07/816,283
;
; FILING DATE: 01-DEC-1991
;
; ATTORNEY/AGENT INFORMATION:
;
; NAME: Wilson, Mark B.
;
; REGISTRATION NUMBER: 37,259
;
; REFERENCE/DOCKET NUMBER: ARCD:144
;
; TELECOMMUNICATION INFORMATION:
;
; TELEPHONE: (512) 418-3000
;
; TELEFAX: (512) 474-7577
;
; INFORMATION FOR SEQ ID NO: 8:
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 369 amino acids
;
; TYPE: amino acid
;
; TOPOLOGY: linear
;
; MOLECULE TYPE: protein
;
; US-08-417-103-8

```

```

Query Match          24.1%; Score 533; DB 1; Length 369;
Best Local Similarity 31.7%; Pred. No. 3.3e-36;
Matches 118; Conservative 77; Mismatches 131; Indels 46; Gaps 10;

```

```

QY 62 EQATGCG-WM----DEASLPTGPNASNTSDGPDNLTSAGSPRTGISIYINIMPSVF 116
   ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
DB 6  EQLNQVQVWVSSPFDLNGSLGPS--NGSNQTEPYDMTS-----NAVLTFIY 50

QY 117 GTTCLGIIGNSVTFYAVVKKSLHMCNNVPDIFIINLSVVDLFLGLMPF-----MIH 170
   ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
DB 51 FVVCVGLGNTLVITVILYIKAKM--KTTNITILNLADLDELFLGLPFLAMQVALVH 107

QY 171 QLMNGVMHFGETMCTLTITAMANDSOFTSTYITLTAIDRYLATVHPISSTFRKPSVAT 230
   ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
DB 108 -----WFGKALCRVMTVDGINSQFTSIFCLTVMSIDRYLAVHPIKSAKMRPRPTAK 160

QY 231 LVICLIMAFSISTPVMYLARLIPPGAVCGCIRLPNDTDLV-WFTLYQFLAFLAP 289
   ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
DB 161 MIVAVWCVSLVILPIMIVAGLRSNQWGRSSCTINMPGSGAMVTFIYAFILGLVLP 220

QY 290 FVYITAAVYRILORMSSVAPASQSRIRLTKRVTRTALAIQVFEVCMAPYVLOLTOL 349
   ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
DB 221 LRTICLCYFIIIRKSSGIRVSSSKRKSEKVTIRAVSIVAVFPCWLPFIYFNSSV 280

QY 350 SIS-RPTLTFVYLYNAISIGYANSCINPFYIVLCETFRRLVLSVKKPAQGLRAVSN 408
   ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
DB 281 SVALSPFPAKGMDFVVLITVANSKANPILYAFLSDNFK-----SFQNVLCIVKY 332

QY 409 AQTADERTESK 420
   ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
DB 333 SGTEDGERSDSK 344

```

```

RESULT 14
US-07-816-283-6
; Sequence 6, Application US/07816283
; Patent No. 5436155
; GENERAL INFORMATION:
; APPLICANT: Bell, Graeme I.
; APPLICANT: Yamada, Yuichiro
; APPLICANT: Saino, Susumu
; TITLE OF INVENTION: SOMATOSTATIN RECEPTORS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee

```

```

;
; STREET: PO Box 4433
;
; CITY: Houston
;
; STATE: Texas
;
; COUNTRY: USA
;
; ZIP: 77210
;
; COMPUTER READABLE FORM:
;
; MEDIUM TYPE: Floppy disk
;
; COMPUTER: IBM PC compatible
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
;
; SOFTWARE: Patentin Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
;
; APPLICATION NUMBER: US/07/816,283
;
; FILING DATE: 19911231
;
; CLASSIFICATION: 435
;
; ATTORNEY/AGENT INFORMATION:
;
; NAME: McDaniel, C. Steven
;
; TELECOMMUNICATION INFORMATION:
;
; TELEPHONE: 713-787-1400
;
; TELEFAX: 713-789-2679
;
; TELEX: 79-0924
;
; INFORMATION FOR SEQ ID NO: 6:
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 369 amino acids
;
; TYPE: AMINO ACID
;
; TOPOLOGY: linear
;
; MOLECULE TYPE: protein
;
; US-07-816-283-6

```

```

Query Match          24.0%; Score 531.5; DB 1; Length 369;
Best Local Similarity 31.6%; Pred. No. 4.4e-36;
Matches 115; Conservative 76; Mismatches 128; Indels 45; Gaps 9;

```

```

QY 69 WM----DEASLPTGPNASNTSDGPDNLTSAGSPRTGISIYINIMPSVFTCLLGI 124
   ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
DB 14 WLSIPEDLNGSVYST--NTSNQTEPYDITLS-----NAVLTFIYVVCITGL 58

QY 125 IGSSTVFAYVKKSKLHMCNNVPDIFIINLSVVDLFLGLMPF-----MIHQLMGVW 178
   ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
DB 59 CGNTLVITVILYIKAKM--KTTNITILNLADLDELFLGLPFLAMQVALVH-----W 108

QY 179 HFGETMCTLTITAMANDSOFTSTYITLTAIDRYLATVHPISSTFRKPSVATVLCILMA 238
   ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
DB 109 PFGKALCRVMTVDGINSQFTSIFCLTVMSIDRYLAVHPIKSAKMRPRPTAKMITMAVWG 168

QY 239 LSPSTPVMYLARLIPPGAVCGCIRLPNDTDLV-WFTLYQFLAFLAPVYITAAV 297
   ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
DB 169 VSLVILPIMIVAGLRSNQWGRSSCTINMPGSGAMVTFIYAFILGLVPLIICLCY 228

QY 298 VRILORMSSVAPASQSRIRLTKRVTRTALAIQVFEVCMAPYVLOLTOLSTS-RPTL 356
   ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
DB 229 LRTICLCYFIIIRKSSGIRVSSSKRKSEKVTIRAVSIVAVFPCWLPFIYFNSSV 288

QY 357 TFVYLYNAISIGYANSCINPFYIVLCETFRRLVLSVKKPAQGLRAVSNQADDEER 416
   ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
DB 289 ALKGMDFVYVVLVYANSKANPILYAFLSDNFK-----SFQNVLCIVKVSQTDGGER 340

QY 417 TESK 420
   ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
DB 341 SDSK 344

```

```

RESULT 15
US-08-417-103-6
; Sequence 6, Application US/08417103
; Patent No. 5723299
; GENERAL INFORMATION:
; APPLICANT: Bell, Graeme I.
; APPLICANT: Yamada, Yuichiro
; APPLICANT: Saino, Susumu
; TITLE OF INVENTION: SOMATOSTATIN RECEPTORS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee

```

STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30C
CURRENT APPLICATION NUMBER: US/08/417,103
FILING DATE: 05-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/816,263
FILING DATE: 01-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: ARCO:144
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 369 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-417-103-6

Db	781	GTGGGGCTGGGGCATAGGCTCTGCCCAACCCAGACTGACTTACTGTTACCTGTAC	840
QY	841	CAGTTTTTCCGTGGCCCTTTGGCCCTGCTTTTGTGTCATCACAGCCGATPAGCTGAGATC	900
Db	841	CAGTTTTTCCGTGGCCCTTTGGCCCTGCTTTTGTGTCATCACAGCCGATPAGTGAGATC	900
QY	901	CTGAGCGCATGACGTCTCATGTGAGCCCCCGCTCCAGCGAGATCCGCTGGGACA	960
Db	901	CTGAGCGCATGACGTCTCATGTGAGCCCCCGCTCCAGCGAGATCCGCTCGGACA	960
QY	961	AAGAGGCTGACCCGACACAGCATCGGCATCTGTCGTCCTTTTGTGTGGGACACC	1020
Db	961	AAGAGGCTGACCCGACACAGCATCGGCATCTGTGTGTCCTTTTGTGTGGGACACC	1020
QY	1021	TACTATGTGTACAGCTGACCCAGTTGTCCATCAGCCGCGACCCCTTGTGTAC	1080
Db	1021	TACTATGTGTACAGCTGACCCAGTTGTCCATCAGCCGCGACCCCTTGTGTAC	1080
QY	1081	TTTATACATCGGGCATCAGCTTGGGCTATGCCAACAGCTGCTTAACCCCTTGTGTAC	1140
Db	1081	TTTATACATCGGGCATCAGCTTGGGCTATGGCAACAGCTGCTTAACCCCTTGTGTAC	1140
QY	1141	ATCGTGTCTGTGAGAGCTTCCGCAAAACGCTTGTGCTGTGGTGAACCTGTGACCCAG	1200
Db	1141	ATCGTGTCTGTGAGAGCTTCCGCAAAACGCTTGTGCTGTGGTGAACCTGTGACCCAG	1200
QY	1201	GGGCGAGCTTGGCGCTGTGACAAACGCTCAGACGGCTGACGAGAGAGGACAGAAAGCAA	1260
Db	1201	GGGCGAGCTTGGCGCGTGTGACAAACGCTCAGACGGGCTGACGAGAGAGGACAGAAAGCAA	1260
QY	1261	GGCACCTGA 1269	
Db	1261	GGCACCTGA 1269	

```

RESULT 3
US-09-478-602-1
; Sequence 1, Application US/09478602
; Patent No. 6291195
; GENERAL INFORMATION:
; APPLICANT: Salom, John A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Nagorny, Raisa
; APPLICANT: Wilson, Amy E.
; TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
; TITLE OF INVENTION: Receptor (MCH1) And Uses Thereof
; FILE REFERENCE: 57453\JPW
; CURRENT APPLICATION NUMBER: US/09/478,602
; CURRENT FILING DATE: 2000-01-06
; EARLIER APPLICATION NUMBER: 09/224,426
; EARLIER FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1269
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-478-602-1

Query Match          100.0%; Score 1269; DB 4; Length 1269;
Best Local Similarity 100.0%; Pred. No. 7.5e-283;
Matches 1269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  ATGTCAGTGGAGCCATGAAAGAAGGAGTGGGGAGGCGACGTTGGGCTTGGAGGCGGACG 60
        |||||||
DB       1  AAGTCAGTGGAGCCATGAAAGAAGGAGTGGGGAGGCGACGTTGGGCTTGGAGGCGGACG 60

QY      61  GGCTCCAGAGCTACAGGAGAGAGACCCCTTCCGCACTGGGGGGCTTGGGCTCCGGGACAA 120
        |||||||
DB       61  GGCTCCAGAGCTACAGGAGAGAGACCCCTTCCGCACTGGGGGGCTTGGGCTCCGGGACAA 120

QY      121  GGTGGCAGGCGCTGAGAGGCTGCCGAGCGCTGGTGGGTGGAGGGAGCTCAGCTCGGTTG 180

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Db	121	GGTGGCAGGCGCTGGAGGCTGGCCAGGCTGGTGGGTTGGAGGGAGGCTCAGCTGGTTG	180
Qy	181	TGGGAGCAGGCGAGCCGGCAGCTGGCTGGATGGAGCCTGGAAAGCCTCCCTCTGACCCACTGGT	240
Db	181	TGGGAGCAGGCGAGCCGGCAGCTGGCTGGATGGAGCCTGGAAAGCCTCCCTCTGACCCACTGGT	240
Qy	241	CCCAATGCCAGACACACCTCTGATGGCCCCGATTAACCTTCACTTCAGCAGGATCACCTCTC	300
Db	241	CCCAATGCCAGCACAACCTCTGATGGCCCCGATTAACCTTCACTTCAGCAGGATCACCTCTC	300
Qy	301	CGCAGGGGGAGCAATCTCTATCAACATCATCATGAGCCTGGGTGGTGGACCAATCGC	360
Db	301	CGCAGGGGGAGCAATCTCTATCAACATCATCATGAGCCTGGGTGGTGGACCAATCGC	360
Qy	361	CTCTTGGGACATCATCGGGAACCTCACGGTCAATCTTCGCGGTGTAAAGATCCAAAGCTG	420
Db	361	CTCTTGGGACATCATCGGGAACCTCACGGTCAATCTTCGCGGTGTAAAGATCCAAAGCTG	420
Qy	421	CACGTGTGCACAACAGTCCCGCAGCATCTTCATCATCAACCTCTGSGTGTAGTAAATCTCTC	480
Db	421	CACGTGTGCACAACAGTCCCGCAGCATCTTCATCATCAACCTCTGSGTGTAGTAAATCTCTC	480
Qy	481	TTTCTCTGGGCAATGCCCTTCAATGATCCACAGCTCATATGGGCAATGGGGTGTGGACCTT	540
Db	481	TTTCTCTGGGCAATGCCCTTCAATGATCCACAGCTCATATGGGCAATGGGGTGTGGACCTT	540
Qy	541	GGGAGAGCAATGTGACACCCCTCATCAGGGCATGGATGGCAATGACAGTTCACCGACCC	600
Db	541	GGGAGAGCAATGTGACACCCCTCATCAGGGCATGGATGGCAATGACAGTTCACCGACCC	600
Qy	601	TACATCTCTGACCCGCATGGCCATTGACCGCTACCTGGCCACTGTGCACCCCACTCTTCC	660
Db	601	TACATCTCTGACCCGCATGGCCATTGACCGCTACCTGGCCACTGTGCACCCCACTCTTCC	660
Qy	661	ACGAAGTTCGGGAAAGCCCTCTGTGGCAACCTGTGTGATCTGCTCTCTGTGGGACCTCTCC	720
Db	661	ACGAAGTTCGGGAAAGCCCTCTGTGGCAACCTGTGTGATCTGCTCTCTGTGGGACCTCTCC	720
Qy	721	TTTCATCAGCAATCCCTGTGTGGGCTAATGGCAGACTATCCCTCCACAGAGAGTGTCA	780
Db	721	TTTCATCAGCAATCCCTGTGTGGGCTAATGGCAGACTATCCCTCCACAGAGAGTGTCA	780
Qy	781	GTGGGCTGCGGCAATACGCTGTGCCCAACCCAGACACAGCATCTCTACTGGTTACCCCTGTAC	840
Db	781	GTGGGCTGCGGCAATACGCTGTGCCCAACCCAGACACAGCATCTCTACTGGTTACCCCTGTAC	840
Qy	841	CAGTTTTTCTGGGCTTGTGCCCTGTGTTGTGTGTCATCAACAGCCGATACGTGTAGATC	900
Db	841	CAGTTTTTCTGGGCTTGTGCCCTGTGTTGTGTGTCATCAACAGCCGATACGTGTAGATC	900
Qy	901	CTGAGGGGCAATGAGTCTCTAGTGGGCCCCGCCCTCCACAGCAGATCCGGCTGTGGGACA	960
Db	901	CTGAGGGGCAATGAGTCTCTAGTGGGCCCCGCCCTCCACAGCAGATCCGGCTGTGGGACA	960
Qy	961	AAGAGGCTGACCCGACAGGCATTCGCAATCTGTCTGTCTTGTGTGTGGTGGGACACC	1020
Db	961	AAGAGGCTGACCCGACAGGCATTCGCAATCTGTCTGTCTTGTGTGTGGTGGGACACC	1020
Qy	1021	TACTATGTGTACAGCTGACCCAGTTGTCCATCAGCGCGCCGACCCCTCAACCTTGTGTAC	1080
Db	1021	TACTATGTGTACAGCTGACCCAGTTGTCCATCAGCGCGCCGACCCCTCAACCTTGTGTAC	1080
Qy	1081	TTTATACAAATGGGGCATACTTGGGCTAATGCCAATAGCTGGCTCAACCCCTTGTGTAC	1140
Db	1081	TTTATACAAATGGGGCATACTTGGGCTAATGCCAATAGCTGGCTCAACCCCTTGTGTAC	1140
Qy	1141	ATGCTGCTCTGTGAGAGTTCGCCAAAGCTTGTCTCTCGGTAAAGCTGTACAGCCAG	1200
Db	1141	ATGCTGCTCTGTGAGAGTTCGCCAAAGCTTGTCTCTCGGTAAAGCTGTACAGCCAG	1200
Qy	1201	GGGCAAGCTTGCGCTGTGCAGCAAGCTCAGAGGGCTGACGAGAGAGGACAGAAAGCAAA	1260

Db 1201 GGGCAGCTTCGCCCTGTCAGCAGCAGCTCAGAGGCTGACAGAGAGAGAGGACAGAAAGCAAA 1280

QY 1261 GGCACCTGA 1269

Db 1261 GGCACCTGA 1269

RESULT 4

```

US-08-984-288-1
: Sequence 1, Application US/08984288
: Patent No. 6033872
:
: GENERAL INFORMATION:
:
: APPLICANT: BERGSMÄ, DEREK
: TITLE OF INVENTION: NOVEL HUMAN 11CB SPLICE V
: TITLE OF INVENTION: NOVEL HUMAN 11CB SPLICE V
: NUMBER OF SEQUENCES: 6
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: RATNER, E PRESTITA
: STREET: P.O. BOX 960
: CITY: VALLEY FORGE
: STATE: PA
: COUNTRY: USA
: ZIP: 19482
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FASTSEQ for Windows Version 2.0
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/984,288
: FILING DATE: 03-DEC-1997
:
: CLASSIFICATION:
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 60/032,763
: FILING DATE: 11-DEC-1996
:
: ATTORNEY/AGENT INFORMATION:
: NAME: PRESTITA, PAUL F
: REGISTRATION NUMBER: 23,031
: REFERENCE/DOCKET NUMBER: P50599
:
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 610-407-0700
: TELEFAX: 610-407-0701
:
: TELEX: 846169
:
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1385 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
:
: MOLECULE TYPE: CDNA
:
: US-08-984-288-1

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Query Match	97.5%;	Score 1237.4;	DB 3;	Length 1385;
Best Local Similarity	99.9%;	Pred. No. 1.4e-275;		
Matches 1238; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

QY	31	GGAGAGGCGAGTTGGGCTTGGAGGGCGGAGGGGCTGGCAGGCTAACGAGAGAGACCCCTT	90
Db	66	GGAGAGGCGAGTTGGGCTTGGAGGGCGGAGGGGCTGGCAGGCTAACGAGAGAGACCCCTT	125
QY	91	CCCGACTGCGGGGCTTGGCTCCCGGGAAGAAGTGGCAGGCGGTGGAGGGCTGCGGACCT	150
Db	126	CCCGACTGCGGGGCTTGGCTCCCGGGAAGAAGTGGCAGGCGGTGGAGGGCTGCGGACCT	185
QY	151	GGCTGGGTGGAAGGAGAGCTCAGCTCGGTTGGGAGCAGGCGAGCCGGACTGGGTGATG	210
Db	186	GGCTGGGTGGAAGGAGAGCTCAGCTCGGTTGGGAGCAGGCGAGCCGGACTGGGTGATG	245
QY	211	GAGCTGGAGAGCTCGCTCTCTCTCCACCTAGTGTCCTCAATGTCAGCAACACTCTGATGGCCCC	270
Db	246	GAGCTGGAGAGCTCGCTCTCTCTCCACCTAGTGTCCTCAATGTCAGCAACACTCTGATGGCCCC	305

QY	271	GAAACCTCACTGACGAGGATCAACCTCTCCGACGGGGAGGACATCTCTACATCAACATC	330
Db	306	GATAACCTCACTTGCGGACGAGATCACTCTCTCCGACGGGGAGCATCTCTACATCAACATC	365
QY	331	ATCATGCTCTGGGGTTCGCGACCATCTGGCTCTCGGGGATCATCGGGAACCTCCAGGTC	390
Db	366	ATCATGCTCTGGGGTTCGCGACCATCTGGCTCTCGGGGATCATCGGGAACCTCCAGGTC	425
QY	391	ATCTTCGCGGTTCGTGAAGAGTCCAACTGCACTGCTGACAAACAGTCCCCGACATCTTC	450
Db	426	ATCTTCGCGGTTCGTGAAGAGTCCAACTGCACTGCTGACAAACAGTCCCCGACATCTTC	485
QY	451	ATCATCAACCTCTGGGATAGTATCTCTCTTCTCTCTGGGGCATAGCCCTTCATGATCAAC	510
Db	486	ATCATCAACCTCTGGGATAGTATCTCTCTTCTCTCTGGGGCATAGCCCTTCATGATCAAC	545
QY	511	CAGCTCATGGGCAATGGGGGTGTGGACATTTTGGGGAGACATGTGCAACCCCTCATACAGGCC	570
Db	546	CAGCTCATGGGCAATGGGGGTGTGGACATTTTGGGGAGACATGTGCAACCCCTCATACAGGCC	605
QY	571	ATGGATGGCAATATGTCAGTTTCACGAGACTACATCTTACGCCCATGGCATTTGACCGC	630
Db	606	ATGGATGGCAATATGTCAGTTTCACGAGACTACATCTTACGCCCATGGCATTTGACCGC	665
QY	631	TACCGGGCACTGTGCCAACCCCATCTCTTCCACGAAGTTCGGAAAGCCCTGTGGGCAAC	690
Db	666	TACCGGGCACTGTGCCAACCCCATCTCTTCCACGAAGTTCGGAAAGCCCTGTGGGCAAC	725
QY	691	CTGGTATCTGCCTCTGTGTGGGCCCTCTCTCATCAAGCATCAACCCCTGTGTGGCTGAT	750
Db	726	CTGGTATCTGCCTCTGTGTGGGCCCTCTCTCATCAAGCATCAACCCCTGTGTGGCTGAT	785
QY	751	GCCAGACTCAATCCCCCTTCCAGAGAGTGGAGTGGCGGGCATATAGCCCTGCCCAACCCA	810
Db	786	GCCAGACTCAATCCCCCTTCCAGAGAGTGGAGTGGCGGGCATATAGCCCTGCCCAACCCA	845
QY	811	GACACTGACCTCTACTGGTTCACCCCTTACACAGTTTTCCTGGACCTTGGCCGACCTTTT	870
Db	846	GACACTGACCTCTACTGGTTCACCCCTTACACAGTTTTCCTGGACCTTGGCCGACCTTTT	905
QY	871	GTTGTCATCACAGCCGACATAGTGAAGATCTTGAGGCGATGACGTCCTCAAGTGGCCCC	930
Db	906	GTTGTCATCACAGCCGACATAGTGAAGATCTTGAGGCGATGACGTCCTCAAGTGGCCCC	965
QY	931	GCTTCACAGGCGACATCTCGGCTGGCGGAGAAAGGGGTGACCCGCAACGATCGGCATC	990
Db	966	GCTTCACAGGCGACATCTCGGCTGGCGGAGAAAGGGGTGACCCGCAACGATCGGCATC	1025
QY	991	TGTCGTGCTCTTTGTGTGCTGGGACCCCTACTATGTGCTACAGCTGACCCAGTTGTCC	1050
Db	1026	TGTCGTGCTCTTTGTGTGCTGGGACCCCTACTATGTGCTACAGCTGACCCAGTTGTCC	1085
QY	1051	ATCAGCGCCCGGACCCCTACCTTTGTACTTTATACAATGCGGCATCAAGCTTGGGCTAT	1111
Db	1086	ATCAGCGCCCGGACCCCTACCTTTGTACTTTATACAATGCGGCATCAAGCTTGGGCTAT	1144
QY	1111	GCCAAACAGCTGACCAACCCCTTGTGTACTATGCTGCTGTAGAGACTTCCGCAAAAGC	1177
Db	1146	GCCAAACAGCTGACCAACCCCTTGTGTACTATGCTGCTGTAGAGACTTCCGCAAAAGC	1201
QY	1171	TTGGTCTGTGTGTAAGACCTTGACGCCAGCGGGGACATTCGCGCTTCAGCAACGCTCAG	1230
Db	1206	TTGGTCTGTGTGTAAGACCTTGACGCCAGCGGGGACATTCGCGCTTCAGCAACGCTCAG	1265
QY	1231	ACGGCTACAGAGAGAGAGACAAAGCAAAAGGACCTGA	1269
Db	1266	ACGGCTACAGAGAGAGAGACAAAGCAAAAGGACCTGA	1304

RESULT 5

US-09-218-467B-1
; Sequence 1, Application US/09218467B
; Patent No. 6362326

GENERAL INFORMATION:

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1 APPLICANT: SATHE, GANESH
2 APPLICANT: ELLIS, CATHERINE
3 APPLICANT: HALSEY, WENDY
4 APPLICANT: BERGSMAN, DEBK
5 TITLE OF INVENTION: 11cby Genomic Sequences
6 FILE REFERENCE: GP-50010
7 CURRENT APPLICATION NUMBER: US/09/218,467B
8 CURRENT FILING DATE: 2001-06-22
9 NUMBER OF SEQ. ID NOS: 8
10 SOFTWARE: FASTSEQ for Windows Version 3.0
11 SEQ. ID NO. 1
12 LENGTH: 3488
13 TYPE: DNA
14 ORGANISM: HOMO SAPIENS
15 US-09-218-467B-1

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Query Match	77.68;	Score 984.4;	DB 4;	Length 3488;
Best Local Similarity	99.48;	Pred. No. 2.6e-217;		
Matches 988; Conservative	0;	Mismatches 6;	Indels 0;	Gaps 0;

QY	276	CCCTACCTTCAGAGAGATTCACACTCTCTGGCACGGGGAGACATCTCTTCATCAATCAACATCAT	335
Db	2056	CCCTTCCTGCCAGAGATCAACACTCTCTGCACGGGGAGCATCTCTCTCATCAACATCATCAT	2115
QY	336	GCCTCGGCTGTGGGACACATCTGCCTCTCTGGGCATCATCGGGAACTCCACAGGTCATCTT	395
Db	2116	GCCTTCGGCTGTGGGACACATCTGCCTCTCTGGGCATCATCGGGAACTCCACAGGTCATCTT	2175
QY	396	CGCGGCTGTAGAGAGCTCCAAAGCTGCATCGTGGCAACAACGTCGCCGACATCTTCATCAT	455
Db	2176	CGCGGCTGTAGAGAGCTCCAAAGGCTGCATCGTGGCAACAACGTCGCCGACATCTTCATCAT	2235
QY	456	CAACCTCTCGGTAAGTAATCTCTCTTCTTCTCCGGGCATGCCCTTCATGATCCACACT	515
Db	2236	CAACCTCTCGGTAAGTAATCTCTCTTCTCTCGGCATGCCCTTCATGATCCACACT	2295
QY	516	CATGCGCAATGSGGTGTGGCATTCTTTGGGAGACATGTGCACCCCTCATACAGGCCATGGA	575
Db	2296	CATGCGCAATGSGGTGTGGCATTCTTTGGGAGACATGTGCACCCCTCATACAGGCCATGGA	2355
QY	576	TGCCAATAGTCAGATTACACAGCACTACATACCTGTGACCGGCATGSGCATGTGACCCGTACTT	635
Db	2356	TGCCAATAGTCAGATTACACAGCACTACATACCTGTGACCGGCATGTGACCCGTACTT	2415
QY	636	GGCCACATGCTACCCCATCTCTTCACAGAAATTCGGGAAAGCCCTGTGGGACACCTGTGT	695
Db	2416	GGCCACATGCTACCCCATCTCTTCACAGAAATTCGGGAAAGCCCTGTGGGACACCTGTGT	2475
QY	696	GATCTGCTCTCTGTGGGCTCTCTCTTCATCAAGCATCACCCCTGTGTGGCTGTATGCAG	755
Db	2476	GATCTGCTCTCTGTGGGCTCTCTCTTCATCAAGCATCACCCCTGTGTGGCTGTATGCAG	2535
QY	756	ACTCATCCCCCTCCACAGAGGTGCATGTGGGCTGGGCATATACCTGTGCCAACCCAGAAC	815
Db	2536	ACTCATCCCCCTCCACAGAGGTGCATGTGGGCTGGGCATATACCTGTGCCAACCCAGAAC	2595
QY	816	TGACCTCTACTGCTGTCAACCTGTACAGATTTTCTGTGGCTTTGCCCTGTCTTTGTGTGT	875
Db	2596	TGACCTCTACTGCTGTCAACCTGTACAGATTTTCTGTGGCTTTGCCCTGTCTTTGTGTGT	2655
QY	876	CATCACAGCCGATACGTAGTAGATTCCTGTAGGCGCATGAGTCTCATAGTGCCGCCGCTCT	935
Db	2656	CATCACAGCCGATACGTAGTAGATTCCTGTAGGCGCATGAGTCTCATAGTGCCGCCGCTCT	2715
QY	936	CCACGAGGAGATCCGGGTGTGGGCAANAAGGGGTGACCCGCAAGGCATGTGCATGTGCT	995
Db	2716	CCACGAGGAGATCCGGGTGTGGGCAANAAGGGGTGACCCGCAAGGCATGTGCTGTCT	2775
QY	996	GGCTCTCTTTGTGTGCTGGGACCCCTCATATGTGCTACAGCTGACCCAGTGTCTCATCAG	1055
Db	2776	GGCTCTCTTTGTGTGCTGGGACCCCTCATATGTGCTACAGCTGACCCAGTGTCTCATCAG	2835

QY	1056	CCGCCGACCTCACCTTTGTCTACTTATACATAGGGGCATACACTTGGGTATGCCAA	1115
Db	2836	CCGCCGACCTCACCTTTGTCTACTTATACATAGGGGCATACACTTGGGTATGCCAA	2895
QY	1116	CAGCTGCCTCAACCCCTTTGTGTATCATCGTGTCTGTGAGAGCTTCCGCAACGCTTGGT	1175
Db	2896	CAGTGCCTCAACCCCTTTGTGTATCATCGTGTGTGAGAGCTTCCGCAACGCTTGGT	2955
QY	1176	CGTGTGCGTGAAGCCTTGCAGCCGAGGGGCAAGCTTGCCTGTGCACCAACGCTCAAGCGGC	1235
Db	2956	CGTGTGCGTGAAGCCTTGCAGCCGAGGGGCAAGCTTGCCTGTGCACCAACGCTCAAGCGGC	3015
QY	1236	TGACGAGGAGAGGAGCAAAAGCAAAAGCAACCTGA	1269
Db	3016	TGACGAGGAGAGGAGCAAAAGCAAAAGCAACCTGA	3049

RESULT 6
US-08-602-809-1
; Sequence 1, Application US/08602809

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1 GENERAL INFORMATION:
2 APPLICANT: BERGSMAN, DEK
3 APPLICANT: ELLIS, CATHERINE
4 TITLE OF INVENTION: HUMAN SOMATOSTATIN-LIKE R
5 TITLE OF INVENTION: ECEPTOR
6 NUMBER OF SEQUENCES: 3
7 CORRESPONDENCE ADDRESS:
8 ADDRESSEE: Ratner & Prestia
9 STREET: P.O. Box 980
10 CITY: Valley Forge
11 STATE: PA
12 COUNTRY: US
13 ZIP: 19482-0980
14
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE: Diskette
17 COMPUTER: IBM Compatible
18 OPERATING SYSTEM: DOS
19 SOFTWARE: FASTSEQ for Windows Version 2.0
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER: US/08/602,809
22 FILING DATE: 13-JUN-1997
23 CLASSIFICATION: 536
24
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER: PCT/US95/14472
27 FILING DATE: 15-DEC-1995
28 APPLICATION NUMBER: US 08/357,675
29 FILING DATE: 16-DEC-1994
30 ATTORNEY/AGENT INFORMATION:
31 NAME: Prestia, Paul F
32 REGISTRATION NUMBER: 23,031
33 REFERENCE/DOCKET NUMBER: P50277
34 TELECOMMUNICATION INFORMATION:
35 TELEPHONE: 601-407-0700
36 TELEFAX: 610-407-0701
37 TELEX: 846169
38
39 INFORMATION FOR SEQ ID NO: 1:
40 SEQUENCE CHARACTERISTICS:
41 LENGTH: 1316 base pairs
42 TYPE: nucleic acid
43 STRANDEDNESS: single
44 TOPOLOGY: linear
45
46 MOLECULE TYPE: cDNA
47
48 US-08-602-809-1

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Query Match:	77.5%;	Score 983;	DB 3;	length 1316;
Best Local Similarity	100.0%;	Pred. NO. 4e-217;		
Matches 983;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
QY	287	CAGGATCACCTCTCTCCACGGGAGACATCTCCATACATCATCATATGCTTGGGTG	346	
ob	253	CAGGATCACCTCTCTCCACGGGAGACATCTCCATACATCATCATATGCTTGGGTG	312	

Thu Feb 20 11:14:23 2003

us-09-885-478-1.rni

Page 6

OY	347	TCGGACACATCTGCTCCCTGGGCAATCATCGGAAATCACAAGTCATCTTCCGGGCTGA	406
Db	313	TCGGACACATCTGCTCCCTGGGCAATCATCGGAAACTCAGAGTCATCTTCCGGGCTGA	372
OY	407	AGAAAGTCCAAGCTGCGCATCTGTGTGCAACAACGTCCCGACATCTTTCATCATCAACTCTGG	466
Db	373	AGAAAGTCCAAGCTGCGCACTGTGTGCAACAACGTCCCGACATCTTTCATCATCAACTCTCGG	432
OY	467	TAGTAGATCTCCTCTTTCCTGGGCATAGCCCTTTCATGTATCCACCAAGCTCATGGGCATG	526
Db	433	TAGTAGATCTCCTCTTTCCTGGGCATAGCCCTTTCATGTATCCACCAAGCTCATGGGCATG	492
OY	527	GGGCTGTGGCATCTTGGGGAGACATGTGACACCTCATACAGGCGCATGGATGCAATGATGC	586
Db	493	GGGCTGTGGCATCTTGGGGAGACCAATGTGACACCTCATACAGGCGCATGGATGCAATGATGC	552
OY	587	AGTTACACAGACCTTACATACCTCTGACCCGCGCATGGCCATTTGACCGCTACCTGGCCACTGTC	646
Db	553	AGTTACACAGACACCTTACATACCTCTGACCCGCGCATTTGACCGCTACCTGGCCACTGTC	612
OY	647	ACCCCATCTCTTCACAGAAAGTCCGGAAGGCCCTGTGGGCACACCGGGATGATCCCTGC	706
Db	613	ACCCCATCTCTTCACAGAAAGTTCGGAAGGCCCTGTGGGCACACCTGGTATCTGCTTCC	672
OY	707	TGTGGGCCCTCTCTCTTTCATCAGCATCACCCCTGTGTGCTGTATGTGCACAGACTCATCCCT	766
Db	673	TGTGGGCCCTCTCTCTTTCATCAGCATCACCCCTGTGTGCTGTATGTGCACAGACTCATCCCT	732
OY	767	TCCAGGAGGTGAGTGGGGCTGCGGCATATAGCCGCGCCAAACCAGACACTACCTACT	826
Db	733	TCCAGGAGGTGAGTGGGGCTGCGGCATATAGCCGCGCCAAACCAGACACTACCTACT	792
OY	827	GGTTTACACCTCTTACCAAGTTTTTCTGGGCTTTTGCCCTTTTGTGTGTCATCACACCG	886
Db	793	GGTTTACACCTCTTACCAAGTTTTTCTGGGCTTTTGCCCTTTTGTGTGTCATCACACCG	852
OY	887	CATACGTGAGAGATCTCGACAGCGCATATGACGTCCTACGTAGGCCCCGCCCTCCAGAGCAGCA	946
Db	853	CATACGTGAGAGATCTCGACAGCGCATATGACGTCCTACGTAGGGCCCGCCTCCAGAGCAGCA	912
OY	947	TCCGGCTCGGGCAANAAGAGGGGACCCGACACCATAGCCCATCTGTGTGCTTTCTTGG	100
Db	913	TCCGGCTCGGGCAANAAGAGGGGACCCGACACCATAGCCCATCTGTGTGCTTTCTTGG	972
OY	1007	TGTGCTGTGGACCTTACTAGTGTGTAGACGTGACCCAGTATGTCATACAGCCGCCGACC	1067
Db	973	TGTGCTGTGGACCTTACTAGTGTGTGTAGACGTGACCCAGTATGTCATACAGCCGCCGACC	1033
OY	1067	TCACTTTGTCTACTTATATACATAGGGGCATACAGCTTGGGGTATGCAANAAGCTGCCTCA	112
Db	1033	TCACTTTGTCTACTTATATACATAGGGGCATACAGCTTGGGGTATGCAANAAGCTGCCTCA	109
OY	1127	ACCCCTTTGTGTACATCGTGTCTGTGTGAGAGCTTTCGCAACAGCTGTGCTGTGGTGA	118
Db	1093	ACCCCTTTGTGTACATCGTGTCTGTGTGTGAGAGCTTTCGCAACAGCTGTGCTGTGGTGA	115
OY	1187	AGCCTCAGCCCAAGGGAGAGCTGTGCGCTGTGACGAACACCTCAGACGGCTCAGCAGAGA	124
Db	1153	AGCCTCAGCCCAAGGGAGCAAGCTGTGCGCTGTGTGACGAACACCTCAGAGCGCTCAGCAGAGA	121
OY	1247	GGACAGAAAGCAAAAGCAGCTTGA	1269
Db	1213	GGACAGAAAGCAAAAGCAGCTTGA	1235

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RESULT 7
PCT-US95-16472-1
: Sequence 1, Application PC/TUS9516472
: GENERAL INFORMATION:
:
: APPLICANT: Bergsma, Derek J
:
: APPLICANT: Ellis, Catherine E
:
: TITLE OF INVENTION: Human Somatostatin Receptor
:
: NUMBER OF SEQUENCES: 3

```

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Smithkline Beecham Corporation/corporate
ADDRESSEE: Intellectual Property
STREET: P. O. Box 1539-0W2220
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16472
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sueton, Jeffrey A
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P502277
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610 270 5024
TELEFAX: 610 270 5090
INFORMATION FOR SEQ. ID NO.: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1316 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: misc.feature
LOCATION: 27..1232
OTHER INFORMATION: /note="The coding sequence is from
OTHER INFORMATION: nucleotides 27 to 1232."
PCT-US95-16472-1

Query Match 77.5%; Score 983; DB 5; Length 1316;
Best Local Similarity 100.0%; Pred. No. 4e-217;
Matches 983; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

OY 287 CAGATCACCTCCCTCGACGCGGAGGAGCATCTCCTACATCAACATCATGATGCTCGGT 346
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DB 253 CAGATCACTCTCTCGACGCGGAGGAGCATCTCCTACATCAACATCATGATGCTCGGT 312
OY 347 TCGCACCAATCTGCTCTCGGATCATATGGAACCTCCACGCTATCTCTGGCGTGTGA 406
|||
DB 313 TCGCACCAATCTGCTCTCGGATCATATGGAACCTCCACGCTATCTCTGGCGTGTGA 372
OY 407 AGAAGTCACGCTGACACTGGTGCAACACAGTCCCGGACATCTTATCATCAACCTCTCG 466
|||
DB 373 AGAAGTCACGCTGACACTGGTGCAACAGTCCCGGACATCTTATCATCAACCTCTCG 432
OY 467 TAGTAGATCTCCCTTTCCTGCGGGATGACCCCTTCATGATGCACACGATCATGGGCAATG 526
|||
DB 433 TAGTAGATCTCCCTTTCCTGCGGGATGACCCCTTCATGATGCACACGATCATGGGCAATG 492
OY 527 GGGGTGGCACTTGGGGAGACCATATGTGACCTTCATACGCGCATGATGCCAATATGTC 586
|||
DB 493 GGGGTGGCACTTGGGGAGACCATATGTGACCTTCATACGCGCATGATGCCAATATGTC 552
OY 587 AGTTACACACACCTTCATATCTGACGCGCATGAGCATGAGACGCTACTGTGGACACTGTTC 646
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DB 553 AGTTACACACACCTTCATATCTGACGCGCATGAGCATGAGACGCTACTGTGGACACTGTTC 612
OY 647 ACCCAATCTTTCACAGAGTTCGCGGAACCCCTCTGTGGCCACACCTGTGATATCGCTCC 706
|||
DB 613 ACCCAATCTTTCACAGAGTTCGCGGAACCCCTCTGTGGCCACACCTGTGATATCGCTCC 672
OY 707 TGTGGGCGCTCTCTTCATACACATCACCCCTGTGTGGCTGTATGCCAGCATCATCCCT 766
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DB 673 TGTGGGCGCTCTCTTCATACACATCACCCCTGTGTGGCTGTATGCCAGCATCATCCCT 732

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Db 361 AACCATGTGCACCCCTCATTCACAGCCATGGACGCCAACAGTACGTTCACTACGACCTTACAT 420

Db 894 TTGTGACCTTGTGTGCTCCTACACCTATGCTTAACAGCTGTGCCAACCCCTATCTATATGCG 953

QY 1144 GTGCTCTGTGAGACGCTTCCGCAACGCTT 1172

Db 954 TTCTTGTCTGACAACTTCAAGAAAGAGCTT 982

RESULT 14

US-07-816-283-5

; Sequence 5, Application US/07816283

; Patent No. 5436155

; GENERAL INFORMATION:

; APPLICANT: Bell, Graeme I.

; APPLICANT: Yamada, Yulchiro

; APPLICANT: Saino, Susumu

; TITLE OF INVENTION: SOMATOSTATIN RECEPTORS

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Arnold White & Durkee

; STREET: PO Box 4433

; CITY: Houston

; STATE: Texas

; COUNTRY: USA

; ZIP: 77210

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/816,283

; FILING DATE: 19911231

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: McDaniel, C. Steven

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 713-787-1400

; TELEFAX: 713-789-2679

; TELEX: 79-0924

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1351 base pairs

; TYPE: NUCLEIC ACID

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

US-07-816-283-5

Query Match 11.6%; Score 147.4; DB 1; Length 1351;

Best Local Similarity 52.6%; Pred. No. 4.3e-25;

Matches 394; Conservative 0; Mismatches 346; Indels 9; Gaps 3;

QY 430 AACACGTCGCCGACATCTTCATCATCACTCTGCGTAGATCTCTCTTCTCCTG 489

Db 305 AAGACATACACCAATTTACATCTCACTGCGACGAGATGAGCTCTTCATGCTG 364

QY 490 GGCAAGCCCTTCATATCCACAGCTCATGCGCAATGGGCAATGGCACTTTGGGAGAC 549

Db 365 GGTGCTCTTCTGTGTATGAGG--TGGCTGTGTGCTCACTGGCCCTTTGGCAAGGCC 421

QY 550 ATGTGACCCCTCATCAGCGCATGGATGCCAATAGTCACTTACACGACCATCATCTG 609

Db 422 ATTTCCGGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 481

QY 610 ACCGCAATGGCCATTTGACCGCTACTGCGCACTGTCCACCCCATCTCTTCCAGAAAT 669

Db 482 ACAGTATGAGCATGACGATGATGATGATGATGATGATGATGATGATGATGATGATG 541

QY 670 GGGAGCCCTCTGTGCGACCCCTGGTGAATGCTCTCTGTGGCCCTCTCTTCTTACG 729

Db 542 AGGAGAGCCCGGAGCGCCAGATGATGATGATGATGATGATGATGATGATGATGATG 601

QY 730 ATCACCCCTGTGTGTGTATGATGATGATGATGATGATGATGATGATGATGATGATG 789

Db 602 ATCTTGCCCATCATGATATATATGCTGGGCTCGGAGCAACAGTAGTGGGAGAAAGCAGCTGC 661

QY 790 GGCATACCCCTGCC---CAACCCAGACACATGACCTCTACAGTGTTCACCCGTGACAGTT 846

Db 662 AACATCAACTGGCCAGAGTGAATCTGGGGCTGTGATACAGAGGCTTCATCATCTTACCTTTC 721

QY 847 TTCCGTGGCTTTGGCCCTGCTTTTGTGTGTCATCAAGCCCATGATGAGATTCCTGAC 906

Db 722 ATTTGGGGGTTCCTGTGATACCCCTCAGCATCATCTGTCTTTCGTACGTTCATATATCATC 781

QY 907 CGCATGACGCTTCAGTGGCCCCCGCTCCAGCGGACGATCCGAGTGGGACCAAGAG 966

Db 782 AAGTGAAAGTCTCTGGAATCCAGAGTGGGCTCTTAAGAGAAAGATGAGAGAAAG 841

QY 967 GTGACCCGACAGCATGCGCATCTGTGTGCTCTTGTGTGTGTGTGTGTGTGTGTGTGTGT 1026

Db 842 GTACCCGAAATGTGTTCATGCTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 901

QY 1027 GTGCTACAGCTGACCCAGTGTGCTAT--CAAGCCCGCCGACCCCTGACCTTTGTCTACTTA 1083

Db 902 ATATTCACAGTTTCTTCGCTTCATGGGCAATCAGCCCGCCCTTAAAGGCATG 961

QY 1084 TACAAATGGGCCATCAGCTTGGGCTATGCAACAGCTGCTTCACCCCTTGTGTATATC 1143

Db 962 TTGTGACTTTGT 1021

QY 1144 GTGCTCTGTGAGACGCTTCCGCAACGCTT 1172

Db 1022 TTCTTGTCTGACAACTTCAAGAAAGCTT 1050

RESULT 15

US-08-417-103-5

; Sequence 5, Application US/08417103

; Patent No. 5723299

; GENERAL INFORMATION:

; APPLICANT: Bell, Graeme I.

; APPLICANT: Yamada, Yulchiro

; APPLICANT: Saino, Susumu

; TITLE OF INVENTION: SOMATOSTATIN RECEPTORS

; NUMBER OF SEQUENCES: 16

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Arnold, White & Durkee

; STREET: P.O. Box 4433

; CITY: Houston

; STATE: Texas

; COUNTRY: United States of America

; ZIP: 77210

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/417,103

; FILING DATE: 05-APR-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/816,283

; FILING DATE: 01-DEC-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Wilson, Mark B.

; REGISTRATION NUMBER: 37,259

; REFERENCE/DOCKET NUMBER: ARCD:144

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (512) 418-3000

; TELEFAX: (512) 474-7577

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1351 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 13, 2003, 13:50:36 ; Search time 13.7494 Seconds
(without alignments)
1273.004 Million cell updates/sec

Title: US-09-885-478-2
Perfect score: 2212
Sequence: 1 MSVGAMKGVRAVGLGGGS.....LRAVSNQTADEPRTESKGT 422

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1763	79.7	353	1	GP24_RAT
2	1696	76.7	402	1	GP24_HUMAN
3	533	24.1	369	1	SSR2_MOUSE
4	531.5	24.0	369	1	SSR2_HUMAN
5	528	23.9	368	1	SSR2_BOVIN
6	527	23.8	369	1	SSR2_RAT
7	525.5	23.8	369	1	SSR2_PIG
8	514	23.2	391	1	SSR1_HUMAN
9	513.5	23.2	388	1	SSR4_HUMAN
10	508	23.0	391	1	SSR1_MOUSE
11	504.5	22.8	418	1	SSR3_HUMAN
12	497.5	22.5	391	1	SSR1_RAT
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15	480.5	21.7	428	1	SSR3_RAT
16	478.5	21.6	364	1	SSR5_HUMAN
17	472	21.3	428	1	SSR3_MOUSE
18	470.5	21.3	363	1	SSR5_RAT
19	457	20.7	401	1	OPRM_BOVIN
20	456	20.6	362	1	SSR5_MOUSE
21	453.5	20.5	398	1	OPRM_MOUSE
22	452	20.4	401	1	OPRM_PIG
23	451.5	20.4	372	1	OPRD_HUMAN
24	451.5	20.3	400	1	OPRM_RAT
25	450	20.3	400	1	OPRM_MACMU
26	448	20.3	400	1	OPRM_HUMAN
27	446.5	20.2	372	1	OPRD_RAT
28	441	19.9	372	1	OPRD_MOUSE
29	435.5	19.7	380	1	OPRK_HUMAN
30	431.5	19.5	380	1	OPRK_CAVPO
31	426	19.3	370	1	OPRX_CAVPO
32	421	19.0	328	1	OPRX_HUMAN
33	420.5	19.0	380	1	OPRK_MOUSE

34	419	18.9	380	1	OPRK_RAT	P34975	rattus norv
35	413	18.7	370	1	OPRX_HUMAN	P41146	homo sapien
36	411.5	18.6	367	1	OPRX_MOUSE	P35377	mus muscicu
37	410.5	18.6	367	1	OPRX_RAT	P35370	rattus norv
38	409.5	18.5	333	1	OPR8_HUMAN	P48146	homo sapien
39	398	18.0	370	1	OPRX_PIG	P79292	sus scrofa
40	372.5	16.8	359	1	AG2R_CHICK	P79785	gallus gall
41	372.5	16.8	359	1	AG2R_METGA	P33396	meleagris g
42	370	16.7	363	1	AG2S_XENLA	P35373	xenopus lae
43	368	16.6	362	1	AG2R_XENLA	P32303	xenopus lae
44	359.5	16.3	352	1	P217_HUMAN	O15722	homo sapien
45	350	15.8	353	1	CKR8_MOUSE	P56484	mus muscicu

ALIGNMENTS

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RESULT 1
ID GP24_RAT
AC P97639;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Probable G protein-coupled receptor GPR24 (SLC-1).
GN GPR24 OR SLC1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA MEDLINE=98193144; PubMed=9531978;
RX lakaye B., Minet A., Zorzi W., Grisar T.,
RT "Cloning of the rat brain cDNA encoding for the SLC-1 G protein-
RL coupled receptor reveals the presence of an intron in the gene.";
RN [2]
RP SEQUENCE OF 143-300 FROM N.A.
RX MEDLINE=97131607; PubMed=8977118;
RA Kolakowski L.F. Jr., Jung B.P., Nguyen T., Johnson M.P., Lynch K.R.,
RT Cheng R., Heng H.H.Q., George S.R., O'Dowd B.F.;
RT "Characterization of a human gene related to genes encoding
RL somatostatin receptors.";
RX FEBS Lett. 398:253-258(1996).
CC -1- FUNCTION: ORPHAN RECEPTOR. DOES NOT SEEM TO BIND TO SOMATOSTATIN.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC SIMILAR TO SOMATOSTATIN RECEPTORS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb.ch/announce/
CC or send an email to license@isb.ch).
CC -----
DR EMBL: AF008650; AAC27977.1; -.
DR EMBL: U77953; AAC14588.1; -.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR InterPro: IPR004047; MCHR1receptor.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCR_Rhodopsn.
DR PRINTS: PR01507; MCHR1RECEPTOR.
DR PROSITE: PS00237; G-PROTEIN_RECEP_FL1; FALSE_NEG.
DR PROSITE: PS00262; G-PROTEIN_RECEP_FL2; 1.
KW G-protein coupled receptor; Transmembrane.
FT DOMAIN 1 45 66 1 (POTENTIAL).
FT TRANSMEM 46 66 79 1 (POTENTIAL).
FT DOMAIN 67 79 100 2 (POTENTIAL).
FT TRANSMEM 80 100 2 (POTENTIAL).

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FT DOMAIN 101 118 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 119 139 3 (POTENTIAL).
FT DOMAIN 139 161 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 140 161 4 (POTENTIAL).
FT DOMAIN 162 182 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 183 204 5 (POTENTIAL).
FT TRANSMEM 205 225 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 226 256 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 257 277 6 (POTENTIAL).
FT DOMAIN 278 294 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 295 315 7 (POTENTIAL).
FT DOMAIN 316 353 CYTOPLASMIC (POTENTIAL).
SQ SEQUENCE 353 AA; 39063 MW; F6EBB2DF381084A9 CRC64;

Query Match
Best Local Similarity 79.7%; Score 1763; DB 1; Length 353;
Matches 339; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 70 MDLEASLPTGPNASNTSGPDNLTSAGSPRTGSIYINIMPSVGTICLLGIIGNST 129
DB 1 MDLQSLSTGPNASNTSGDNLTLPGSPRTGSIYINIMPSVGTICLLGIIGNST 60

QY 130 VIFAVVKKSKLMKNNPDIITNLVVDLLFLGMPFMHOLMGKVMHFGEMCLIT 189
DB 61 VIFAVVKKSKLMKSNVDFIITNLVVDLLFLGMPFMHOLMGKVMHFGEMCLIT 120

QY 190 AMDANSOFTSYITLTAADRYLATVHPISSTKRPKSVATLVICLMAISFISPPVWL 249
DB 121 AMDANSOFTSYITLTAMTIDRYLATVHPISSTKRPKSMATLVICLMAISFISPPVWL 180

QY 250 YARLIPPGAGVGGCIRLPNDPDLVWFTLYQGFELAPLFPVYITAAVRILOMTSSVA 309
DB 181 YARLIPPGAGVGGCIRLPNDPDLVWFTLYQGFELAPLFPVYITAAVRILOMTSSVA 240

QY 310 PASORSTRKRTKRTAATACVFCVCAPIYVLOLTQISISPTLTFYLYLNAASISLG 369
DB 241 PASORSTRKRTKRTAATACVFCVCAPIYVLOLTQISISPTLTFYLYLNAASISLG 300

QY 370 YANSCLNPFYIVLCETFRKRLVSVKPAAGOLRAVSNMOTADEERTESKGT 422
DB 301 YANSCLNPFYIVLCETFRKRLVSVKPAAGOLRAVSNMOTADEERTESKGT 353

RESULT 2
GP24_HUMAN STANDARD; PRT; 402 AA.
ID GP24_HUMAN
AC 099705;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Probable G protein-coupled receptor GPR24 (SLC-1).
GN GPR24 OR SLC1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97131607; Pubmed=8977118;
RA Kolakowski L.F. Jr., Jung B.P., Nguyen T., Johnson M.P., Lynch K.R.,
RA Cheng R., Heng H.H.Q., George S.R., O'Dowd B.F.;
RT "Characterization of a human gene related to genes encoding
RT somatostatin receptors."
RL FEBS Lett. 398:253-258(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20057165; Pubmed=10591208;
RA Dunham I., Hunt A.R., Collins J.E., Bruskiewicz R., Beare D.M.,
RA Clump M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,
RA Baguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
RA Bird C.P., Blakey S.E., Bridgman A.M., Buck D., Burgess J.,
RA Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,

```

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RA Dhani P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
RA Evans K.L., Fay J.M., Fleming K., French L., Garner A.A.,
RA Gilbert J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C.,
RA Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,
RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.W., King A.,
RA Laird G.K., Langford C.F., Leverisha M.A., Lloyd C., Lloyd D.M.,
RA Marilyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,
RA Mcclay J., McLaren S., McMuray A.A., Milne S.A., Mortimore B.J.,
RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,
RA Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,
RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,
RA Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,
RA Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,
RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
RA Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,
RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyama S.,
RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,
RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shauli S., Sloan D., Song L.,
RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu M.L.,
RA Zhan M., Zhang G., Chisoe S., Murray J., Miller N., Minx P.,
RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
RA Hinds K., Kemp K., Latreille P., Layman D., Ozerky P., Rohlfing T.,
RA Scheet P., Walker C., Wamsley A., Wohlmann P., Pepin K., Nelson J.,
RA Kort I., Bedell J.A., Hillier L., Kurashiki H., Saita S., Budarf M.L.,
RA Emanuel B.S., Shaikh T., Kurashiki H., Saita S., Budarf M.L.,
RA McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E., Edelmann L.,
RA Kim U.J., Shizuya H., Simon M.I., Dunanski J.P., Peyard M., Kedra D.,
RA Serousi E., Franssen I., Tapia I., Bruder C.E., O'Brien K.P.,
RA Wilkinson P., Bodemleisch A., Hartman K., Hu X., Khan A.S., Lane L.,
RA Tiliun Y., Wright H.;
RT The DNA sequence of human chromosome 22."
RL Nature 402:489-495(1999).
CC -1- FUNCTION: ORPHAN RECEPTOR. DOES NOT SEEM TO BIND TO SOMATOSTATIN.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: GREATEST ABUNDANCE IN BRAIN, PARTICULARLY IN
CC THE FRONTAL CORTEX AND HYPOTHALAMUS. A LOWER LEVEL EXPRESSION IS
CC SEEN IN THE LIVER AND HEART.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC SIMILAR TO SOMATOSTATIN RECEPTORS.
CC -----
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CC -----
DR EMBL: U71092; AAC14587.1; -.
DR EMBL: Z86090; CAB62943.1; -.
DR GeneW: HGNC:4479; GPR24.
DR MIM: 601751; -.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR InterPro: IPR004047; MCHR1receptor.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PRINTS: PR01507; MCHR1RECEPTOR.
DR PROSITE: PS00237; G-PROTEIN_RECP_F1_1; FALSE_NEG.
DR PROSITE: PS00262; G-PROTEIN_RECP_F1_2; 1.
FT G-protein coupled receptor; Transmembrane.
FT DOMAIN 1 94 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 95 115 1 (POTENTIAL).
FT DOMAIN 116 128 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 129 149 2 (POTENTIAL).
FT DOMAIN 150 167 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 168 188 3 (POTENTIAL).
FT DOMAIN 189 210 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 211 231 4 (POTENTIAL).
FT DOMAIN 232 253 EXTRACELLULAR (POTENTIAL).

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FT TRANSMEM 254 274 5 (POTENTIAL).
RT DOMAIN 275 305 6 (POTENTIAL).
FT TRANSMEM 306 326 6 (POTENTIAL).
RT DOMAIN 327 343 6 (POTENTIAL).
FT TRANSMEM 344 364 7 (POTENTIAL).
FT DOMAIN 365 402 7 (POTENTIAL).
SQ SEQUENCE 402 AA: 44454 MW: 5D24B72E76C4F82 CRC64;

Query Match
Best Local Similarity 83.2%; Score 1696; DB 1; Length 402;
Matches 341; Conservative 7; Mismatches 14; Indels 48; Gaps 4;

QY 50 PAWEGS--SARLMEQATGTGMDLEASLPTGPNASNTSDGPDN----- 92
   | : | | : | : | | | | | | | | | | | | | | | | | | | | | |
Db 4 PSKTDGSGHSGRIHQETHGGRND-----KISN--SEGRENGRGRQNMGSLEAE 52
   | : | | : | : | | | | | | | | | | | | | | | | | | | | | |
QY 93 -----LTSAGSPRTGSIYINIMPSVFGITCLGIGNSTVIF 132
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 53 HASRMSVLRKPMNSQRLLLSPGSPPTGSIYINIMPSVFGITCLGIGNSTVIF 112
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 133 AAYKSKLHMCNNVPDIFINLSVDLFLFGMPFMIHOLMGVWHFGFTGTLITAMD 192
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 113 AAYKSKLHMCNNVPDIFINLSVDLFLFGMPFMIHOLMGVWHFGFTGTLITAMD 172
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 193 ANSQFTSYILTAADRYLATVHPISSTKFRKPSVATVLCMLALSFISITPVMLYAR 252
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 173 ANSQFTSYILTAADRYLATVHPISSTKFRKPSVATVLCMLALSFISITPVMLYAR 232
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 253 LIPEPGAGCGIRLNPDTLWFTLQFFLALPFTVITAAVRIIORMSSVAPAS 312
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 233 LIPEPGAGCGIRLNPDTLWFTLQFFLALPFTVITAAVRIIORMSSVAPAS 292
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 313 QRSIRTRKVTETAICLFEVCNAPRYVQLTOLISRPITLFTFYILNAISIGYAN 372
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 293 QRSIRTRKVTETAICLFEVCNAPRYVQLTOLISRPITLFTFYILNAISIGYAN 352
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 373 SCINPFIYVLCETFRKRLVLSYKPAAGQLRAVSAQADEBRTESKGT 422
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 353 SCINPFIYVLCETFRKRLVLSYKPAAGQLRAVSAQADEBRTESKGT 402
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 3
SSR2_MOUSE STANDARD; PRT; 369 AA.
AC P30875; P30934;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Somatostatin receptor type 2 (SS2R) (SRIF-1) (SS2RA and SS2RB).
GN SSR2 OR SMSR2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OC NCBI_TaxID=10090;
RP [1]
RX MEDLINE-92108031; PubMed-1346068;
RT "Cloning and functional characterization of a family of human and
RT mouse somatostatin receptors expressed in brain, gastrointestinal
RT tract, and kidney."
RL Proc. Natl. Acad. Sci. U.S.A. 89:251-255(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-93012001; PubMed-1397330;
RX Vanetti M., Kouba M., Wang X., Vogt G., Hoellt V.;
RT "Cloning and expression of a novel mouse somatostatin receptor
RT (SSR2B).";
RL FEBS Lett. 311:290-294(1992).
RN [3]
RP SEQUENCE OF 99-309 FROM N.A.
RX MEDLINE-94300079; PubMed-7913111;
RX Elliott D.E., Metwalli A., Blum A.M., Sandor M., Lynch R.,

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RA Weissstock J.V.;
RT "T lymphocytes isolated from the hepatic granulomas of schistosome-
RT infected mice express somatostatin receptor subtype II (SSR2)
RT messenger RNA.";
RL J. Immunol. 153:1180-1186(1994).
RN [4]
RX CHARACTERIZATION.
RP MEDLINE-93387480; PubMed-8104154;
RT Vanetti M., Hoellt V.;
RT "The two isoforms of the mouse somatostatin receptor (msSR2A and
RT msSR2B) differ in coupling efficiency to adenylylate cyclase and in
RT agonist-induced receptor desensitization.";
RL FEBS Lett. 331:260-266(1993).
RN [5]
RX FUNCTION: RECEPTOR FOR SOMATOSTATIN-14 AND -28. THIS RECEPTOR IS
RX COUPLED VIA PERTUSSIS TOXIN SENSITIVE G PROTEINS TO INHIBITION OF
RX ADENYLYL CYCLASE. IN ADDITION IT STIMULATES PHOSPHOTRANSFER
RX PHOSPHATASE AND PLC VIA PERTUSSIS TOXIN INSENSITIVE AS WELL AS
RX SENSITIVE G PROTEINS. IN RIN 5F CELLS, THIS RECEPTOR INHIBITS
RX CALCIUM ENTRY BY SUPPRESSING VOLTAGE DEPENDENT CALCIUM-CHANNELS.
RX -1 SUBUNIT: The C-terminus interacts with SHANK1 PDZ domain (by
RX similarity).
RX -1 SUBCELLULAR LOCATION: Integral membrane protein.
RX -1 ALTERNATIVE PRODUCTS: 2 ISOFORMS; SS2RA (SHOWN HERE) AND SS2RB;
RX ARE PRODUCED BY ALTERNATIVE SPLICING.
RX -1 TISSUE SPECIFICITY: CEREBRUM AND KIDNEY.
RX -1 SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
RX -----
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RX -----
CC EMBL; M81832; AAA8236.1; -.
CC EMBL; X68951; CAA48766.1; -.
CC EMBL; S71756; -. NOT_ANNOTATED_CDS.
CC PIR; D41795; D41795.
CC PIR; S29248; S29248.
CC HSSP; P02699; 1BOU.
CC MGD; MGI:98328; Smt2.
CC InterPro; IPR000276; GPCR_Rhodopsin.
CC Pfam; PF00001; 7tm.1; 1.
CC DR PRINTS: PR00237; GPCR_RHODOPSIN.
CC DR PROSITE: PS00237; G-PROTEIN_RECP_FL1; 1.
CC DR PROSITE: PS00262; G-PROTEIN_RECP_FL2; 1.
CC KW Multigene family; Lipoprotein; Palmitate; Alternative splicing.
CC FT DOMAIN 1 43
CC FT TRANSMEM 44 67
CC FT DOMAIN 68 78
CC FT TRANSMEM 79 103
CC FT DOMAIN 104 118
CC FT TRANSMEM 119 138
CC FT DOMAIN 139 161
CC FT TRANSMEM 162 181
CC FT DOMAIN 182 207
CC FT TRANSMEM 208 229
CC FT TRANSMEM 230 253
CC FT DOMAIN 254 278
CC FT TRANSMEM 279 288
CC FT DOMAIN 289 303
CC FT TRANSMEM 304 369
CC FT DOMAIN 369 389
CC FT CARBOHYD 9
CC FT CARBOHYD 22
CC FT CARBOHYD 29
CC FT CARBOHYD 32
CC FT DISULFID 115
CC FT LIPID 328
CC FT VARSPDIC 332
CC FT CONFLICT 179

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FT CONFLICT 305 305 S -> T (IN REF. 2).
SQ SEQUENCE 369 AA; 41321 MW; A78845AF74823039 CRC64;

Query Match
Best Local Similarity 31.78; Score 533; DB 1; Length 369;
Matches 118; Conservative 77; Mismatches 131; Indels 46; Gaps 10;

QY 62 EQATGTG-WM---DLEASLPTGPNASNTSDGPDNLTASASPRTGSISYINIMPSVF 116
DB 6 EQNGSQWVSSPFDLNGSLGPS--NSNGQREPYDMS-----NAVLFIFV 50
QY 117 GTICLLGIGNSVYFAVVKSKLHMCNNVPDIFITINSVVDLLFLGMPE-----MIH 170
DB 51 FVVCVVGCGMTLYVILYLRKAKM---KTITNIYILNLAIADLFMLGLPFLAMQVALVH 107
QY 171 QLMGCVHHEGEMTCTLTAMDANSQFTSYIILFAMADRLAVVHPISKREKPEPVAT 230
DB 108 -----WPFGRALCRVMTVDGNIQFTSICLTVMSIDRLAVVHPISKAKWRPRTRAK 160
QY 231 LVICLLMALSPFISITPVLVYARLLPFPAGAVGCGIRLPNPDTDY-WFTIXOFPLAALP 289
DB 161 MINVAVWCVSLILVILPIMIVAGLSNMGGRSSCIINMPGESGAMYTGFIITAFILGLFV 220
QY 230 FVVTAAVYVRILOKRTSSVAPASQSRILRKRVYTRFAIAICLVFVCMADYVYLQTL 349
DB 221 LTIIICLCYLIILIKVSSGIRVSSKRSKSEKRYTAMVSIYVAVIFICWLPFYIFNVSSV 280
QY 350 SIS-RPDLTFYVYVMAAISLGANSCLNPFYIYLCEFFERRLVLSKPAAGSLRAVSN 408
DB 261 SVAISPTPALKGMEFVVLITVYANSCANPILLYAFLLSDNFK-----SFQVNLCLVYV 332
QY 409 AQTADERTESK 420
DB 333 SGTEDGERSDK 344

RESULT 4
ID SSR2_HUMAN STANDARD; PRT; 369 AA.
AC P30874;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Somatostatin receptor type 2 (SS2R) (SRIF-1).
GN SSR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92108031; PubMed=1346068;
RA Yamada Y., Post S.R., Wang K., Tager H.S., Bell G.I., Seino S.;
RT "Cloning and functional characterization of a family of human and
RT mouse somatostatin receptors expressed in brain, gastrointestinal
RT tract, and kidney.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:251-255(1992).
RN [2]
RP ALTERNATIVE SPLICING.
RX MEDLINE=9123586; PubMed=8386508;
RA Patel Y.C., Greenwood M., Kent G., Panetta R., Strikant C.B.;
RT "Multiple gene transcripts of the somatostatin receptor SSR2: tissue
RT selective distribution and cAMP regulation.";
RL Biochem. Biophys. Res. Commun. 192:288-294(1993).
RN [3]
RP INTERACTION WITH SHANK1.
RX MEDLINE=20020275; PubMed=10551867;
RA Zilzer H., Hennek H.-H., Baechner D., Richter D., Kretzenkamp H.-D.;
RT "Somatostatin receptor interacting protein defines a novel family of
RT multidomain proteins present in human and rodent brain.";
RL J. Biol. Chem. 274:32997-33001(1999).
CC -1- FUNCTION: RECEPTOR FOR SOMATOSTATINS-14 AND -28. THIS RECEPTOR IS
CC COUPLED VIA PERTUSSIS TOXIN SENSITIVE G PROTEINS TO INHIBITION OF

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CC ADENYLYL CYCLASE. IN ADDITION IT STIMULATES PHOSPHOTYROSINE
CC PHOSPHATASE AND PLC VIA PERTUSSIS TOXIN INSENSITIVE AS WELL AS
CC SENSITIVE G PROTEINS. IN RIN 5F CELLS, THIS RECEPTOR INHIBITS
CC CALCIUM ENTRY BY SUPPRESSING VOLTAGE DEPENDENT CALCIUM-CHANNELS.
CC -1- SUBUNIT: The C-terminus interacts with SHANK1 PDZ domain.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A (SHOWN HERE) AND B; ARE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: CEREBRUM AND KIDNEY. IN LESSER AMOUNTS IN
CC JEJUNUM, COLON, AND LIVER.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC -----
DB EMBL; M81830; AAA58248.1; -.
DB F81R; B41795; B41795.
DB HSSP; P02699; 1BC0.
DB Genew; HGNC:11331; SSR2.
DB MIM; 182452; -.
DB InterPro; IP000276; GPCR_Rhodpsn.
DB Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECCEP_F1.1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECCEP_F1.2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Lipoprotein; Palmitate; Alternative splicing.
FT DOMAIN 1 43
FT TRANSMEM 44 67
FT DOMAIN 68 78
FT TRANSMEM 79 103
FT DOMAIN 104 118
FT TRANSMEM 119 138
FT DOMAIN 139 161
FT TRANSMEM 162 181
FT DOMAIN 182 207
FT TRANSMEM 208 229
FT DOMAIN 230 253
FT TRANSMEM 254 278
FT DOMAIN 279 288
FT TRANSMEM 289 303
FT DOMAIN 304 369
FT CARBOHYD 9
FT CARBOHYD 22
FT CARBOHYD 29
FT CARBOHYD 32
FT DISULFID 115 193
FT LIPID 328 328
FT VARSPIC 332 369
SQ SEQUENCE 369 AA; 41332 MW; 3B5D78BA9AC246C6 CRC64;

Query Match
Best Local Similarity 31.68; Score 531.5; DB 1; Length 369;
Matches 115; Conservative 76; Mismatches 128; Indels 45; Gaps 9;

QY 69 WM---DLEASLPTGPNASNTSDGPDNLTASASPRTGSISYINIMPSVGTICLGI 124
DB 14 WLSIPFDLNGSVST--NSNGQREPYDLS-----NAVLFIFVCCIIGL 58
QY 125 IGNSVYFAVVKSKLHMCNNVPDIFITINSVVDLLFLGMPE-----MIHQLMGNGV 178
DB 59 CGNTIVYVILYLRKAKM---KTITNIYILNLAIADLFMLGLPFLAMQVALVH-----W 108
QY 179 HEGEMTCTLTAMDANSQFTSYIILFAMADRLAVVHPISKREKRSVATVYICLLMA 238
DB 109 PFGALCRVMTVDGNIQFTSICLTVMSIDRLAVVHPISKAKWRPRTRAKMTTMAVWG 168

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OY 239 LSFSTIPVWLYARLIPFGAGVGIRLPNDTDLX-WFTLYOFPLAFALPFVITAY 297
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 169 VSLVILPIMYIAGLRBNQMRSSCTINWPGESGAMTGFILYIFLIGLPLILICLY 228
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 298 VRILOMTSSVAPASQSRIRLRTKRVTRTAICLVFEVVCAPRYVLOLQSLIS-REPL 356
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 229 LFIIRKXSSGIRVSSSKRRKSEKKTIRMVSIYAVFIFCWLPPIYFNSSVSMAISPTP 288
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 357 TFVYLVNAALISLGYANSCINPFYIVLCFEPFRKRLVSVKRAAGQLRAVNAQTAEER 416
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 289 ALKMFEPVYVLYANSCANPILYAFISDNKK-----SFQNVLCVAVSGTDGER 340
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 417 TESK 420
      : : : :
Db 341 SSK 344

RESULT 5
SSR2_BOVIN STANDARD; PRT; 368 AA.
AC P34993;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Somatostatin receptor type 2 (SS2R) (SRIF-1).
GN SSR2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_Taxid=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Xian W.W., Wong M.-L., Rimland J., Nestler E.J., Duman R.S.;
RL submitted (xxx-1992) to the EMBL/Genbank/DBD databases.
CC -1- FUNCTION: RECEPTOR FOR SOMATOSTATIN-14 AND -28. THIS RECEPTOR IS
CC COUPLED VIA PERTUSSIS TOXIN SENSITIVE G PROTEINS TO INHIBITION OF
CC ADENYLYL CYCLASE. IN ADDITION IT STIMULATES PHOSPHORYLATION
CC PHOSPHATASE AND PLC VIA PERTUSSIS TOXIN INSENSITIVE AS WELL AS
CC SENSITIVE G PROTEINS. IN RIN 5F CELLS, THIS RECEPTOR INHIBITS
CC CALCIUM ENTRY BY SUPPRESSING VOLTAGE DEPENDENT CALCIUM CHANNELS.
CC -1- SUBUNIT: The C-terminus interacts with SHANK1 PDZ domain (by
CC similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC -----
DR EMBL: I06613: AAA30764.1: -.
DR HSSP: P02699: 1BOJ.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1: 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G-PROTEIN_RECEPTOR_F1_1; 1.
DR PROSITE: PS50262; G-PROTEIN_RECEPTOR_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Lipoprotein; Palmitate.
FT DOMAIN 1 42
FT TRANSMM 43 66
FT TRANSMM 67 77
FT TRANSMM 78 102
FT TRANSMM 103 117
FT TRANSMM 118 137
FT TRANSMM 138 160
FT TRANSMM 161 180
FT TRANSMM 181 206
FT DOMAIN 181 206
FT EXTRACELLULAR (POTENTIAL).

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FT TRANSMM 207 228
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FT TRANSMM 278 287
FT TRANSMM 288 302
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FT TRANSMM 369 416
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RT GH4C1 pituitary cells."
RL Biochem. Biophys. Res. Commun. 184:131-136(1992).
RN [3]
RP ALTERNATIVE SPLICING.
RX MEDLINE=93236586; PubMed=8386508;
RA Patel Y.C., Greenwood M., Kent G., Panetta R., Srikanth C.B.;
RT "Multiple gene transcripts of the somatostatin receptor STR2: tissue
RT selective distribution and cAMP regulation."
RL Biochem. Biophys. Res. Commun. 192:288-294(1993).
CC -1- FUNCTION: RECEPTOR FOR SOMATOSTATINS-14 AND -28. THIS RECEPTOR IS
CC COUPLED VIA PERTUSSIS TOXIN SENSITIVE G PROTEINS TO INHIBITION OF
CC ADENYLATE CYCLASE. IN ADDITION IT STIMULATES PHOSPHORYLATION
CC PHOSPHATASE AND PLC VIA PERTUSSIS TOXIN INSENSITIVE AS WELL AS
CC SENSITIVE G PROTEINS. IN RAT 5F CELLS, THIS RECEPTOR INHIBITS
CC CALCIUM ENTRY BY SUPPRESSING VOLTAGE DEPENDENT CALCIUM CHANNELS.
CC -1- SUBUNIT: The C-terminus interacts with SHANK1 PDZ domain (by
CC similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A (SHOWN HERE) AND B; ARE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: CORTEX, HIPPOCAMPUS, PITUITARY GLAND, COLON
CC ADRENALS, PANCREAS-DERIVED CELL LINE, AND PANCREATIC TUMOR.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC -----
DR EMBL: M96817; AAA42166.1; -
DR EMBL: M93273; AAA42165.1; -
DR HSR: A45291; A45291.
DR HSSP: P02699; 1BOJ.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_Rhodopsn.
DR PROSITE: PS00237; G-PROTEIN RECEPTOR FL1; 1.
DR PROSITE: PS50262; G-PROTEIN RECEPTOR FL2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Lipoprotein; Palmitate; Alternative splicing.
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FT LIPID 328 328
FT VAPSLIC 332 369
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Best Local Similarity 31.5%; Pred. No. 4.6e-23;
Matches 11; Conservative 77; Mismatches 132; Indels 46; Gaps 10;
62 EQATGNG-WM---DLFASILPTGPNASNTSDPDLNLTSGSPPTGTSISYINIMPVSF 116

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QY 117 GTICLLGIIGNSVIFPAVVKSKSLHMCNNVPDIFINISVVDLFLGMP-----MIH 170
Db 51 FVYCVGLGCGNLLVIVIRAKM---KTIINIIILNLAIDELFMGLPPLAQAQVALVH 107
QY 171 QLMGNGVHFGEFTMCTLTITANDANSQFTSYITLMAIDRYLAVHPISSTKRPSSVAT 230
Db 108 -----MPEGKAICGVVTVTGINGQIFISIFCLVMSIDRYLAVHPKSAKMRPRPTAK 160
QY 231 LVICLMAISFISIPVWVLYARLIPFGAVCGIRLNPPTDLY-WFTLYQFLAALP 289
Db 161 MIVVAWGSVSLVILPIMTLAGLRNOMRSCITINWEGSANTGTITIAFLGLVLP 220
QY 290 FVITAAVYRIILQMTSSVAPASQSRIRLKRVTRTAIAICLVFVCWADYVLTQL 349
Db 221 LTIICLCYFIIITKVSISRGSKRKSEKRYRMSIYAVIFECMLFFIYFNVSIV 280
QY 350 SIS-RETLFVLYLNALISLGYANGCLNPVYIVICEFRKRLVSVKPAAGOLRAVSN 408
Db 281 SVASIPPLAKGWFDEVLITVYANGCANFLIATLSDNFKK-----SQNVLCVYK 332
QY 409 AQTADERTESEK 420
Db 333 SGAEDGERSDSK 344
RESULT 7
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ID SSR2_PIG
AC P34994;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Somatostatin receptor type 2 (SSR2) (SRIF-1).
GN SSR2.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_Taxid=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94168590; PubMed=8123027;
RA Matsumoto K., Yokogoshi Y., Fujinaka Y., Zhang C., Saito S.;
RT "Molecular cloning and sequencing of porcine somatostatin receptor
RT 2."
RL Biochem. Biophys. Res. Commun. 199:298-305(1994).
CC -1- FUNCTION: RECEPTOR FOR SOMATOSTATINS-14 AND -28. THIS RECEPTOR IS
CC COUPLED VIA PERTUSSIS TOXIN SENSITIVE G PROTEINS TO INHIBITION OF
CC ADENYLATE CYCLASE. IN ADDITION IT STIMULATES PHOSPHORYLATION
CC PHOSPHATASE AND PLC VIA PERTUSSIS TOXIN INSENSITIVE AS WELL AS
CC SENSITIVE G PROTEINS. IN RAT 5F CELLS, THIS RECEPTOR INHIBITS
CC CALCIUM ENTRY BY SUPPRESSING VOLTAGE DEPENDENT CALCIUM CHANNELS.
CC -1- SUBUNIT: The C-terminus interacts with SHANK1 PDZ domain (by
CC similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D21338; BAA04810.1; -
DR PIR: JC2083; JC2083.
DR HSSP: P02699; 1BOJ.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_Rhodopsn.

```


DB 95 IYIINLADELMLSPFLVTSILRH-WPGALLCHLVSDAVNMFTSYICLVLSV 153
 QY 209 DRYLATVHPISSTKFRKPSVATVYICLMLALSFISTPFWYLARLPFGGAVCGIRLP 268
 DB 154 DRYVAVHPDKAARRRRTAVKYNVLGWVLSLVILPIVVFSTNADSGTAVCNMLMP 213
 QY 269 NP-DTDLWFTLYOPFLAFLPFPVYITAAVYRIIQRMVTSSVAPASQSRIRLKRVTPTA 327
 DB 214 BPAQRMVLGFLVYFLMGLFLLPVGAICLCYVLIIAKMMVALKAGWQKRSEKRITLMV 273
 QY 328 IAIICVFVCPAPYAVYLDTOLISRPITFEVYLYNNAISIGYANSCINPFYIYVLCETF 387
 DB 274 MMVAVFVICMMPFYVOLVNVFAEDDQATVSQL---SVILIGANSCANPILYGFILSDNF 330
 QY 388 RK 389
 DB 331 KR 332

RESULT 9
 SSR4_HUMAN STANDARD: PRT; 388 AA.
 ID SSR4_HUMAN
 AC P31391; OGU1Y1;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Somatostatin receptor type 4 (SS4R).
 GN SSTR4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93290656; PubMed=8512564;
 RA Xu Y., Song J., Bruno J.F., Berelowitz M.;
 RT "Molecular cloning and sequencing of a human somatostatin receptor,
 RL hSSTR4.";
 RL Biochem. Biophys. Res. Commun. 193:648-652(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93248256; PubMed=8483934;
 RA Kohner L., Raulf F., Bruns C., Buettner R., Hofstaedter F.,
 RA Schuele R.;
 RT "Cloning and characterization of a fourth human somatostatin
 RT receptor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:4196-4200(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93384611; PubMed=8373420;
 RA Yamada Y., Kagimoto S., Kubota A., Yasuda K., Masuda K., Someya Y.,
 RA Ihara Y., Li Q., Imura H., Seino S., Seino Y.;
 RT "Cloning, functional expression and pharmacological characterization
 RT of a fourth (hSSTR4) and a fifth (hSSTR5) human somatostatin receptor
 RT subtype.";
 RL Biochem. Biophys. Res. Commun. 195:844-852(1993).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93302729; PubMed=8100352;
 RA Demchyshyn L.L., Strikant C.B., Sunahara R.K., Kent G., Seeman P.,
 RA van Tol H.H.M., Panetta R., Patel Y.C., Niznik H.B.;
 RT "Cloning and expression of a human somatostatin-14-selective receptor
 RT variant (somatostatin receptor 4) located on chromosome 20.";
 RL Mol. Pharmacol. 43:894-901(1993).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21638749; PubMed=11780052;
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baguley C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Beadle L.M., Beare D.M.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,

RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
 RA Coulson A., Coville G.J., Deaman R., Dhali P.D., Dunn M.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Grahm D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Hockley E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Levasialho M.H., Leverisha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConnachie L.J., McIay K., McMurtry A.A.,
 RA Malne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Pothalingam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Ross M.T., Scott C.E., Selva H.K., Showkhen R., Sims S.,
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whitaker P., Wille D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:865-871(2001).
 CC -I- FUNCTION: RECEPTOR FOR SOMATOSTATIN-14. THE ACTIVITY OF THIS
 CC CYCLASE. IT IS FUNCTIONALLY COUPLED NOT ONLY TO INHIBITION OF
 CC ADENYLATE CYCLASE, BUT ALSO TO ACTIVATION OF BOTH ARACHIDONATE
 CC RELEASE AND MITOGEN-ACTIVATED PROTEIN (MAP) KINASE CASCADE.
 CC MEDIATES ANTIPROLIFERATIVE ACTION OF SOMATOSTATIN IN TUMOR CELLS.
 CC -I- TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED IN FETAL AND ADULT
 CC BRAIN, LUNG TISSUE, STOMACH, AND IN LESSER QUANTITIES IN THE
 CC KIDNEY, PITUITARY, AND ADRENALS.
 CC -I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC
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 CC
 DR EMBL: D16826; BAAD4106.1; -
 DR EMBL: L14856; AAA623.1; -
 DR EMBL: L07833; AAA60565.1; -
 DR EMBL: L07061; -; NOT ANNOTATED_CDS.
 DR EMBL: AL049651; CAB51953.1; -
 DR PIR: JN0605; JN0605.
 DR PIR: JN0762; JN0762.
 DR HSSP: P02699; 1BOJ.
 DR GeneW: HGNC:11333; SSTR4.
 DR MIM: 182454; -
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1.1.
 DR PRINTS: PR00237; GPCRHHODOPSN.
 DR PROSITE: PS00237; G_PROTEIN_RECPEP_F1_1; 1.
 DR PROSITE: PS50262; G_PROTEIN_RECPEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family; Lipoprotein; Palmitate; Phosphorylation;
 KW Polymorphism.
 FT DOMAIN 1 46
 FT TRANSMEM 47 73
 FT DOMAIN 74 83
 FT TRANSMEM 84 104
 FT DOMAIN 105 120
 FT TRANSMEM 121 142
 FT DOMAIN 143 161
 FT TRANSMEM 162 185
 FT DOMAIN 186 208
 FT TRANSMEM 209 232
 FT DOMAIN 233 260
 FT TRANSMEM 261 280
 FT DOMAIN 281 291
 FT TRANSMEM 292 314
 FT TRANSMEM 314

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CC DOMAIN 315 388 CYTOPLASMIC (POTENTIAL).
CC CARBOHYD 24 24 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC DISULFID 119 198 BY SIMILARITY.
CC LIPID 327 327 PALMITATE (POTENTIAL).
CC VARIANT 83 83 N->T (IN DBSNP:1065191).
CC CONFLICT 284 284 /FTID=VAR_011703.
CC CONFLICT 321 321 V->F (IN REF. 4 AND 5).
CC CONFLICT 365 365 S->F (IN REF. 5).
CC SEQUENCE 388 AA; 41894 MW; 8BC0695F3BC2F5 CRC64;

Query Match 23.2%; Score 513.5; DB 1; Length 388;
Best Local Similarity 31.7%; Pred. No. 2.7e-22;
Matches 107; Conservative 74; Mismatches 118; Indels 39; Gaps 9;

QY 62 E0A0TGM0MLELALPTGPASNTSDGPDNLTSAGSPPTGTSYINIMPSVETICTL 121
DB 12 E0G1GTAM-----PSANASSAPAEAEAVAGPGDARAAGM-VAIQCIYALVCL 59
QY 122 LGIIGNSTVIFAAYVKSKSLHWCNNVDPDIFIIINLSVVDLFLFLGMEPI-----HOLMGN 175
DB 60 VGLVGNMLVIFVLIRYAKMTATN---IYLINLAVADELFMLSVFPVASSALNRH----- 111
QY 176 GWAHFGTMTCLITAMANDANSQFTSYLLTAMADRLATVHPISSTFKRSPVATVITCL 235
DB 112 --WFGSVLCRAVLSDVGLMFTSVECLTVLSYDRYAVAVHPLRAATYRRSPVAKLINLG 169
QY 236 LMAFSFISITPVMVLYARLIPFPGG-AVGGCIRLPNPTDLTX---FTLYQFLAFALPEY 291
DB 170 VWLASLVLPFAIFATPFRARAGQAVACMLQMPHP---AMSAVFVYFLLGLFPLV 225
QY 292 VITAAVRIIQRMSTSSVAPASQSRIRLRTKRTAIALICLFEVCAWAPYVQLTQLST 351
DB 226 AIGLCYLLIYGKMAVALRAGMOQRSEKTRVLVLMVVVAVLCMPFYVQLNLIV 285
QY 352 SRPTFVLYNNAISGVANSCLNPRVYVLCETPRK 389
DB 286 TSLDAT---VNVHSLILSTANSCANPLTGLFISDNFRR 320

RESULT 10
SSRL_MOUSE STANDARD; PRT; 391 AA.
AC P30873;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Somatostatin receptor type 1 (sstr) (SRIF-2).
GN SSTR1 OR SMSSTR1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92108031; PubMed=1346068;
RA Yamada Y., Post S.R., Kang K., Tager H.S., Bell G.I., Seino S.;
RT "Cloning and functional characterization of a family of human and
RT mouse somatostatin receptors expressed in brain, gastrointestinal
RT tract, and kidney.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:251-255(1992).
CC -1- FUNCTION: RECEPTOR FOR SOMATOSTATIN WITH HIGHER AFFINITY FOR
CC SOMATOSTATIN-14 THAN -28. THIS RECEPTOR IS COUPLED VIA PERTUSSIS
CC TOXIN SENSITIVE G PROTEINS TO INHIBITION OF ADENYLYL CYCLASE. IN
CC ADDITION IT STIMULATES PHOSPHOTRANSFERASE PHOSPHATASE AND NA+/H+
CC EXCHANGER VIA PERTUSSIS TOXIN INSENSITIVE G PROTEINS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: JEJUNUM AND STOMACH.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
CC EMBL; M81831; AAA8255.1; -.
CC PIR; C41795; C41795.
CC MGD; MGI:98327; Smstr1.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm1; 1.
CC PRINTS; PR00237; GPCR_RHODPSN.
CC PROSITE; PS00337; G_PROTEIN_REC_P1.1; 1.
CC PROSITE; PS50262; G_PROTEIN_REC_P1.2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein;
CC Multigene family; Lipoprotein; Palmitate.
CC DOMAIN 1 56
CC TRANSMEM 57 84 1 (POTENTIAL).
CC DOMAIN 85 94 2 (POTENTIAL).
CC TRANSMEM 95 120 2 (POTENTIAL).
CC DOMAIN 121 131 3 (POTENTIAL).
CC TRANSMEM 132 153 3 (POTENTIAL).
CC DOMAIN 154 175 4 (POTENTIAL).
CC TRANSMEM 176 196 4 (POTENTIAL).
CC DOMAIN 197 219 5 (POTENTIAL).
CC TRANSMEM 220 244 5 (POTENTIAL).
CC DOMAIN 245 270 6 (POTENTIAL).
CC TRANSMEM 271 296 6 (POTENTIAL).
CC DOMAIN 297 303 7 (POTENTIAL).
CC TRANSMEM 304 327 7 (POTENTIAL).
CC DOMAIN 328 391 7 (POTENTIAL).
CC CARBOHYD 4 4 4
CC CARBOHYD 44 44 4
CC CARBOHYD 48 48 4
CC DISULFID 130 208 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC LIPID 339 339 BY SIMILARITY.
CC SEQUENCE 391 AA; 42718 MW; 4461673956F2BD22 CRC64;

Query Match 23.0%; Score 508; DB 1; Length 391;
Best Local Similarity 30.7%; Pred. No. 5.6e-22;
Matches 111; Conservative 73; Mismatches 134; Indels 44; Gaps 8;

QY 29 PLPDCGACAPGGGGRMRMLPQPAWEGSSARLMEQATGTGWMDEASLPTGPNASNTSD 88
DB 14 PPSPPGSCG-----EGACSR-----GPSGAD---GHEEGRNASONGT 50
QY 89 GPDNLTSGSPPTGTSYINIMPSVFGTICLIGTIGNSTVIFAAYKSKSLHWCNNVPP 148
DB 51 LSEGGSA-----ILISFIYSVCLVGLCGNSMVIYVILRYAKMTATN--- 94
QY 149 IFIINLSVVDLFLGMPFIHOLMNGVHMGFMCTLITAMANDANSQFTSYLLTMAI 208
DB 95 IYIINLALADELMISVFFLVTSILLRH-WPFGALCLCLVLSVAVNMVFSITCLVLSV 153
QY 209 DRYLATVHPISSTFKRKSVAFLVLCMLALSFISITPVMVLYARLIPFGAGVCGIRLP 268
DB 154 DRYAVAVHPIKARARYRRTVAKVNLGVVSLVILIPVFSRTAANSQGTACNNMLP 213
QY 269 NP-DTDLWFTLXQFLAFALPFPVYITAAVRIIQRMSTSSVAPASQSRIRLRTKRTA 327
DB 214 EPAORMLVGFVLYFLFMGLFLLPVGALICLVLLIAKKRMVALKGMQORRSEKRTILAV 273
QY 328 IALCLVEFVCAWAPYVQLTQLSTISRPTLPFVLYNNAISGVANSCLNPRVYVLCETP 387
DB 274 MAAVWVWFICMMPFYVQLVAVFADQDATVSQL---SVILGTANSCANPLTGLFISDNF 330
QY 388 RK 389
DB 331 KR 332

RESULT 11
SSR3_HUMAN STANDARD; PRT; 418 AA.
ID SSR3_HUMAN
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AC P32745; 01-OCT-1993 (Rel. 27, Created)

DT 01-OCT-1993 (Rel. 27, Last sequence update)

DT 01-OCT-1993 (Rel. 27, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Somatostatin receptor type 3 (SS3R) (SSR-28).

GN SSR3.

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxId=9606;

XP MEDLINE=93149123; PubMed=1337145;

RA Yamada Y., Reisine T., Law S.F., Ihara Y., Kubota A., Kagimoto S.,

RA Seino M., Seino Y., Bell G.I., Seino S.;

RT "Somatostatin receptors, an expanding gene family: cloning and

RT functional characterization of human SSR3, a protein coupled to

RT adenylyl cyclase";

RL Mol. Endocrinol. 6:2136-2142(1992).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=93238970; PubMed=8097479;

RA Corness J.D., Demchishyn L.L., Seeman P., van Tol H.H.M.,

RA Strikant C.B., Kent G., Patel Y.C., Niznik H.B.;

RT "A human somatostatin receptor (SSR3), located on chromosome 22,

RT displays preferential affinity for somatostatin-14 like peptides."

RL FEBS Lett. 321:279-284(1993).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=20057165; PubMed=10591208;

RA Dunham I., Hunt A.R., Collins J.E., Bruskiewicz R., Beare D.M.,

RA Clamp M., Smit L.J., Ainscough R., Almeida J.P., Babage A.K.,

RA Baguley C., Bailey S.E., Barlow K.F., Bates K.N., Beasley O.P.,

RA Bird C.P., Blakey S.E., Bridgman A.M., Buck D., Burgess J.,

RA Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,

RA Clegg S.M., Cobley V.E., Cole G.G., Collier R.E., Connor R.,

RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,

RA Dhami P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,

RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,

RA Gilbert J.G.R., Goward M.E., Graefm D.V., Griffiths M.N.D., Hall C.,

RA Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,

RA Hunt R.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,

RA Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,

RA Martin I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,

RA Mcclay J.C.N., McLaren S., McMuray A.A., Milne S.A., Mortimore B.J.C.T.,

RA Phillips S.H., Platt R., Pearce A.V., Pearson D., Phillimore B.J.,

RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,

RA Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,

RA Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,

RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,

RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,

RA Wnoshima S., Kawasaki K., Sasaki T., Asakawa S., Kodoh J.,

RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyama S.,

RA Roe B.A., Chen F., Chu Y., Hu P., Hua A., Kenton S., Lai H., Do T.,

RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Do T.,

RA Lewis J., Lewis S., Lin S.-P., Loh P., Mala J., Nguyen T., Pan H.,

RA Pan S., Qi S., Qian Y., Ray L., Ren O., Shaull S., Sloan D., Song L.,

RA Wang Q., Wang Y., Wang Z., White J., Williamson D., Wu H., Yao Z.,

RA Zhan M., Zhang G., Chisome S., Murray J., Miller N., Minx P.,

RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw B., Bourne S.,

RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,

RA Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfing T.,

RA Schuet P., Walker C., Wamsley A., Wohlmann P., Pepin K., Nelson J.,

RA Kofit I., Bedell J.A., Hillier L., Mardis E., Waterston R., Wilson R.,

RA Emanuel B.S., Shaikh T., Kurihashi H., Saitta S., Budarf M.L.,

RA Mcmurd H.E., Johnson A., Wong A.C.C., Morrow B.E., Edelmann L.,

RA Kim U.J., Shizuya H., Simon M.I., Dumanski J.P., Peyraud M., Keda D.,

RA Seroussi E., Fransson I., Tapia I., Bruder C.E., O'Brien K.P.,

RA Wilkison P., Bodenteich A., Hartman K., Hu X., Khan A.S., Lane L.,

RA Tiahun Y., Wright H.;

RT "The DNA sequence of human chromosome 22."

RL Nature 402:489-495(1999).

CC -1- FUNCTION: RECEPTOR FOR SOMATOSTATINS-14 AND -28. THIS RECEPTOR IS

CC COUPLED VIA PERTUSSIS TOXIN SENSITIVE G PROTEINS TO INHIBITION OF

CC ADENYLYL CYCLASE

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- TISSUE SPECIFICITY: BRAIN, PITUITARY AND PANCREAS.

CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

CC -----

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CC -----

DR EMBL: M96738; AAA60592.1; -

DR EMBL: Z82188; CAB45263.1; -

DR PIR: S32501; S32501.

DR PIR: A46226; A46226.

DR HSP: P34996; 1DD.

DR Gene: HGNC:11332; SSR3.

DR MIM: 182453; -

DR InterPro: IPR00276; GPCR_Rhodopsn.

DR Pfam: PF00001; 7tm_1; 1.

DR PRINTS: PR00237; GPCR_RHODOPSN.

DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.

DR PROSITE: PS0262; G-PROTEIN_RECEP_F1_2; 1.

KM G-protein coupled receptor; Transmembrane; Glycoprotein;

KM Multigene family; Polymorphism.

FT DOMAIN 1 43

FT TRANSMEM 44 69

FT DOMAIN 70 79

FT TRANSMEM 80 101

FT DOMAIN 102 116

FT TRANSMEM 117 138

FT DOMAIN 139 161

FT TRANSMEM 162 181

FT TRANSMEM 182 205

FT TRANSMEM 206 231

FT TRANSMEM 232 257

FT TRANSMEM 258 279

FT DOMAIN 280 293

FT TRANSMEM 294 316

FT DOMAIN 317 418

FT CAROHD 17 17

FT CAROHD 30 30

FT DISULFID 116 191

FT DOMAIN 346 360

FT VARIANT 411 411

S -> T (IN DBSNP:229568).

/FTID-VAR_011853.

SQ SEQUENCE 418 AA; 45847 MW; 1227095F801190C4 CRC64;

Query Match 22.8%; Score 504.5; DB 1; Length 418;

Best Local Similarity 32.5%; Pred. No. 9.2e-22;

Matches 118; Conservative 76; Mismatches 134; Indels 35; Gaps 11;

QY 81 PNASNTSDGPDNLTSAGSP-----PRGTSIYINIMPSVFGICLLGIGNSTY 130

DB 6 PSSVSTSEPENASSAMPDATALGNVSAGPSAGLAVSGVLLPLVYLVAVGVGLGNSLV 65

QY 131 IRAYVKKSLHMCNPNDFIINLSVDFLLFLGPMFIHLMNGV--MHFGETMCTLI 188

DB 66 IYVNLHTN---SPSTNYITLNLADBLFMLGIPFLAAQ---NALSYWPGSLMCLTV 119

QY 189 TAMDANSQFTSYIITLMAIDRYLTVHPDISSTKFRKSVATLVICLLMAISITPWW 248

DB 120 MAVDGINQSTIFCLTVMSVDRYLAVHPTBSARMTAVARTVSAAVASAVVLPVV 179

QY 249 LVARLIPPGAGVGCIRLPNDTDLV--FTLQFLAFALPVPVITAAYVRLQWMT 305

DB 180 VFSGV--PRGMSCHMWPDEPA--AMRAGFIITYAALGFGLPLVLCCLLVAVR 234

QY 306 SS-----VAPASQSRIRLIRKRYTRAIAICLVFPCMAPIYVLAQTQISIRP--TLTRYV 360

D6	235	SAGRRVAMPSCQRR-RSERERVTGMVAIVAVLFLVCWMPFEYVLNVNVCPLPEEPAPFCG	293
OY	361	LYNNAISIGVANSCLINPFVYLCEETFR--KRLVLKYKPAAGQLRAVNSAQTADERT	417
DB	294	LYFLVALPVPANSCANPIIFYGLSYRFKQGRFVRLLRPSSRRVRSGQEPTVGPEKTEEDE	353
OY	418	ESK 420	
DB	354	EEE 356	
 RESULT 12			
SSRL_RAT	ID	SSRL_RAT	STANDARD; PRT; 391 AA.
AC	P28646;		
DT	01-DEC-1992 (Rel. 24, Created)		
DT	01-FEB-1992 (Rel. 24, Last sequence update)		
DT	01-FEB-1996 (Rel. 33, Last annotation update)		
DE	Somatostatin receptor type 1 (SSIR) (SRIF-2).		
GN	SSRI.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_TaxID=10116;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=Wistar; TISSUE=Brain;		
RX	MEDLINE=92096119; PubMed=1661599;		
RA	Meyerhof W., Faust H.J., Schoenrock C., Richter D.;		
RT	"Cloning of a cDNA encoding a novel putative G-protein-coupled		
RT	receptor expressed in specific rat brain regions."		
RL	DNA Cell Biol. 10:689-694(1991).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Brain;		
RX	MEDLINE=93016064; PubMed=1400442;		
RA	Li X.-T., Forte M., North R.A., Ross C.A., Snyder S.H.;		
RT	"Cloning and expression of a rat somatostatin receptor enriched in		
RT	brain."		
RL	J. Biol. Chem. 267:21307-21312(1992).		
CC	-1- FUNCTION: RECEPTOR FOR SOMATOSTATIN WITH HIGHER AFFINITY FOR		
CC	SOMATOSTATIN-14 THAN -28. THIS RECEPTOR IS COUPLED TO		
CC	PHOSPHOTRANSFERASE PHOSPHATASE AND NA+/H+ EXCHANGER VIA PERTUSSIS		
CC	TOXIN INSENSITIVE G PROTEINS.		
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.		
CC	-1- TISSUE SPECIFICITY: BRAIN, PITUITARY, ISLET, JEJUNUM, STOMACH,		
CC	HEART, SPLEEN.		
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.		
CC	-----		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -		
CC	the European Bioinformatics Institute. There are no restrictions on its		
CC	use by non-profit institutions as long as its content is in no way		
CC	modified and this statement is not removed. Usage by and for commercial		
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/or-		
CC	or send an email to license@isb-sib.ch).		
CC	-----		
DR	EMBL; X62314; CA44193.1; -		
DR	EMBL; M97656; -: NOT_ANNOTATED_CDS.		
DR	PIR; A39297; A39297.		
DR	PIR; A45102; A45102.		
DR	InterPro; IPR000276; GPCR_Rhodpsn.		
DR	Pfam; PF00001; 7tm.1; 1.		
DR	PRINTS; PR000237; GPCRRHODPSN		
DR	PROSITE; PS00237; G-PROTEIN_RECEP_FL_1; 1.		
DR	PROSITE; PS50262; G-PROTEIN_RECEP_FL_2; 1.		
KW	G-protein coupled receptor; Transmembrane; Glycoprotein;		
KW	Multiogene family; Lipoprotein; Palmitate.		
FT	DOMAIN 1	EXTRACELLULAR (POTENTIAL).	
FT	TRANSMM 57	84	1 (POTENTIAL).
FT	DOMAIN 85	94	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 95	120	2 (POTENTIAL).

Query Match	Best Local Similarity	Matches	Score	DB	Length
Query 78	PTGPASNTSGP-----DNLTSAG-SEPPRGSISY--INIMPVSGTICLLGIIGNS	128	22.5%; 32.38%; 72; 129; 17; Gaps	DB	391
DB	18 POGCGEYCSNGSPGSGADMGEEPRGNSQNGTISEGGASALLSFISYVCLVGLGNS	77			
QY	129 TVTEAVAKSKLHMCONVPDIFFIINLSVDDLFTLGMPEMHIQLMGNGWHEGETMCTLI	186			
DB	78 MWIYVILYFAKKMKATN---IYIINLALADLEMLMSVPELVTSTLIRH-WPFGALLCRVY	133			
QY	189 TAMDANSQFTSYIITLTAIDRYLATVPISTPFKRSVATVETIICLMLASFISTPPW	248			
DB	134 LSVDAVNFSTSYICLTIVLSVRYVAVNHPIAARIRRTAKVNLGVWLSLVLPIV	199			
QY	249 IYARLIPPGGAVGCGIRLPNP-DTDLVTFPLVQFFLAFLAPFVITAAYVRIQRMSS	307			
DB	194 VFSRIANSDGVACNMMLPEPDAQRWLGFLVFTFLMGFLPVGALICLYLIIAKRMV	255			
QY	308 VAPASORSIRLTKRKVYRTAATLCLVEFCVCAPIYVQLNLQLSISRPTLFFVLYNNAIS	367			
DB	254 ALKAGMQQRKSEKRTILMAMVWVWVFEVICWMPFVYVQLVNVFAEODATVSQL---SVI	310			
QY	368 IGYANSCNPFYIYVLCETPKR	389			
DB	311 LGYANSCANPLIYGLFSLDNFKR	332			
RESULT 13					
SSR4_RAT	SSR4_RAT	STANDARD:	PRT:	384 AA.	
AC	P30937;				
DT	01-JUL-1993 (Rel. 26, Created)				
DT	01-JUL-1993 (Rel. 26, Last sequence update)				
DT	01-FEB-1996 (Rel. 33, Last annotation update)				
DE	Somatostatin receptor type 4 (SS4r).				
GN	SSR4.				
OS	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus				
OX	NCBI_TaxID=10116;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Brain;				
RX	MEDLINE=93087484; PubMed=1360663;				
RA	Bruno J.F., Xu Y., Song J., Berezowltz M.;				
RT	"Molecular cloning and functional expression of a brain-specific				
RT	proc. Natl. Acad. Sci. U.S.A. 89:11151-11155(1992).				
RL	[2]				
RN	SEQUENCE FROM N.A.				
RC	STRAIN=Sprague-Dawley; TISSUE=Hippocampus;				
RA	MEDLINE=94230347; PubMed=91755684;				
RX	Bito H., Mori M., Sakanaka C., Takano T., Honda Z., Gotoh Y.,				

RA Nishida E., Shimizu T.;
 RT "Functional coupling of SSR4, a major hippocampal somatostatin
 receptor, to adenylate cyclase inhibition, archidonate release and
 RT activation of the mitogen-activated protein kinase cascade.";
 RL J. Biol. Chem. 269:12722-12730(1994).
 CC -1- FUNCTION: RECEPTOR FOR SOMATOSTATIN-14. THE ACTIVITY OF THIS
 CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH INHIBITS ADENYLATE
 CC CYCLASE. IT IS FUNCTIONALLY COUPLED NOT ONLY TO INHIBITION OF
 CC ADENYLATE CYCLASE, BUT ALSO TO ACTIVATION OF BOTH ARACHIDONATE
 CC RELEASE AND MITOGEN-ACTIVATED PROTEIN (MAP) KINASE CASCADE.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: BRAIN, LUNGS, HEART AND ISLETS. MODERATE
 CC LEVELS IN THE HIPPOCAMPUS, CORTEX, AND OLFACTORY BULB.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL: M96544; AAA42180.1; -;
 DR EMBL: U04738; AAA1519.1; -;
 DR PIR: A47249; A47249.
 DR HSSP: P02699; IBOJ.
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm1.1;
 DR PRINTS: PR00237; GPCR_Rhodpsn.
 DR PROSITE: PS00237; G-PROTEIN_REC_P1_1;
 DR PROSITE: PS00262; G-PROTEIN_REC_P1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family; Lipoprotein; Palmitate.
 FT DOMAIN 1
 FT 42 69
 FT 70 79
 FT TRANSMEM 80 105
 FT DOMAIN 106 116
 FT TRANSMEM 117 138
 FT DOMAIN 139 160
 FT TRANSMEM 161 181
 FT DOMAIN 182 203
 FT TRANSMEM 204 228
 FT DOMAIN 229 254
 FT TRANSMEM 255 280
 FT DOMAIN 281 287
 FT TRANSMEM 288 311
 FT DOMAIN 312 384
 FT CARBOHYD 21 21
 FT DISULFID 115 194
 FT LIPID 323 323
 FT SEQUENCE 384 AA; 42087 MW; 04454284922411E5 CRC64;

Query Match 22.4%; Score 494.5; DB 1; Length 384;
 Best Local Similarity 33.0%; Pred. No. 3.1e-21;
 Matches 104; Conservative 66; Mismatches 116; Indels 29; Gaps 8;

QY 85 NTSQPDNLTSAGSPRTSISYINIIIMPVFGTICLLGIIGSTVFAYVKKSKLMCN 144
 Db 21 NASNAPDEEDAVASDGTGAGMTI--QCITAYLCVLGVALVLFVILRKAKMTAT 78
 QY 145 NVPDFIINISVVDLLFLGPMFI-----HQLMGNGVHFGTMCCTLTITANDANSQFT 198
 Db 79 N---IYLLNLAVDELFLSVFVASAALRH-----WPGFVLCRAVLSVDGLMFT 128
 QY 199 STYIIITAMADRYLATAPHSISTFKRPSVATLVICLMLSPSTIPVWLVARLPFG 238
 Db 129 SVECTIVISVDRYVAVHPRAATYRRPSVAKLINTLCVWLASLVTLPVAVFADTRPARG 188
 QY 259 G-AVGGGRLNPDLDLW--FTLYQFELAFALPFVITAAVRIILQRTSSVAAPSQR 314
 Db 189 GEAVACNLHMFHP-----AMSADVITYTFLGFLPVLAIGLCITLLIVGKMAVALRGMQ 244

QY 315 STLRKRTVTRTAICLVFVCWAPYVYLQTLQSLSPRTLTFVLYNAALSLGIANSC 374
 Db 245 QRRSRSEKRTVLMVTVFVLCWMPFYVOLLNFTSLDAT---VNHVSLLSYANSC 301
 QY 375 LNPFFYVLCETPERK 389
 Db 302 ANPLTIGFLSDNRR 316

RESULT 14

SSR4_MOUSE
 ID SSR4_MOUSE STANDARD; PRT; 384 AA.
 AC P49660;
 DT 01-FEB-1996 (rel. 33, Created)
 DT 01-FEB-1996 (rel. 33, Last sequence update)
 DT 30-MAY-2000 (rel. 39, Last annotation update)
 DE Somatostatin receptor type 4 (SS4R).
 GN SSR4 OR SMSR4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/Svj; TISSUE=liver;
 RX MEDLINE=96194903; PubMed=8654950;
 RA Schwabe W., Brennan M.B., Hochgeschwender U.;
 RT "Isolation and characterization of the mouse (Mus musculus)
 RT somatostatin receptor type-4-encoding gene (SMSR4).";
 RL Gene 168:233-235(1996).
 CC -1- FUNCTION: RECEPTOR FOR SOMATOSTATIN-14. THE ACTIVITY OF THIS
 CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH INHIBITS ADENYLATE
 CC CYCLASE. IT IS FUNCTIONALLY COUPLED NOT ONLY TO INHIBITION OF
 CC ADENYLATE CYCLASE, BUT ALSO TO ACTIVATION OF BOTH ARACHIDONATE
 CC RELEASE AND MITOGEN-ACTIVATED PROTEIN (MAP) KINASE CASCADE.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----

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 CC use by non-profit institutions as long as its content is in no way
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL: U26176; AAA67561.1; -;
 DR HSSP: P02699; IBOJ.
 DR MGD: MGI:105372; Ssstr4.
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm1.1;
 DR PRINTS: PR00237; GPCR_Rhodpsn.
 DR PROSITE: PS00237; G-PROTEIN_REC_P1_1;
 DR PROSITE: PS00262; G-PROTEIN_REC_P1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family; Lipoprotein; Palmitate.
 FT DOMAIN 1
 FT 42 69
 FT 70 79
 FT TRANSMEM 80 105
 FT DOMAIN 106 116
 FT TRANSMEM 117 138
 FT DOMAIN 139 160
 FT TRANSMEM 161 181
 FT DOMAIN 182 203
 FT TRANSMEM 204 228
 FT DOMAIN 229 254
 FT TRANSMEM 255 280
 FT DOMAIN 281 287
 FT TRANSMEM 288 311
 FT DOMAIN 312 384
 FT CARBOHYD 21 21

[illegible]

Sequence 14,	Appl
Sequence 84,	App
Sequence 84,	App
Sequence 21,	Appl
Sequence 13,	Appl
Sequence 4,	Appl
Sequence 25,	Appl
Sequence 26,	Appl
Sequence 19,	Appl
Sequence 29,	Appl
Sequence 83,	App
Sequence 83,	App
Sequence 20,	Appl
Sequence 27,	Appl
Sequence 17,	Appl
Sequence 28,	Appl
Sequence 4,	Appl
Sequence 20,	App
Sequence 16,	Appl
Sequence 1,	Appl
Sequence 1,	Appl
Sequence 2,	Appl
Sequence 79,	Appl
Sequence 79,	Appl
Sequence 80,	Appl
Sequence 80,	Appl

GLUCAGON-LIKE HORMONE RECEPTOR (M

	Query Match	100.0%	Score 2212	DB 10	Length 422
	Best Local Similarity	100.0%	Pred. No. 4	8e-182	
	Matches 422	Conservative 0	Mismatches 0	Indels 0	Gaps
QY	1	MSYGAHKKGYGKRVGLGGSSGQATEEDPLPDGCACAPGGGGRMLPDPANVESSARL	60		
Db	1	MSYGAHKKGKGRVVGSGGSGQATEEDPLPDGCACAPGGGGRMLPDPANVESSARL	60		
QY	61	WEQATGTGMWDLASLLPTGPNASNTSDGPDNLTLSAGSPRTGISYINIIIMPVFGTIC	120		
Db	61	WEQATGTGMWDLASLLPTGPNASNTSDGPDNLTLSAGSPRTGISYINIIIMPVFGTIC	120		
QY	121	LLGIINSTVIFAAYVKKSLKLCNNVDPDIFINLSYVDLLFLTGMPMTHOLMGQVHFE	180		
Db	121	LLGIINSTVIFAAYVKKSLKLCNNVDPDIFINLSYVDLLFLTGMPMTHOLMGQVHFE	180		
QY	181	GFEMCLLITRAMANQPFSTYLLTMAADRYLATVHPISSTFKRPSVATLYICLMAALS	240		
Db	181	GFEMCLLITRAMANQPFSTYLLTMAADRYLATVHPISSTFKRPSVATLYICLMAALS	240		

Db 181 GETMCTLTAMANDANSOFTSTYILITAMADRYLATVHPISSTKFRKPSVATLVICLLMALS 240
QY 241 FISTIPVWLYARLIPPGGAVGCGIRLPNDPDLWFTLYOFELAFALPFVITAAVRI 300
Db 241 FISTIPVWLYARLIPPGGAVGCGIRLPNDPDLWFTLYOFELAFALPFVITAAVRI 300
QY 301 LQRMSSVAPASORSIRLTKRVTRTAICLVFVCNAPYVVLQTLQLSISRPITLTFVY 360
Db 301 LQRMSSVAPASORSIRLTKRVTRTAICLVFVCNAPYVVLQTLQLSISRPITLTFVY 360
QY 361 LYNAAISLGANSCLNPFYIYLCEFFRKRLVLSVKPAAGOLRAVSNQTADEERTESK 420
Db 361 LYNAAISLGANSCLNPFYIYLCEFFRKRLVLSVKPAAGOLRAVSNQTADEERTESK 420
QY 421 GT 422
Db 421 GT 422

RESULT 2
US-09-885-478-26
; Sequence 26, Application US/09885478
; Patent No. US2002011306A1
; GENERAL INFORMATION:
; APPLICANT: SALON, JOHN A
; APPLICANT: LAZ, THOMAS M
; APPLICANT: MAGORNY, RAISA
; APPLICANT: WILSON, AMY E
; TITLE OF INVENTION: DNA ENCODING A HUMAN MELANIN CONCENTRATING HORMONE RECEPTOR (MCHT)
; FILE REFERENCE: 1795/57453-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/885,478
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US99/31169
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 422
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: MUTATED MCH RECEPTOR
US-09-885-478-26

Query Match 99.7%; Score 2206; DB 10; Length 422;
Best Local Similarity 99.8%; Pred. No. 1,6e-181;
Matches 421; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSVGAMKKGVGRAVGLGGSGCQATEEDPLPDCGACAPGGGGRMRRLPOPAMVEGSSARL 60
Db 1 MSVGAMKKGVGRAVGLGGSGCQATEEDPLPDCGACAPGGGGRMRRLPOPAMVEGSSARL 60
QY 61 WEQATGTGMDLEASLLPTGPNASNTSDGPDNLTSAGSPRTGSIYINIMPSVFTIC 120
Db 61 WEQATGTGMDLEASLLPTGPNASNTSDGPDNLTSAGSPRTGSIYINIMPSVFTIC 120
QY 121 LGGTIGNSTVIFAVYKSKSLHMCNNVPDIFINLSVVDLFLGMPFMIHQLMGNGVWHF 180
Db 121 LGGTIGNSTVIFAVYKSKSLHMCNNVPDIFINLSVVDLFLGMPFMIHQLMGNGVWHF 180
QY 181 GETMCTLTAMANDANSOFTSTYILITAMADRYLATVHPISSTKFRKPSVATLVICLLMALS 240
Db 181 GETMCTLTAMANDANSOFTSTYILITAMADRYLATVHPISSTKFRKPSVATLVICLLMALS 240
QY 241 FISTIPVWLYARLIPPGGAVGCGIRLPNDPDLWFTLYOFELAFALPFVITAAVRI 300
Db 241 FISTIPVWLYARLIPPGGAVGCGIRLPNDPDLWFTLYOFELAFALPFVITAAVRI 300
QY 301 LQRMSSVAPASORSIRLTKRVTRTAICLVFVCNAPYVVLQTLQLSISRPITLTFVY 360
Db 301 LQRMSSVAPASORSIRLTKRVTRTAICLVFVCNAPYVVLQTLQLSISRPITLTFVY 360

QY 361 LYNAAISLGANSCLNPFYIYLCEFFRKRLVLSVKPAAGOLRAVSNQTADEERTESK 420
Db 361 LYNAAISLGANSCLNPFYIYLCEFFRKRLVLSVKPAAGOLRAVSNQTADEERTESK 420
QY 421 GT 422
Db 421 GT 422

RESULT 3
US-09-885-478-27
; Sequence 27, Application US/09885478
; Patent No. US2002011306A1
; GENERAL INFORMATION:
; APPLICANT: SALON, JOHN A
; APPLICANT: LAZ, THOMAS M
; APPLICANT: MAGORNY, RAISA
; APPLICANT: WILSON, AMY E
; TITLE OF INVENTION: DNA ENCODING A HUMAN MELANIN CONCENTRATING HORMONE RECEPTOR (MCHT)
; FILE REFERENCE: 1795/57453-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/885,478
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US99/31169
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 422
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: MUTATED MCH RECEPTOR
US-09-885-478-27

Query Match 99.5%; Score 2200; DB 10; Length 422;
Best Local Similarity 99.5%; Pred. No. 5,1e-181;
Matches 420; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSVGAMKKGVGRAVGLGGSGCQATEEDPLPDCGACAPGGGGRMRRLPOPAMVEGSSARL 60
Db 1 MSVGAMKKGVGRAVGLGGSGCQATEEDPLPDCGACAPGGGGRMRRLPOPAMVEGSSARL 60
QY 61 WEQATGTGMDLEASLLPTGPNASNTSDGPDNLTSAGSPRTGSIYINIMPSVFTIC 120
Db 61 WEQATGTGMDLEASLLPTGPNASNTSDGPDNLTSAGSPRTGSIYINIMPSVFTIC 120
QY 121 LGGTIGNSTVIFAVYKSKSLHMCNNVPDIFINLSVVDLFLGMPFMIHQLMGNGVWHF 180
Db 121 LGGTIGNSTVIFAVYKSKSLHMCNNVPDIFINLSVVDLFLGMPFMIHQLMGNGVWHF 180
QY 181 GETMCTLTAMANDANSOFTSTYILITAMADRYLATVHPISSTKFRKPSVATLVICLLMALS 240
Db 181 GETMCTLTAMANDANSOFTSTYILITAMADRYLATVHPISSTKFRKPSVATLVICLLMALS 240
QY 241 FISTIPVWLYARLIPPGGAVGCGIRLPNDPDLWFTLYOFELAFALPFVITAAVRI 300
Db 241 FISTIPVWLYARLIPPGGAVGCGIRLPNDPDLWFTLYOFELAFALPFVITAAVRI 300
QY 301 LQRMSSVAPASORSIRLTKRVTRTAICLVFVCNAPYVVLQTLQLSISRPITLTFVY 360
Db 301 LQRMSSVAPASORSIRLTKRVTRTAICLVFVCNAPYVVLQTLQLSISRPITLTFVY 360
QY 361 LYNAAISLGANSCLNPFYIYLCEFFRKRLVLSVKPAAGOLRAVSNQTADEERTESK 420
Db 361 LYNAAISLGANSCLNPFYIYLCEFFRKRLVLSVKPAAGOLRAVSNQTADEERTESK 420
QY 421 GT 422
Db 421 GT 422

RESULT 4

```

US-09-925-776-2
; Sequence 2, Application US/09925776
; Patent No. US20020038007A1
; GENERAL INFORMATION:
; APPLICANT: AMES, ROBERT S., JR.
; APPLICANT: SARAU, HENRY M.
; APPLICANT: FOLEY, JAMES J.
; APPLICANT: BERGSMAN, DEK J.
; APPLICANT: ELLIS, CATHERINE E.
; APPLICANT: CHAMBERS, JON K.
; TITLE OF INVENTION: A METHOD OF FINDING AGONIST AND
; FILE REFERENCE: GP-50003-D2
; CURRENT APPLICATION NUMBER: US/09/925,776
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/032,763
; PRIOR FILING DATE: 1996-12-11
; PRIOR APPLICATION NUMBER: 08/984,288
; PRIOR FILING DATE: 1997-12-03
; PRIOR APPLICATION NUMBER: 60/073,747
; PRIOR FILING DATE: 1998-02-05
; PRIOR APPLICATION NUMBER: 09/060,504
; PRIOR FILING DATE: 1998-04-15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 2
; LENGTH: 353
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-925-776-2

Query Match      82.5%; Score 1824; DB 10; Length 353;
Best Local Similarity 100.0%; Pred. No. 6,8e-149;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 MDEASLPLTGPNASNTSDGPDNLTSAGSPPTGSIYINIMPSVFGTICLLIGTGNST 129
DB 1 MDEASLPLTGPNASNTSDGPDNLTSAGSPPTGSIYINIMPSVFGTICLLIGTGNST 60

QY 130 VIFAAYKSKSLHMCNNVPDIFIINLSYVDLLFLGMPFMIHOLMGNGVWHFGETMCTLT 189
DB 61 VIFAAYKSKSLHMCNNVPDIFIINLSYVDLLFLGMPFMIHOLMGNGVWHFGETMCTLT 120

QY 190 AMDANSQFTSYILTAADRYLATVHPISSTFKRPSVATLVICLMAISFISTPVM 249
DB 121 AMDANSQFTSYILTAADRYLATVHPISSTFKRPSVATLVICLMAISFISTPVM 180

QY 250 YARLIPPGAVGCGIRLPNPDLDLYFTLYQFFLAFLPFIYVITAAVRILOMTSSVA 309
DB 181 YARLIPPGAVGCGIRLPNPDLDLYFTLYQFFLAFLPFIYVITAAVRILOMTSSVA 240

QY 310 PASORSIRLRTKRYRTAIAICLVFVCWAPYVLOLTQLSISRPPLTFEYLYNAAISLG 369
DB 241 PASORSIRLRTKRYRTAIAICLVFVCWAPYVLOLTQLSISRPPLTFEYLYNAAISLG 300

QY 370 YANSLNPFYIYLCETFRKRLVLSVKPAAGQLRAVSNAGTADERTESKGT 422
DB 301 YANSLNPFYIYLCETFRKRLVLSVKPAAGQLRAVSNAGTADERTESKGT 353

RESULT 5
US-09-885-478-28
; Sequence 28, Application US/09885478
; Patent No. US2002011306A1
; GENERAL INFORMATION:
; APPLICANT: SALON, JOHN A.
; APPLICANT: LAZ, THOMAS M.
; APPLICANT: NAGORNY, RAISA
; APPLICANT: WILSON, AMY E.
; TITLE OF INVENTION: DNA ENCODING A HUMAN MELANIN CONCENTRATING HORMONE RECEPTOR (MCH)
; FILE REFERENCE: 1795/57453-A-PCF-US
; CURRENT APPLICATION NUMBER: US/09/885,478

```

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; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US99/31169
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 28
; LENGTH: 353
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: MUTATED MCH RECEPTOR
US-09-885-478-28

Query Match      82.5%; Score 1824; DB 10; Length 353;
Best Local Similarity 100.0%; Pred. No. 6,8e-149;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 MDEASLPLTGPNASNTSDGPDNLTSAGSPPTGSIYINIMPSVFGTICLLIGTGNST 129
DB 1 MDEASLPLTGPNASNTSDGPDNLTSAGSPPTGSIYINIMPSVFGTICLLIGTGNST 60

QY 130 VIFAAYKSKSLHMCNNVPDIFIINLSYVDLLFLGMPFMIHOLMGNGVWHFGETMCTLT 189
DB 61 VIFAAYKSKSLHMCNNVPDIFIINLSYVDLLFLGMPFMIHOLMGNGVWHFGETMCTLT 120

QY 190 AMDANSQFTSYILTAADRYLATVHPISSTFKRPSVATLVICLMAISFISTPVM 249
DB 121 AMDANSQFTSYILTAADRYLATVHPISSTFKRPSVATLVICLMAISFISTPVM 180

QY 250 YARLIPPGAVGCGIRLPNPDLDLYFTLYQFFLAFLPFIYVITAAVRILOMTSSVA 309
DB 181 YARLIPPGAVGCGIRLPNPDLDLYFTLYQFFLAFLPFIYVITAAVRILOMTSSVA 240

QY 310 PASORSIRLRTKRYRTAIAICLVFVCWAPYVLOLTQLSISRPPLTFEYLYNAAISLG 369
DB 241 PASORSIRLRTKRYRTAIAICLVFVCWAPYVLOLTQLSISRPPLTFEYLYNAAISLG 300

QY 370 YANSLNPFYIYLCETFRKRLVLSVKPAAGQLRAVSNAGTADERTESKGT 422
DB 301 YANSLNPFYIYLCETFRKRLVLSVKPAAGQLRAVSNAGTADERTESKGT 353

RESULT 6
US-09-895-686-2
; Sequence 2, Application US/09895686
; Patent No. US20020106655A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN GPCR PROTEINS
; FILE REFERENCE: PC-0044 CIP
; CURRENT APPLICATION NUMBER: US/09/895,686
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PERL Program
; SEQ ID NO: 2
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020106655A1 1459432C01
US-09-895-686-2

Query Match      81.7%; Score 1808; DB 10; Length 353;
Best Local Similarity 99.2%; Pred. No. 1,6e-147;
Matches 350; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 70 MDEASLPLTGPNASNTSDGPDNLTSAGSPPTGSIYINIMPSVFGTICLLIGTGNST 129
DB 1 MDEASLPLTGPNASNTSDGPDNLTSAGSPPTGSIYINIMPSVFGTICLLIGTGNST 60

```

```

RESULT 7
US-09-885-478-4
: Sequence 4, Application US/09885478
: Patent No. US20020111306A1
: GENERAL INFORMATION:
: APPLICANT: SALON, JOHN A
: APPLICANT: LAZ, THOMAS M
: APPLICANT: NAGORNY, RAISA
: APPLICANT: WILSON, AMY E
: TITLE OF INVENTION: DNA ENCODING A HUMAN MELANIN CONCENTRATING HORMONE RECEPTOR (MCHT)
: TITLE OF INVENTION: USES THEREOF
: FILE REFERENCE: 1/95/57453-A-PCT-US
: CURRENT APPLICATION NUMBER: US/09/885,478
: CURRENT FILING DATE: 2001-09-24
: PRIOR APPLICATION NUMBER: PCT/US99/31169
: PRIOR FILING DATE: 1999-12-30
: NUMBER OF SEQ ID NOS: 28
: SOFTWARE: patentIn version 3.1
: SEQ ID NO 4
: LENGTH: 353
: TYPE: PRT
: ORGANISM: RATTUS NORVEGICUS
US-09-885-478-4

```

```

RESULT 8
US-09-990-940-19
; Sequence 19, Application US/09990940
; Publication No. US20030027252A1
GENERAL INFORMATION:
APPLICANT: Tian, Hui
APPLICANT: Zhao, Jiayang
APPLICANT: Chen, Jin-Long
APPLICANT: Cutler, Gene
APPLICANT: An, Songzhu
APPLICANT: Dai, Kang
APPLICANT: Gupta, Jamila S.
APPLICANT: Tularik Inc.
TITLE OF INVENTION: No. US20030027252a1e1 Receptors
FILE REFERENCE: 018781-007410US
CURRENT APPLICATION NUMBER: US/09/990,940
CURRENT FILING DATE: 2001-11-21
PRIORITY APPLICATION NUMBER: US 60/252,841
PRIORITY FILING DATE: 2000-11-22
PRIORITY APPLICATION NUMBER: US 60/257,636
PRIORITY FILING DATE: 2000-12-22
PRIORITY APPLICATION NUMBER: US 60/261,377
PRIORITY FILING DATE: 2001-01-12
PRIORITY APPLICATION NUMBER: US 60/279,554
PRIORITY FILING DATE: 2001-03-28
PRIORITY APPLICATION NUMBER: US 60/280,696
PRIORITY FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 19
LENGTH: 402
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human melanin-concentrating hormone receptor
US-09-990-940-19

```

	Query Match	76.7%;	Score 1696;	DB 9;	Length 402;
	Best Local Similarity	83.2%;	Pred. No.7.5e-138;		
	Matches 344;	Conservative	7;	Mismatches 14;	Indels 48;
					Gaps 4;
QY	50	PAMVGS--SARLEQATGTGMDLEASLPTGPNASNTSDGPDN-----	92		
		: : : : : : : : : : : : : :			
Db	4	PSKIDGSGHSORIRHETHEGKRD-----KISN-SEGRENGGRGFQNGGSLBAE	52		
QY	93	-----LTSAGSPRTGISITINIMSVFCTLLGLIGNSTYIF	132		
Db	53	HASRMSTVLAKPMNSQSRLLLSPESPRTGISITINIMSVFCTLLGLIGNSTYIF	112		
QY	133	AVVKKSKLHKMCNNVPDIFITINLSYVDLFLFGMPMIHOLMGNGVWHGETMCTITAMD	192		
Db	113	AVVKKSKLHKMCNNVPDIFITINLSYVDLFLFGMPMIHOLMGNGVWHGETMCTITAMD	172		
QY	193	ANSQSTSYIITLAMAIDRYLATVHPISSSTKRRKPSVAFLVLCMLALSFISITTPWLYAR	252		
Db	173	ANSQSTSYIITLAMAIDRYLATVHPISSSTKRRKPSVAFLVLCMLALSFISITTPWLYAR	232		
QY	253	LIPFGGAVGGGIRLPNDPTDLVYPTLQOFLAPLAPFVYITAAVRLIQRRTSSVAPAS	312		
Db	233	LIPFGGAVGGGIRLPNDPTDLVYPTLQOFLAPLAPFVYITAAVRLIQRRTSSVAPAS	292		
QY	313	QRSILRFRKRYTRFAIAICLVEFYCWMAYYVYLQQLQSLISRPITLFFVLYLNAAISLGYAN	372		
Db	293	QRSILRFRKRYTRFAIAICLVEFYCWMAYYVYLQQLQSLISRPITLFFVLYLNAAISLGYAN	352		
QY	373	SCLNDFVYIVLCETFRKRLVLSVCPAAGQQLRAVSNNAQTADBEERESGCT	422		
Db	353	SCLNDFVYIVLCETFRKRLVLSVCPAAGQQLRAVSNNAQTADBEERESGCT	402		

```
RESULT 9
US-09-864-761-38414
; Sequence 38414, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aemulca-X-1
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 38414
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO 286090.10
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.67
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.78
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.74
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.72
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.1
; OTHER INFORMATION: EST_HUMAN HIT: BE701073.1, EVALU6 6.00e-44
; OTHER INFORMATION: SWISSPROT HIT: Q99705, EVALU6 0.00e+00
US-09-864-761-38414

Query Match      55.3%; Score 1224; DB 10; Length 239;
Best Local Similarity 100.0%; Pred. No. 1.1e-97;
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Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 184 MCTLTITMDANSQFTSYIITLTAIDRYLATVHPDISSTKRKRSVATLVICLMAISFIS 243
|||||
Db 1 MCTLTITMDANSQFTSYIITLTAIDRYLATVHPDISSTKRKRSVATLVICLMAISFIS 60
QY 244 ITTPTVLTARLIPPGGAVGGGIRLPNPDITLYWFTLQFPLAFAPVVTAAVRLIQR 303
|||||
Db 61 ITTPTVLTARLIPPGGAVGGGIRLPNPDITLYWFTLQFPLAFAPVVTAAVRLIQR 120
|||||
QY 304 MTSVAPASQSRIRLRTKRYTRTAIAICLVFVCMAFYVYLQTLQSLSPRTLTFVLYN 363
|||||
Db 121 MTSVAPASQSRIRLRTKRYTRTAIAICLVFVCMAFYVYLQTLQSLSPRTLTFVLYN 180
|||||
QY 364 AAISLGYANSCINPFYIVICETFRKLVYSVPAAGQIRANVNAQTADERTESKGT 422
|||||
Db 181 AAISLGYANSCINPFYIVICETFRKLVYSVPAAGQIRANVNAQTADERTESKGT 239
|||||

RESULT 10
US-09-791-932-117
; Sequence 117, Application US/09791932
; Publication No. US2003003451A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Paredi, Luis A.
; APPLICANT: Hiebsch, Ronald R.
; APPLICANT: Lind, Peter
; APPLICANT: Kayles, Paul S.
; APPLICANT: Ruff, Valerie
; APPLICANT: Huff, Rita M.
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: No. US2003003451A1e1 G Protein-Coupled Receptors Cross-Refe
; FILE REFERENCE: 00325.US1
; CURRENT APPLICATION NUMBER: US/09/791,932
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/184,305
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,304
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,303
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,397
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,880
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,247
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,397
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/217,369
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/217,370
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/218,492
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: 60/186,810
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/188,064
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: 60/186,457
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: 60/213,861
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/194,344
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: 60/218,337
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 117
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-932-117
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Db      35 VILPSPMIGIICSGVLGNLIVFTIIISRSK-----KYVPDIYICLNAAVDLVHYGMFELI   90
               : : | | | : : | | : : : | | | | : | | | : : | | | : : | | | :
QY      170 HOLMGNGVWHFGETMCTLTITAMDANSOFTSTYYILTAMADRYLATVHPDISYTKRKRCSVA   229
               || : | | : | | : | | : | | : | | : | | : | | : | | : | | :
Db      91 HOMARGEWEVGGLCTTIITSIDTCNOFACSAIMTVMSVPRYFALVOPFLTRIRTRYKT    150
QY      230 TLIVCLLMIAFSITFPVMYLARLIIPPGGAVGCCIRLPNDPTDLWFTLYQFFLAFLP    289
               : | | | | : | | : | | : | | : | | : | | : | | : | | : | | :
Db      151 IRLUGIMASFIPLAEVWYWSKYIKFKDGVCSCAPFLTSPD-DVLMVTXLTLITTFEFP    209
QY      290 FVVITTAAYRLL-----QRMTSVAPASQRSI-RLRTKRVTRTAAICLVEFCWAPIYV   343
               : | | : | | : | | : | | : | | : | | : | | : | | : | | :
Db      210 LPLIIVCIILLICTYMEWOQNKDARCNCNSVPRQBYMKLTKMLVLYVVVFILISAIFYHV   269
QY      344 LOLTLQSLRPTELFVLYLYNAISLSGYANSCINFEFYITCEPFRRKLRYLSVKPPAAGOL   403
               : | | : | | : | | : | | : | | : | | : | | : | | : | | :
Db      270 IQVLNLDMEOPTLFIFYGYIYSICLSYASSINFFLIILLSGNOKRLPOLQRATEKEI    329
QY      404 RAVSN 408
               : |
Db      330 NNMGN 334

RESULT 12
US-09-885-478-16
; Sequence 16, Application US/09885478
; Patent No. US20020111306A1
; GENERAL INFORMATION:
; APPLICANT: SALON, JOHN A
; APPLICANT: LAZ, THOMAS M
; APPLICANT: MAGORNY, RAISA
; APPLICANT: WILSON, AMY E
; TITLE OF INVENTION: DNA ENCODING A HUMAN MELANIN CONCENTRATING HORMONE RECEPTOR (M
; FILE REFERENCE: 1795/57453-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/885,478
; PRIORITY FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US99/31169
; PRIORITY FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 16
; LENGTH: 100
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: MUTATION CLONE
; US-09-885-478-16

Query Match          24.3%; Score 538; DB 10; Length 100;
Best Local Similarity 98.0%; Pred. No. 2,3e-39;
Matches 98; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 MSVGAMKKGVGRAVGLGGSGCAATEEDPLPDGCAGAPGCGRRMRRLQPAPWEGSSARKL 60
               ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| |||||
Db      1 MSVAMMKGVGTAVGLGGSGCAATEEDPLPDGCAGAPGCGRRMRRLQPAPWEGSSARKL 60
QY      61 WEATGTGMMDLFASILPTGPNASNTSDGPNLTGSAGSPP 100
               ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| |||||
Db      61 WEATGTGMMDLFASILPTGPNASNTSDGPNLTGSAGSPP 100

RESULT 13
US-09-885-478-17
; Sequence 17, Application US/09885478
; Patent No. US20020111306A1
; GENERAL INFORMATION:
; APPLICANT: SALON, JOHN A
; APPLICANT: LAZ, THOMAS M
; APPLICANT: MAGORNY, RAISA
; APPLICANT: WILSON, AMY E
; TITLE OF INVENTION: DNA ENCODING A HUMAN MELANIN CONCENTRATING HORMONE RECEPTOR (M

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;; TITLE OF INVENTION: USES THEREOF
;; FILE REFERENCE: 1795/57453-A-PCT-US
;; CURRENT APPLICATION NUMBER: US/09/885,478
;; CURRENT FILING DATE: 2001-09-24
;; PRIOR APPLICATION NUMBER: PCT/US99/31169
;; PRIOR FILING DATE: 1999-12-30
;; NUMBER OF SEQ ID NOS: 28
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 17
;; LENGTH: 100
;; TYPE: PRT
;; ORGANISM: ARTIFICIAL SEQUENCE
;; OTHER INFORMATION: MUTATION CLONE
US-09-885-478-17

Query Match 24.3%; Score 538; DB 10; Length 100;
Best Local Similarity 98.0%; Pred. No. 2, 3e-39;
Matches 98; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSVGA MKKGVRAVGLGGSCQATEEDPLPCGACAPGGGRRRLPQPAWEGSSARL 60
Db 1 MSVGA MKKGVRAVGLGGSCQATEEDPLPCGACAPGGGRRRLPQPAWEGSSARL 60
QY 61 WEQATGTGMDLEASLPTGPNASNTSDGPDNLTSAGSP 100
Db 61 WEQATGTGMDLEASLPTGPNASNTSDGPDNLTSAGSP 100

RESULT 14

US-09-823-114-9
; Sequence 9, Application US/09823114
; Patent No. US20020061554A1

;; GENERAL INFORMATION:
;; APPLICANT: EVANS, CHRISTOPHER J.
;; KEITH, DUANE E.
;; TITLE OF INVENTION: OPIOID RECEPTOR GENES
;; NUMBER OF SEQUENCES: 25
;; CORRESPONDENCE ADDRESSES:
;; ADDRESSEE: MORRISON & FOERSTER
;; STREET: 2000 PENNSYLVANIA AVENUE, NW, Suite 5500
;; CITY: WASHINGTON
;; STATE: DC
;; COUNTRY: USA
;; ZIP: 20006-1888
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/823,114
;; FILING DATE: 29-Mar-2001
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 09/148,351
;; FILING DATE: <Unknown>
;; ATTORNEY/AGENT INFORMATION:
;; NAME: MURASHIGE, KATE H.
;; REGISTRATION NUMBER: 29,959
;; REFERENCE/DOCKET NUMBER: 22000-20526.22
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 887-1500
;; TELEFAX: (202) 887-0763
;; TELE: 90-4030 MRSNFOERSWSH
;; INFORMATION FOR SEQ ID NO: 9:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 369 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-09-823-114-9

Query Match 23.8%; Score 527; DB 10; Length 369;
Best Local Similarity 31.5%; Pred. No. 1e-37;
Matches 117; Conservative 77; Mismatches 132; Indels 46; Gaps 10;

QY 62 EQATGTG-WM----DEASLPLTPGPNASNTSDGPDNLTSAGSPPTGSGISYINIIIMPVSF 116
Db 6 EQFGSQWIPSPEDLNGSLGPS--NGSNQTEPYDMTS-----NAVLTFLY 50
QY 117 GTICLLIGNSYVIFAVVAKSKLHMCONVDPDIFILNSVDDLFLGMPF-----MII 170
Db 51 FVVCVAGLCGNTLYIVYIIRYAKK---KTTNIIYIINLAIDELFMGLPFLAMQVALVH 107
QY 171 QLMGNGVHPEGETNCTLIITAMDNSQFTSYIITANAIIDRYLATVHPISSTFKRPSVAT 230
Db 108 -----WPEGKAICRYVMTVDGINQFTSYFCLTVMSIDRYLAVHPIRKSAWRPRRTAK 160
QY 231 LVICLLMALSPISITPWLARLIPFPFGAVGGGIRLPNDVDLY-NFTLYQFLAFLAP 289
Db 161 MINVAVGVSLLVILPIMITAGLRSNOMGRSSCTIMPGSGAMTYGFIITAFILGFLVP 220
QY 290 FVITAAVYRLLQMTSSVAPASQSRIRLRTKRYTRTAIALCLFVFCAPYYVILQTLQ 349
Db 221 LTIIICLYFIIRKSSGIRVSSKRRKSEKRYTRVSVIVAVFIICWLPFIYFVSSV 280
QY 350 SIS-RPTITFYILNNAISIGYANSCINPFYIVLCETPFKRLVLSVKPAAGQGLRAVSN 408
Db 281 SVALSPPALGMDFEVVILITVANSCLPILVAFILSDNEK-----SFQNVLCVAV 332
QY 409 AQTADERTESK 420
Db 333 SGAEIDGERSDK 344

RESULT 15

US-09-990-940-20
; Sequence 20, Application US/09990940
; Publication No. US20030027252A1

;; GENERAL INFORMATION:
;; APPLICANT: Tian, Hui
;; APPLICANT: Zhao, Jiegang
;; APPLICANT: Chen, Jin-Long
;; APPLICANT: Cutler, Gene
;; APPLICANT: An, Songzhu
;; APPLICANT: Dai, Kang
;; APPLICANT: Gupta, Jamila S.
;; APPLICANT: Tularik Inc.
;; TITLE OF INVENTION: No. US20030027252A1el Receptors
;; FILE REFERENCE: 018781-007410US
;; CURRENT APPLICATION NUMBER: US/09/990,940
;; CURRENT FILING DATE: 2001-11-21
;; PRIOR APPLICATION NUMBER: US 60/252,841
;; PRIOR FILING DATE: 2000-11-22
;; PRIOR APPLICATION NUMBER: US 60/257,636
;; PRIOR FILING DATE: 2000-12-22
;; PRIOR APPLICATION NUMBER: US 60/261,377
;; PRIOR FILING DATE: 2001-01-12
;; PRIOR APPLICATION NUMBER: US 60/279,554
;; PRIOR FILING DATE: 2001-03-28
;; PRIOR APPLICATION NUMBER: US 60/280,696
;; PRIOR FILING DATE: 2001-03-29
;; NUMBER OF SEQ ID NOS: 54
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 20

;; LENGTH: 391
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: human somatostatin receptor 1 (SSTR1)
US-09-990-940-20

Query Match 23.2%; Score 514; DB 9; Length 391;
Best Local Similarity 30.7%; Pred. No. 1.4e-36;

[illegible]

Db 181 TGGAGACAGGCGACCGGACCTGCTGGATGAGACCTGGAAAGCCTGCTGCTCCACTGCT 240
Qy 241 CCCAATGCGACGACACACCTCTGATGGCCCGATTAACCTCACTTACAGAGATACCTGCT 300
Db 241 CCCAATGCGACGACACACCTCTGATGGCCCGATTAACCTCACTTACAGAGATACCTGCT 300
Qy 301 CGCAGGGGGAGCATCTCTTACATCAATCATCATATGCTTGGGTGGGTGGGACCATCTGC 360
Db 301 CGCAGGGGGAGCATCTCTTACATCAATCATCATATGCTTGGGTGGGTGGGACCATCTGC 360
Qy 361 CTCTTGGGACATCGGGAAGTCCAGGCTATCTTCCGGGTCTGGAAGAAGTCCAGGCTG 420
Db 361 CTCTTGGGACATCGGGAAGTCCAGGCTATCTTCCGGGTCTGGAAGAAGTCCAGGCTG 420
Qy 421 CACTGTGTCACACAGTCCCGACATCTTCATCATCAACCTCTCGGTAGATATCTCTTC 480
Db 421 CACTGTGTCACACAGTCCCGACATCTTCATCATCAACCTCTCGGTAGATATCTCTTC 480
Qy 481 TTTCTCTGGGACATGACCTTCTCATGATCCACAGCTATGGGCAATGGGGTGTGGACTTT 540
Db 481 TTTCTCTGGGACATGACCTTCTCATGATCCACAGCTATGGGCAATGGGGTGTGGACTTT 540
Qy 541 GGGGAGACCATGTGACCTCTCATACAGGCAATGATGATGATGATGATGATGATGATGAT 600
Db 541 GGGGAGACCATGTGACCTCTCATACAGGCAATGATGATGATGATGATGATGATGATGAT 600
Qy 601 TACATCTGACCGGACATGACGCTATGACGCTTACCTGGGCAATGCAACCCCATCTCTTC 660
Db 601 TACATCTGACCGGACATGACGCTATGACGCTTACCTGGGCAATGCAACCCCATCTCTTC 660
Qy 661 ACGAAGTTCGGGAAGCCCTCTGTGGCCACCCCTGATCTGCTCTGTGGGCTCTCTCC 720
Db 661 ACGAAGTTCGGGAAGCCCTCTGTGGCCACCCCTGATCTGCTCTGTGGGCTCTCTCC 720
Qy 721 TTTCTAGCATCAACCTCTGTGGCTATGCCAGACATCTTCCCTTCCAGAGAGTGA 780
Db 721 TTTCTAGCATCAACCTCTGTGGCTATGCCAGACATCTTCCCTTCCAGAGAGTGA 780
Qy 781 GTGGGCTGCGGACATGACGCTGTGGCCCAACCCAGACATGACCTTACCTGACCTGTAC 840
Db 781 GTGGGCTGCGGACATGACGCTGTGGCCCAACCCAGACATGACCTTACCTGACCTGTAC 840
Qy 841 CAGTTTCTCTGCGCTTGTGCTTGTGCTATGACAGCCGCAATACGTGAGATG 900
Db 841 CAGTTTCTCTGCGCTTGTGCTTGTGCTATGACAGCCGCAATACGTGAGATG 900
Qy 901 CTGACGCGCATGAGCTCTGAGTGGGCCCGGCTCCAGGCGAGCATCCGGCTGCGGACA 960
Db 901 CTGACGCGCATGAGCTCTGAGTGGGCCCGGCTCCAGGCGAGCATCCGGCTGCGGACA 960
Qy 961 AAGAGGCTGACCGGACAGCATGCGCATGCTGTGCTTCTTGTGTGTGGGACCC 1020
Db 961 AAGAGGCTGACCGGACAGCATGCGCATGCTGTGCTTCTTGTGTGTGGGACCC 1020
Qy 1021 TACTATGTGCTTACAGCTGACAGTGTGCTATGACGCGCCGCACTTGTGTAC 1080
Db 1021 TACTATGTGCTTACAGCTGACAGTGTGCTATGACGCGCCGCACTTGTGTAC 1080
Qy 1081 TTTTACAAATGCGGCGCATGACCTTGGGCTATGCAACAGCTGCTCAACCCCTTGTGTAC 1140
Db 1081 TTTTACAAATGCGGCGCATGACCTTGGGCTATGCAACAGCTGCTCAACCCCTTGTGTAC 1140
Qy 1141 ATCGTGTCTGTGAGAGCTTCCGAAAGCTTGTGCTGTGGTGAAGCTGTGAGCCGAG 1200
Db 1141 ATCGTGTCTGTGAGAGCTTCCGAAAGCTTGTGCTGTGGTGAAGCTGTGAGCCGAG 1200
Qy 1201 GGGCAGCTTTCGCGCTGTCAAGAACGCTCAAGAGGCTGACGAGAGAGAGAGAGAGAGAG 1260
Db 1201 GGGCAGCTTTCGCGCTGTCAAGAACGCTCAAGAGGCTGACGAGAGAGAGAGAGAGAGAG 1260
Qy 1261 GGCACCTGA 1269
Db 1261 GGCACCTGA 1269

RESULT 2
US-09-925-776-1
; Sequence 1, Application US/09925776
; Patent No. US2002038007A1
; GENERAL INFORMATION:
; APPLICANT: AMES, ROBERT S., JR.
; APPLICANT: SARAU, HENRY M.
; APPLICANT: FOLEY, JAMES J.
; APPLICANT: BERGSMAN, DEBK J.
; APPLICANT: ELLIS, CATHERINE E.
; APPLICANT: CHAMBERS, JON K.
; TITLE OF INVENTION: A METHOD OF FINDING AGONIST AND
; TITLE OF INVENTION: ANTAGONIST TO HUMAN IICB SPLICE VARIANT
; FILE REFERENCE: GP-50003-02
; CURRENT FILING DATE: 2001-08-09
; PRIOR FILING DATE: 1996-12-11
; PRIOR FILING DATE: 1996-12-11
; PRIOR FILING DATE: 1997-12-03
; PRIOR FILING DATE: 1997-12-03
; PRIOR FILING DATE: 1998-02-05
; PRIOR FILING DATE: 1998-02-05
; PRIOR FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FASTSEQ For Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1385
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-925-776-1

Query Match 97.5%; Score 1237.4; DB 10; Length 1385;
Best Local Similarity 99.9%; Pred. No. 7.3e-285;
Matches 1238; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 31 GGGAGGAGAGTGGGCTTGGAGGCGGACGCGGCTGACGAGTACGAGAGAGAGAGAGAGAGAG 90
Db 66 GGGAGGAGAGTGGGCTTGGAGGCGGACGCGGCTGACGAGTACGAGAGAGAGAGAGAGAGAG 125
Qy 91 CCGGACCTGCGGGGCTTGGGCTCCGGGACAGGTGACAGGCTGAGAGCTCCGACGCT 150
Db 126 CCGGACCTGCGGGGCTTGGGCTCCGGGACAGGTGACAGGCTGAGAGCTCCGACGCT 185
Qy 151 GCGTGGTGGAGGAGGAGCTGACGCTGCTGTGGAGAGAGGAGGAGGAGGAGGAGGAGG 210
Db 186 GCGTGGTGGAGGAGGAGCTGACGCTGCTGTGGAGAGAGGAGGAGGAGGAGGAGGAGGAG 245
Qy 211 GACCGGAGAGGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 270
Db 246 GACCGGAGAGGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 305
Qy 271 GATTAACCTCACTTACAGAGATCACTTCCGCAAGGAGGAGATCTCTACATCAATC 330
Db 306 GATTAACCTCACTTACAGAGATCACTTCCGCAAGGAGGAGATCTCTACATCAATC 365
Qy 331 ATCATGCTTGGGTGCTGCGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 390
Db 366 ATCATGCTTGGGTGCTGCGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 425
Qy 391 ATCTTGGGAGGCTGGAAGATGCAAGTGTGCAAGTGTGCAAGTGTGCAAGTGTGCAAGTGTG 450
Db 426 ATCTTGGGAGGCTGGAAGATGCAAGTGTGCAAGTGTGCAAGTGTGCAAGTGTGCAAGTGTG 485
Qy 451 ATCATCACTCTGCTGATGATCTCTCTTCTCTGCGGAGATGCTCTCATGATGATGATGATG 510
Db 486 ATCATCACTCTGCTGATGATCTCTCTTCTCTGCGGAGATGCTCTCATGATGATGATGATG 545
Qy 511 CAGCTCATGAGGCAATGGGAGTGGGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 570
Db 546 CAGCTCATGAGGCAATGGGAGTGGGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 605

OY	571	ATGGATGGCAATTAATGATTACAGAGACCTACATCTGTAACGGCAATGGCCATTACAGC	630
Db	606	ATGGATGGCAATTAATGATTACAGAGACCTACATCTGTAACGGCAATGGCCATTACAGC	665
OY	631	TACCTGGCCACTGTGCACCCCATCTCTCCACGAAATTCCGGGAAGCCCTGTGGCCACC	690
Db	666	TACCTGGCCACTGTGCACCCCATCTCTCCACGAAATTCCGGGAAGCCCTGTGGCCACC	725
OY	681	CTGGGTGATCTTGCCCTCTGTGGGCCCTCTCTTATATAGATCAACCCCTGTGTGGCTGAT	750
Db	726	CTGGGTGATCTTGCCCTCTGTGGGCCCTCTCTTATATAGATCAACCCCTGTGTGGCTGAT	785
OY	751	GCCAGACTATCCCTTCCTCCAGAGAGGTGCAGTGGGTGGGGCATACAGCCTGCCCAACCA	810
Db	786	GCCAGACTATCCCTTCCTCCAGAGAGGTGCAGTGGGTGGGGCATACAGCCTGCCCAACCA	845
OY	811	GACACTGACTCTACTGTGGTTACCCCTGTACCAAGTTTTCCTGTGGCTTGTGCCCTGCTTTT	870
Db	846	GACACTGACTCTCTACTGTGGTTACCCCTGTACCAAGTTTTCCTGTGGCTTGTGCCCTGCTTTT	905
OY	871	GTCGTCATCAACAGCCGGATACGTAGAGAGATCTGCACGGCATACAGCTCCCAATGGGCCCC	930
Db	906	GTCGTCATCAACAGCCGGATACGTAGAGAGATCTGCACGGCATACAGCTCCCAATGGGCCCC	965
OY	931	GCTTCCCAGCGCAGCATTCGGGCTGCGGACAAAGGGGTGACCCGCAACAGCCATCGCCATC	990
Db	966	GCTTCCCAGCGCAGCATTCGGGCTGCGGACAAAGGGGTGACCCGCAACAGCCATCGCCATC	1025
OY	991	TGTCTGGCTCTCTTGTGTGTCTGGGGACCCCTACTATGTCTCTACGCTGACCCAGTTGGCC	1055
Db	1026	TGTCTGGCTCTCTTGTGTGTCTGGGGACCCCTACTATGTCTCTACGCTGACCCAGTTGGCC	1085
OY	1051	ATCAGCGCGCCGACCCCTCACCTTTGTCTACTTATACAAATGCGGCACTACGCTTGGGCTAT	1110
Db	1086	ATCAGCGCGCCGACCCCTCACCTTTGTCTACTTATACAAATGCGGCACTACGCTTGGGCTAT	1145
OY	1111	GCCAAAGCTGCTCCCAACCCCTTGTGTATACATGTGTCTCTGTAGAACGTTCCGCAAAAGC	1170
Db	1146	GCCAAAGCTGCTCCCAACCCCTTGTGTATACATGTGTCTCTGTAGAACGTTCCGCAAAAGC	1205
OY	1171	TTGGTCTGCTGTGGAAGCCTGTGACGCCACAGGGGACACTTCGCGCTGTACGAACCTCAG	1230
Db	1206	TTGGTCTGCTGTGGAAGCCTGTGACGCCACAGGGGACACTTCGCGCTGTGTACGAACCTCAG	1265
OY	1231	ACGGCTGACGAGAGAGAGAACAAAGAACGACCTGA	1269
Db	1266	ACGGCTGACGAGAGAGAGAACAAAGAACGACCTGA	1304

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RESULT 3
US-09-895-686-8
; Sequence 8, Application US/09895686
; Patent No. US20020106655A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN GPCR PROTEINS
; FILE REFERENCE: PC-0044 CIP
; CURRENT APPLICATION NUMBER: US/09/895,686
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PERL Program
; SEQ ID NO 8
; LENGTH: 2138
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020106655A1 1459432CB1
US-09-895-686-8

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Query Match	94.8%	Score 1203	DB 10	Length 2138
Best Local Similarity	99.1%	Pred. No. 1.2e-276		
Matches 1220	Conservative	0	Matches 10	Indels 1
				Gaps 1
QY 39	ACTTGGGCTTGGAGACGGACGGGCTGCCAGGACTACAGAGAGAAAGACCCCTTCCGACATG	98		
Db 20	AATTTGGGCTTGGAGGCGGGA-CGGCTGCCAGGCTACAGAGATGAGACCCCTTCCCACTG	78		
QY 99	CGGGCTTGCGCTCCGGGACAAGTGGCAGGCGCTGGAGGCTGGCCGACGCTGGCTGGGT	158		
Db 79	CGGGCTTGCGCTCCGGGACAAGTGGCAGGCGCTGGAGGCTGGCCGACGCTGGCTGGGT	138		
QY 159	GGAGGGAGGCTCAGCTCGGTTGGGAGGAGGCGACCGGCACTGGCTGGATGGACCTGGA	218		
Db 139	GGAGGGAGGCTCAGCTCGGTTGGGAGGAGGCGACCGGCACTGGCTGGATGGACCTGGA	198		
QY 219	AGCCTTCGCTGCTGCCCACTGCTGCCAATGGCCAGCAACACTTGAATGGGCCGATAACT	278		
Db 199	AGCCTTCGCTGCTGCCCACTGCTGCCAATGGCCAGCAACACTTGAATGGGCCGATAACT	258		
QY 279	CACCTTCAGCAGGATCACCCTCTTCGCGACGGGGAGCATCTCTTACATCAGATCATATGCG	338		
Db 259	CACCTTCGAGGATCACCCTCTTCGCGACGGGGAGCATCTCTTACATCAGATCATATGCG	318		
QY 339	TTGCGTGTTCGGGACCATTCCTGCTGCGGATTCATCAGGGAATCAGCGATCATCTGCG	398		
Db 319	TTGCGGTTCGGGACCATTCCTGCTGCGGATTCATCAGGGAATCAGCGATCATCTGCG	378		
QY 399	GGTGGTGAAGATGCCAGCTGCTGTCGAACAACGTCGCCGACATCTCATCATCA	458		
Db 379	GGTGGTGAAGATGCCAGCTGCTGTCGAACAACGTCGCCGACATCTCATCATCA	438		
QY 459	CCCTTCGAGTACAGATCTCTCTTCTCTCTGGGACATGCCCTTCATGATCAGCAGTGCAT	518		
Db 439	CCCTTCGAGTACAGATCTCTCTTCTCTCTGGGACATGCCCTTCATGATCAGCAGTGCAT	498		
QY 519	GGGCAATGGGGTGTGGCACTTTGGGGAGCAATGTGCAACCCCTCATCAGGCCATGGATGC	578		
Db 499	GGGCAATGGGGTGTGGCACTTTGGGGAGCAATGTGCAACCCCTCATCAGGCCATGGATGC	558		
QY 579	CATATGTACGTTACACAGACCTACATCTGACCGCATGGGCACTTGAACCGTACTAGGC	638		
Db 559	CATATGTACGTTACACAGACCTACATCTGACCGCATGGGCACTTGAACCGTACTAGGC	618		
QY 639	CACGTGCACCCCATCTCTTCCACGAAATTCGGGAAAGCCCTTGTGGCCACCCCTGGTAT	698		
Db 619	CACGTGCACCCCATCTCTTCCACGAAATTCGGGAAAGCCCTTGTGGCCACCCCTGGTAT	678		
QY 699	CTGCTCTCTGTGGGCGCTCTCTTCAATACGATCACCCCTGTGTGGCTATGCCAGACT	758		
Db 679	CTGCTCTCTGTGGGCGCTCTCTTCAATACGATCACCCCTGTGTGGCTATGCCAGACT	738		
QY 759	CATCCCTTCCAGAGAGGTGAGTGGGGTGGGGCACTAGCCCTGGCCAAACCCAGACACTGA	818		
Db 739	CATCCCTTCCAGAGAGGTGAGTGGGGTGGGGCACTAGCCCTGGCCAAACCCAGACACTGA	798		
QY 819	CCTTACTGTGTACCCCTGTACCACTTTTCTGTGGCTTTTGTGGCTTTTGTGGTAT	878		
Db 799	CCTTACTGTGTACCCCTGTACCACTTTTCTGTGGCTTTTGTGGCTTTTGTGGTAT	858		
QY 879	CACAGCGGATACGAGAGATCTGTGAGGAGCATAGAGCTCCTACAGTGGGCCCGGCTCCCA	938		
Db 859	CACAGCGGATACGAGAGATCTGTGAGGAGCATAGAGCTCCTACAGTGGGCCCGGCTCCCA	918		
QY 939	GGCAGACATCGGGCTGGGCAAAAGAGGGTGAACCGCACAGCCATCGCCATCTGTGGT	998		
Db 919	GGCAGACATCGGGCTGGGCAAAAGAGGGTGAACCGCACAGCCATCTGTGTGGT	978		
QY 999	CTTCTTTGTGTCTGGGCACTTACTATGTCTACAGCTGACCCAGTGTTCATCAGCGG	1058		
Db 979	CTTCTTTGTGTCTGGGCACTTACTATGTCTACAGCTGACCCAGTGTTCATCAGCGG	1038		

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OY 1059 CCCGACCTCACCCTTGTCTACTATPACATCGGGCCATCAGCTTGGGCTATGCAACAG 1118
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Db 1039 CCCGACCCCACTTGTCTACTATPACATCGGGCCATCAGCTTGGGCTATGCAACAG 1098
OY 1119 CCGCTCAACCCCTTGTGTACTATGTGCTGTGAGACGTCCCAACGCTTGCTCT 1178
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1099 CCGCTCAACCCCTTGTGTACTATGTGCTGTGAGACGTCCCAACGCTTGCTCT 1158
OY 1179 GTCGGTGAAGCTGACGCCAGCGGCGAGCTTGCCTGTGACCAACGCTCAACGCTGA 1238
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Db 1159 GTCGGTGAAGCTGACGCCAGCGGCGAGCTTGCCTGTGACCAACGCTCAACGCTGA 1218
OY 1239 CGAGGAGAGACAGAAAGCAAGCACTGA 1269
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Db 1219 CGAGGAGAGACAGAAAGCAAGCACTGA 1249

RESULT 4
; Sequence 9721, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 9721
; LENGTH: 1478
; TYPE: DNA
; ORGANISM: Homo sapiens
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; FEATURE:
; OTHER INFORMATION: MAP TO 286090.10
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.2
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.1
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 5.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.7
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.3
US-09-864-761-9721

Query Match 77.6%; Score 984.4; DB 10; Length 1478;
Best Local Similarity 99.4%; Pred. No. 9,1e-225;
Matches 988; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 276 CCTCACTTCAGAGATGATCCCTCCGCGAGGAGGAGCATCTCTATCAATCATCATCAT 335
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Db 406 CCTTCTGTCCAGAGATGATCCCTCCGCGAGGAGGAGCATCTCTATCAATCATCATCAT 465
OY 336 GCCTTCGGTTCGGGACCATTCGCTCCGCGCATCATCGGAACTCCAGCGTATCTT 395
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Db 466 GCCTTCGGTTCGGGACCATTCGCTCCGCGCATCATCGGAACTCCAGCGTATCTT 525
OY 396 CGCGGTGCTGAAGAAGTCCAAAGCTGATGTCACCAAGCTCCCGACATCTTCATCAT 455
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 526 CGCGGTGCTGAAGAAGTCCAAAGCTGATGTCACCAAGCTCCCGACATCTTCATCAT 585
OY 456 CAACCTCTCGTAGTAGATCTCTCTTCTCTGCGCATCGCCCTTCATGATCACCAGCT 515
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Db 586 CAACCTCTCGTAGTAGATCTCTCTTCTCTGCGCATCGCCCTTCATGATCACCAGCT 645
OY 516 CATGGGCAATGGGGTGTGACACTTTGGGAGACCATGTGACCCCTCATGACGGCATGGA 575
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Db 646 CATGGGCAATGGGGTGTGACACTTTGGGAGACCATGTGACCCCTCATGACGGCATGGA 705
OY 576 TGCCATATGTCAGTTACACGAGACCTATCTCTGACCCGCGCATGAGCGCTACTCT 635
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Db 706 TGCCATATGTCAGTTACACGAGACCTATCTCTGACCCGCGCATGAGCGCTACTCT 765
OY 636 GCGCACATGTCACCCCATCTCTTCCACGAGAGTTCGGGAAGCCCTCTGTGGCACCCTGCT 695
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Db 766 GCGCACATGTCACCCCATCTCTTCCACGAGAGTTCGGGAAGCCCTCTGTGGCACCCTGCT 825
OY 696 GATCTGCCCTCTGTGGGCGCTCTCTCTCATGACATCAACCCCTGTGTGCTATGCGAG 755
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Db 826 GATCTGCCCTCTGTGGGCGCTCTCTCTCATGACATCAACCCCTGTGTGCTATGCGAG 885
OY 756 ACTCATCCCTTCCAGAGAGTGCAGTGGGCTGCGGCATATGCGTCCCAACCCAGACAC 815
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Db 886 ACTCATCCCTTCCAGAGAGTGCAGTGGGCTGCGGCATATGCGTCCCAACCCAGACAC 945
OY 816 TGACCTCTATGTTGTTACACCTGTACCAAGTTTCTGCGCTTGTGCTGCTTTGTGCT 875
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Db 946 TGACCTCTATGTTGTTACACCTGTACCAAGTTTCTGCGCTTGTGCTGCTTTGTGCT 1005
OY 876 CATCAAGCGCGATACGTGAGATGCTGAGGAGCATGAGTCTGAGTGGGCCCGCCCTC 935
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Db 1006 CATCAAGCGCGATACGTGAGATGCTGAGGAGCATGAGTCTGAGTGGGCCCGCCCTC 1065
OY 936 CGAGCGAGCATCGGCTGCGGAGCAAGAGGTGACCCGACAGGCATCGCATCTGTCT 995
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Db 1066 CGAGCGAGCATCGGCTGCGGAGCAAGAGGTGACCCGACAGGCATCGCATCTGTCT 1125
OY 996 GGTCTTCTTGTGTGCTGGGACCTTATGTGCTACAGCTGACCCAGTGTTCATCAG 1055
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Db 1126 GGTCTTCTTGTGTGCTGGGACCTTATGTGCTACAGCTGACCCAGTGTTCATCAG 1185
OY 1056 CCGCGGACCCCTCAGCTTGTCTACTATACAAATGGGCGATCAGCTGGGCTATGCCAA 1115
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1186 CCGCGGACCCCTCAGCTTGTCTACTATACAAATGGGCGATCAGCTGGGCTATGCCAA 1245
OY 1116 CAGTGTCTCAACCCCTTGTGTACTATGCTGTGTGAGAGCTTCCGCAAGCGCTGTG 1175
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Db 1246 CAGCTGCTCAACCCCTTTGTGTGATCGTGTGTGAGAGTTCGCCAAGCGTTGGT 1305
QY 1176 CCGTGGGTGAAGCCCTGCGAGCCCGAGAGTTCGCCCTGTCAAGAACGCTCAGAGGCG 1235
Db 1306 CCGTGGGTGAAGCCCTGCGAGCCCGAGAGTTCGCCCTGTCAAGAACGCTCAGAGGCG 1365
QY 1236 TGACGAGAGAGAGACAGAAAGCAAGGCACTGA 1269
Db 1366 TGACGAGAGAGAGACAGAAAGCAAGGCACTGA 1399

RESULT 5
US-09-885-478-3
; Sequence 3, Application US/09885478
; Patent No. US2002011306A1
; GENERAL INFORMATION:
; APPLICANT: SALON, JOHN A
; APPLICANT: LAZ, THOMAS M
; APPLICANT: MAGORNY, RAISA
; APPLICANT: WILSON, AMT E
; TITLE OF INVENTION: DNA ENCODING A HUMAN MELANIN CONCENTRATING HORMONE RECEPTOR (MCH)
; FILE REFERENCE: 1795/57453-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/885,478
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US99/31169
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1214
; TYPE: DNA
; ORGANISM: RATTUS NORVEGICUS
US-09-885-478-3

Query Match 71.9%; Score 912.8; DB 10; Length 1214;
Best Local Similarity 90.1%; Pred. No. 8.7e-208;
Matches 977; Conservative 0; Mismatches 107; Indels 0; Gaps 0;

QY 186 GCAGGGGACCGGACGCTGGTGGTGAAGCTGGAGCGCTGGCGCCAGCTGGTCCAA 245
Db 1 GCAGGGGACCTGCAGCGGCTGGATGATGCAAACTGGTGGCTGGCGCCAA 60
QY 246 TGCCAGCAACACCTCTGATGGCCCGATACCTCACTTCAGAGATCACTCTCGAC 305
Db 61 TGCCAGCAACATCTCCGATGGCAGGATATCTCAATTCGCGGTCACCTCTCGAC 120
QY 306 GGGGAGCATCTCTACATACATATCATATGCTTCGCTCGGTTCGGCAGCATCTGCTCT 365
Db 121 AGGGAGTGTCTCTACATACATATCATATGCTTCGCTCGGTTCGGTACCATCTGCTCT 180
QY 366 GGGCATCATCGGAGACTCCAGGTCATCTTCGCGTCTGTAAGAGTCCAAAGCTGACTG 425
Db 181 GGGCATCTGGGAACTCCAGGTCATCTTCGCTGTTGGTAAGAGTCCAAAGTACTG 240
QY 426 GTCCAAAGAGTTCGCCGAATCTTCATCATCACTCTTCGGTAGATCTCTCTTCT 485
Db 241 GTCCAAAGAGTTCGCCGAATCTTCATCATCACTCTTCGGTAGATCTCTCTTCT 300
QY 486 CCTGGGCAATGCCCTTCATGATCACCAGCTCATGGGCAATGGGGTGTGGCACTTGGGGA 545
Db 301 GCTGGGCAATGCCCTTCATGATCACCAGCTCATGGGGAAGGCGTCTGGCACTTGGGGA 360
QY 546 GACCATGTGACCTCTATACAGGCAATGATGCAATAGTCACTTCACCAAGCACTTACAT 605
Db 361 AACCATGTGACCTCTATACAGGCAATGATGCAATAGTCACTTCACCAAGCACTTACAT 420
QY 606 CTTGACCGCATGGCATTGACCGCTACTGCGCACTGTCCACCCCATCTCTCCACCAA 665
Db 421 CTTGACCGCATGGCATTGACCGCTACTGCGCACTGTCCACCCCATCTCTCCACCAA 480
QY 666 GTTCCGAAGACCTCTGTGGCCACCTGTGATGTGCTCTGTGGCCCTCTCTCTTCTAT 725

|||||
Db 481 TTTCGGGAAGCCCTTCATAGCCAGCCCTGATGATCTGCTCTGTGGGGGCTCTCTTCTAT 540
QY 726 CAGCATCACCCTGTGTGTGTGTATGCCAGACTATCCCTTCCAGAGAGTGCAGTGGG 785
Db 541 CAGTATCACCCTGTGTGTGTGTGTATGCCAGACTATCCCTTCCAGAGAGTGCAGTGGG 600
QY 786 CTGCGCAATACCCCTGCCCCAACCCAGACATGACCTCTACTGTTACCTCTACAGTT 845
Db 601 CTGTGCAATCCGCTGCCCCAACCCAGACATGACCTCTACTGTTACCTCTACAGTT 660
QY 846 TTTCCTGCGCTTTGCGCTGCTTTGTGTGTATCATCAGACCCGATACGTGAGAGATCTGCA 905
Db 661 TTTCCTGCGCTTTGCGCTGCTTTGTGTGTATCATCAGACCCGATACGTGAGAGATCTGCA 720
QY 906 GCGCATGACGTCTCAGTGGGCCCGCTCCAGCGCAGACATCCGGCTGCGGACAAAGAG 965
Db 721 GCGCATGACGTCTTGGGTGGGCCCGCTCCAGCGCAGACATCCGGCTGCGGACAAAGAG 780
QY 966 GGTGACCCGACAGCCATCGCATCTGTCTGTCTTTCTTTGTGTGTGGCACCCTACTA 1025
Db 781 GGTGACCCGACAGCCATCGCATCTGTCTGTCTTTCTTTGTGTGTGGCACCCTACTA 840
QY 1026 TGTGCTACAGCTGACCCAGTGTGTCATCAGACCGCCGACCTCAACCTTGTCTACTATA 1085
Db 841 TGTGCTACAGCTGACCCAGTGTGTCATCAGACCGCCGACCTCAACCTTGTCTACTATA 900
QY 1086 CAATGCGCCATCAGCTGTGGCTATGCCAAGACGTGCTCAACCCCTTGTGTACTGCT 1145
Db 901 CAATGCGCCATCAGCTGTGGCTATGCCAAGACGTGCTCAACCCCTTGTGTACTGCT 960
QY 1146 GCTCTGTGAGAGCTTCCGAAACGCTGTGCTGTGCTGTGAAGCCGTGAGCCGAGGGA 1205
Db 961 GCTCTGTGAGAGCTTCCGAAACGCTGTGCTGTGCTGTGAAGCCGTGAGCCGAGGGA 1020
QY 1206 GCTTGGCGCTGTGACAGACGCTCAAGACGCTGACGAGAGAGACAGAAAGCAAGGCAC 1265
Db 1021 GCTCCGACAGGTCAGACAGCTCAGACAGCTGATGAGAGAGACAGAAAGCAAGGCAC 1080
QY 1266 CTGA 1269
Db 1081 CTGA 1084

RESULT 6
US-09-864-761-21946
; Sequence 21946, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE REFERENCE: Aecmics-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
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? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00669
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00665
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00668
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00663
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00662
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00661
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00670
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: US 60/234,687
? PRIOR FILING DATE: 2000-09-21
? PRIOR APPLICATION NUMBER: US 09/608,408
? PRIOR FILING DATE: 2000-06-30
? PRIOR APPLICATION NUMBER: US 09/774,203
? PRIOR FILING DATE: 2001-01-29
? NUMBER OF SEQ ID NOS: 49117
? SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
? SEQ ID NO 71946
? LENGTH: 720
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? OTHER INFORMATION: MAP TO 286090.10
? OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.67
? OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 1
? OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.78
? OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.74
? OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.3
? OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2
? OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.72
? OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.2
? OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.1
? OTHER INFORMATION: SWISSPROT HIT: Q29705, EVALU0 0.00e+00
? OTHER INFORMATION: NT HIT: g11l418166, EVALU0 0.00e+00
? OTHER INFORMATION: EST_HUMAN HIT: BE701073.1, EVALU0 0.00e+00
? US-09-884-761-21946
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Query Match          56.7%; Score 720; DB 10; Length 720;
Best Local Similarity 100.0%; Pred. No. 4,6e-162;
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 550 ATGTGACCCCTCATCAGGCGCCATGATGCCAATAGTCAGTTCCACGACCCCTCATCTG 609
    |||||
Db 1 ATGTGACCCCTCATCAGGCGCCATGATGCCAATAGTCAGTTCCACGACCCCTCATCTG 60
QY 610 ACCGCGATGGCCATTTAGCCGCTACCTGGCCGCTGCCACCCCATCTCTCCACGAAGTTC 669
    |||||
Db 61 ACCGCGATGGCCATTTAGCCGCTACCTGGCCGCTGCCACCCCATCTCTCCACGAAGTTC 120
QY 670 CGGAAGCCCTGTGTGGCCACCCCTGGTGTGCTGCTCTGTGTGGCCCTCTCTCTCATGAGC 729
    |||||
Db 121 CGGAAGCCCTGTGTGGCCACCCCTGGTGTGCTGCTCTGTGTGGCCCTCTCTCTCATGAGC 180
QY 730 ATCACCCTGTGTGGCTGTATGCCAGACTATCCCTTCCAGAGAGTGCAGTGGGCTGC 789
    |||||
Db 181 ATCACCCTGTGTGGCTGTATGCCAGACTATCCCTTCCAGAGAGTGCAGTGGGCTGC 240
QY 790 GGCATACGCCCTGGCCCAACCCAGACAGACCTGACTTACCTGTTCCACCCGTACAGTTTTC 849
    |||||
Db 241 GGCATACGCCCTGGCCCAACCCAGACAGACCTGACTTACCTGTTCCACCCGTACAGTTTTC 300
QY 850 CTGGCCCTTGGCCCTGCTTTTGTGTGTCATCAGCCGCGATAGAGAGATCCTGCAGCGC 909
    |||||
Db 301 CTGGCCCTTGGCCCTGCTTTTGTGTGTCATCAGCCGCGATAGAGAGATCCTGCAGCGC 360
QY 910 ATGAGCTCTCAGTGGCCCCCGCTCCCAAGCGCAGATCCGGCTGGGACAAAGGGTG 969
    |||||
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Db 361 ATGAGCTCTCAGTGGCCCCCGCTCCCAAGCGCAGATCCGGCTGGGACAAAGAGGGTG 420
QY 970 ACCGCGACAGCCATCGCCATCTGTGTGCTCTTTGTGTGGGACCCCTACTATGTG 1029
    |||||
Db 421 ACCGCGACAGCCATCGCCATCTGTGTGCTCTTTGTGTGGGACCCCTACTATGTG 480
QY 1030 CTACAGCTGACCCAGTTGTCCATCAGCCGCCGACCCCTCACTTGTCTACTATACAT 1089
    |||||
Db 481 CTACAGCTGACCCAGTTGTCCATCAGCCGCCGACCCCTCACTTGTCTACTATACAT 540
QY 1090 GCGGCGATCAGCTTGGGCTATGCCAAGCTGCTCAACCCCTTGTGTACATCGTGTG 1149
    |||||
Db 541 GCGGCGATCAGCTTGGGCTATGCCAAGCTGCTCAACCCCTTGTGTACATCGTGTG 600
QY 1150 TGTGAGAGCTTGGCGAAAGCGTGTGCTCTGTGCTGAAGCTGAGGCCAGGGGACCTT 1209
    |||||
Db 601 TGTGAGAGCTTGGCGAAAGCGTGTGCTCTGTGCTGAAGCTGAGGCCAGGGGACCTT 660
QY 1210 CGCGCTGTACGCAACGCTCAGAGCGGCTGACGAGAGAGAGAGAGCAAGCAAGGACCTGA 1269
    |||||
Db 661 CGCGCTGTACGCAACGCTCAGAGCGGCTGACGAGAGAGAGAGAGCAAGCAAGGACCTGA 720
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RESULT 7

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US-09-895-686-25
? Sequence 25, Application US/09895686
? Patent No. US20020106655A1
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? GENERAL INFORMATION:
? APPLICANT: Bandman, Olga
? APPLICANT: Lal, Preeti
? APPLICANT: Tang, Y. Tom
? APPLICANT: Baughn, Mariah R.
? TITLE OF INVENTION: HUMAN GPCR PROTEINS
? FILE REFERENCE: PC-0044 CIP
? CURRENT APPLICATION NUMBER: US/09/895,686
? CURRENT FILING DATE: 2001-06-28
? NUMBER OF SEQ ID NOS: 74
? SOFTWARE: PERL Program
? SEQ ID NO 25
? LENGTH: 519
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: misc-feature
? OTHER INFORMATION: Incyte ID No. US20020106655A1 SMA00250R1
? US-09-895-686-25
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Query Match          40.8%; Score 517.4; DB 10; Length 519;
Best Local Similarity 99.8%; Pred. No. 5,4e-114;
Matches 518; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 533 GGCACCTTTGGGAGACCATGTGCACCCCTCATCAGGCGCCATGATGCCAATAGTCAGTTCA 592
    |||||
Db 1 GGCACCTTTGGGAGACCATGTGCACCCCTCATCAGGCGCCATGATGCCAATAGTCAGTTCA 60
QY 593 CCAGCACTTACATCTGACCGCCCATGATGCCATGACCGCTACCTGGGCACTGTCCACCCA 652
    |||||
Db 61 CCAGCACTTACATCTGACCGCCCATGATGCCATGACCGCTACCTGGGCACTGTCCACCCA 120
QY 653 TCTCTTCCAGAGTTCGGAAGCCCTGTGTGGCCACCCCTGTGTGATCTGCTCTGTGGG 712
    |||||
Db 121 TCTCTTCCAGAGTTCGGAAGCCCTGTGTGGCCACCCCTGTGTGATCTGCTCTGTGGG 180
QY 713 CCTCTCTCTCATCAGATCACCCTGTGTGTGTGTATGCTCAGACATCTCCCTTCCAG 772
    |||||
Db 181 CCTCTCTCTCATCAGATCACCCTGTGTGTGTGTATGCTCAGACATCTCCCTTCCAG 240
QY 773 GAGGTGAGTGGGCTGGGCGATACGCGTGGCCCAACCAGACATGACCTCTACTGGTTCA 832
    |||||
Db 241 GAGGTGAGTGGGCTGGGCGATACGCGTGGCCCAACCAGACATGACCTCTACTGGTTCA 300
QY 833 CCTGTACAGTTTCTCTGCTTGTGCTTGTGCTTGTGTGTCATCAGCGCGCATAGC 892
    |||||
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Db 301 CCTGTACAGTTTTCCTGGCCCTTGGCCCTTTAGTGTCTACACAGCCGCATACG 360
QY 893 TGAGATCTCTGACGCGCATAGCTCCTAGTGGCCCGCCCTCCAGCGAGCATCCGCG 952
Db 361 TGAGATCTCTGACGCGCATAGCTCCTAGTGGCCCGCCCTCCAGCGAGCATCCGCGC 420
QY 953 TGGGACAAAGAGGGTGACCCCGACAGCATGCGCATCTGTCTGTTCTTTGTGTCT 1012
Db 421 TGGGACAAAGAGGGTGACCCCGACAGCATGCGCATCTGTCTGTTCTTTGTGTCT 480
QY 1013 GGGCACCCTACTATGTGTACAGTGCAGCCAGTGTGTCCA 1051
Db 481 GGGCACCCTACTATGTGTACAGTGCAGCCAGTGTGTCCA 519

RESULT 8
US-09-864-761-10236
; Sequence 10236, Application US/09864761
; Patent No. US2002048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aomics-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 10236
; LENGTH: 459
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO 286090.10

; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.67
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.72
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.78
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.74
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2
US-09-864-761-10236
Query Match
Best Local Similarity 100.0%; Score 459; DB 10; Length 459;
Matches 459; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 545 AGACCATGTGACACCTCATACAGCCATGATGCCAATAGTCAATGACAGCACTTACA 604
Db 1 AGACCATGTGACACCTCATACAGCCATGATGCCAATAGTCAATGACAGCACTTACA 60
QY 605 TCCTGACCGCATGGCCATTTGACCCGCTACCGGACCTGTCCACCCCATCTCTCCACGA 664
Db 61 TCCTGACCGCATGGCCATTTGACCCGCTACCGGACCTGTCCACCCCATCTCTCCACGA 120
QY 665 AGTTCGGAAAGCCCTGTGTGSCCACCCTGTGTATCTGCTCTGTGGCCCTTCTTCA 724
Db 121 AGTTCGGAAAGCCCTGTGTGSCCACCCTGTGTATCTGCTCTGTGGCCCTTCTTCA 180
QY 725 TCAGCATACCCCTGTGTGTGCTGTATGCGACATCATCCCTTCCAGAGAGTGACATGG 784
Db 181 TCAGCATACCCCTGTGTGTGCTGTATGCGACATCATCCCTTCCAGAGAGTGACATGG 240
QY 785 GCTGCGGATAGCGCTGCGCCAAACGACATGACCTTACTGTTACCTGTACAGT 844
Db 241 GCTGCGGATAGCGCTGCGCCAAACGACATGACCTTACTGTTACCTGTACAGT 300
QY 845 TTTTCTGCGCTTTGGCCGCTTTTGTGTATACAGCGGATAGTGTGATCTGTC 904
Db 301 TTTTCTGCGCTTTGGCCGCTTTTGTGTATACAGCGGATAGTGTGATCTGTC 360
QY 905 AGCGCATGACGCTCTCAGTGGCCCGCCCTCCAGCGAGCATCGGCTGGGACAAAGA 964
Db 361 AGCGCATGACGCTCTCAGTGGCCCGCCCTCCAGCGAGCATCGGCTGGGACAAAGA 420
QY 965 GGCTGACCGCGACAGCATGCGCATCTGTCTGTTCT 1003
Db 421 GGCTGACCGCGACAGCATGCGCATCTGTCTGTTCT 459

RESULT 9
US-09-895-686-22
; Sequence 22, Application US/09895686
; Patent No. US20020106655A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN GPCR PROTEINS
; FILE REFERENCE: PC-0044 CIP
; CURRENT APPLICATION NUMBER: US/09/895,686
; CURRENT FILING DATE: 2001-06-28
; SOFTWARE: PERL Program
; SEQ ID NO 22
; LENGTH: 336
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID NO. US20020106655A1 1459432x12
US-09-895-686-22

Query Match
Best Local Similarity 97.9%; Score 314.8; DB 10; Length 336;
Matches 319; Conservative 0; Mismatches 7; Indels 0; Gaps 0;


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PRIORITY APPLICATION NUMBER: US 09/774,203
PRIORITY FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annotmax Sequence Listing Engine vers. 1.1
SEQ ID NO 26501
LENGTH: 274
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO 286090.10
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5.3
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 6.2
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 9.3
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.5
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.9
OTHER INFORMATION: EST HUMAN HIT: BE312542.1, EVALUATE 0.00e+00
OTHER INFORMATION: SWISSPROT HIT: P97639, EVALUATE 1.00e-04
OTHER INFORMATION: NT HIT: AE004060.1, EVALUATE 1.10e-02
US-09-864-761-26501

Query Match
Best Local Similarity 21.2%; Score 269.2; DB 10; Length 274;
Matches 271; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 16 ATGACACAGAGATGGGCGAGGCGACTTGGCTTGAGAGCGGCGACGGCTCCAGGCTTAG 75
Db 1 ATGAAGAAGGAGATGGGAGGCGCACTTGGCTTGAGAGCGGCGACGGCTCCAGGCTTAG 60
QY 76 GAGGAAGACCCCTTCCACACTGCGGGGCTTGCCTCCGGAGCAAGGTGGCAGGCGCTGG 135
Db 61 GAGGAAGACCCCTTCCCAACTGCGGGGCTTGCCTCCGGAGCAAGGTGGCAGGCGCTGG 120
QY 136 AGGCTGCGGAGCGTGGGTGGAGGAGAGCTGAGTGGCTTGGTGGAGAGGGGAGCC 195
Db 121 AGGCTGCGGAGCGCTTGGGTGGAGGAGAGCTGAGTGGCTTGGTGGAGAGGGGAGCC 180
QY 196 GGCAGTGGCTGATGAGGACCTGAGACCTGCGTGGTCCCACTGCTCCCAATGCCAGCAG 255
Db 181 GGCAGTGGCTGATGAGGACCTGAGACCTGCGTGGTCCCACTGCTCCCAATGCCAGCAG 240
QY 256 ACCGTGATGGCCCGATTAACCTCACTTCAGCAG 289
Db 241 ACCGTGATGGCCCGCATTAACCTCACTTCAGCAG 274

RESULT 13
US-09-895-686-57
; Sequence 57, Application US/09895686
; Patent No. US20020106655A1
GENERAL INFORMATION:
APPLICANT: Bandmen, Olga
APPLICANT: Lal, Preeti
APPLICANT: Tang, Y. Tom
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN GPCR PROTEINS
FILE REFERENCE: PC-0044 CIP
CURRENT APPLICATION NUMBER: US/09/895,686
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PERL Program
SEQ ID NO 57
LENGTH: 304
TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID NO. US20020106655A1 70199983H1
US-09-895-686-57

Query Match
20.2%; Score 256; DB 10; Length 304;

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Best Local Similarity 90.1%; Pred. No. 5,6e-52;
Matches 274; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

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QY 645 CCACCCATCTCTCCACGAGTCCGGAAGCCCTGTGTGCGACCCCTGTGTGTGCT 704
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 CCACCCATCTCTCCACGAGTCCGGAAGCCCTGTGTGCGACCCCTGTGTGTGCT 60
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 705 CCGTGTGGCCCTCTCCCTTCATGAGTACACCCCTGTGTGTGTGTGTGTGTGTGTGT 764
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 CCGTGTGGCCCTCTCTCTTCATGAGTACACCCCTGTGTGTGTGTGTGTGTGTGTGT 120
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 765 CTTTCCAGAGAGTGCAGTGGGCTGCGCATACGCTGCCCAACCCAGACTGACTCTTA 824
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 CTTTCCAGAGAGTGCAGTGGGCTGCGCATACGCTGCCCAACCCAGACTGACTCTTA 180
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 825 CTTGTGACCCCTGTACAGTTTCTGTGGCTTTGGCCCTTTTGGTGTGTGTGTGTGTGT 884
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 CTTGTGACCCCTGTACAGTTTCTGTGGCTTTGGCCCTTTTGGTGTGTGTGTGTGTGT 240
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 885 CGCATAGTGAAGATCCCTGCAGCGCATGACGTCCTGAGTGCCGCCGCCCTCCAGCGAG 944
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 241 CGCATAGTGAAGATCCCTGCAGCGCATGACGTCCTGAGTGCCGCCGCCCTCCAGCGAG 300
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 945 CATC 948
      ||| |||
Db 301 CATC 304
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RESULT 14
US-09-895-686-56
; Sequence 56, Application US/09895686
; Patent No. US2002010655A1

GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN GPCR PROTEINS
; FILE REFERENCE: PC-0044 CIP
; CURRENT APPLICATION NUMBER: US/09/895,686
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PERL Program
; SEQ ID NO 56
; LENGTH: 271
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc-feature
; OTHER INFORMATION: Incyte ID No. US2002010655A1 701250242H1
US-09-895-686-56

Query Match 18.2%; Score 231; DB 10; Length 271;
Best Local Similarity 90.8%; Pred. No. 4.7e-46;
Matches 246; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

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QY 406 AAGAAGTCCAAAGTGCAGTGGTGCACAAAGTCCCGACATCTTATCATCAACCTCTG 465
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 AAGAAGTCCAAAGTGCAGTGGTGCACAAAGTCCCGACATCTTATCATCAACCTCTCT 60
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 466 GTAGTAGATCTCCTCTTCTCTGGGAGTCCCTCATGATCAGCAGCTCATGGGCAAT 525
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 GTAGTAGATCTCCTCTTCTCTGGGAGTCCCTCATGATCAGCAGCTCATGGGCAAT 120
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 526 GGGGTGTGGACATTGGGGAGACCATGTGCACCTCATCAGCGCATGGATGCCAATAGT 585
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 GGGGTGTGGACATTGGGGAGACCATGTGCACCTCATCAGCGCATGGATGCCAATAGT 180
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Db 241 CATCCATCTCTCTCCACGAAAGTCCGGAAGC 271

RESULT 15
US-09-895-686-20
; Sequence 20, Application US/09895686
; Patent No. US2002010655A1

GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN GPCR PROTEINS
; FILE REFERENCE: PC-0044 CIP
; CURRENT APPLICATION NUMBER: US/09/895,686
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PERL Program
; SEQ ID NO 20
; LENGTH: 223
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; OTHER INFORMATION: Incyte ID No. US2002010655A1 1459432H1
US-09-895-686-20

Query Match 17.6%; Score 223; DB 10; Length 223;
Best Local Similarity 100.0%; Pred. No. 3.5e-44;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Search completed: February 19, 2003, 12:08:33
Job time : 84 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 19, 2003, 08:30:46 : Search time 3435 Seconds

(without alignments)
10751.517 Million cell updates/sec

Title: US-09-885-478-1

Perfect score: 1269

Sequence: 1 atgtcagtgaggagcactgaa.....cagaaagcaagcaccctga 1269

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : GenBank!*

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- 2: gb_htg:*
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- 37: em_htg_vrt:*
- 38: em_sy:*
- 39: em_htgo_hum:*
- 40: em_htgo_mus:*
- 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1269	100.0	1269	6	AR169785	AR169785 Sequence
2	1267.4	99.9	2042	9	BC001736	BC001736 Homo sapi
3	1267.4	99.9	2042	9	BC021146	BC021146 Homo sapi
4	1264.2	99.6	1275	6	BD013168	BD013168 MCH recep
5	1264.2	99.6	1275	6	AB063174	AB063174 Homo sapi
6	1264.2	99.6	1275	23	BD006649	BD006649 MCH recep
7	1264.2	99.6	1283	6	BD013174	BD013174 MCH recep
8	1264.2	99.6	1283	23	BD006655	BD006655 MCH recep
9	1237.4	97.5	1385	6	AX174768	AX174768 Sequence
10	1115.2	87.9	1444	9	AF513988	AF513988 Macaca mu
11	1058.8	83.4	1062	6	AX280739	AX280739 Sequence
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13	1058.8	83.4	1062	6	AX280747	AX280747 Sequence
14	1058.8	83.4	1062	6	AX280755	AX280755 Sequence
15	1058.8	83.4	1062	6	AX280759	AX280759 Sequence
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21	1057.2	83.3	1062	6	AX280751	AX280751 Sequence
22	1055.6	83.2	1062	6	AX280763	AX280763 Sequence
23	1052.4	82.9	1062	6	AX280731	AX280731 Sequence
24	1014	79.9	1062	9	AY078245	AY078245 Macaca mu
25	999.6	78.8	1349	6	AX280735	AX280735 Sequence
26	984.4	77.6	1877	9	HSU71092	U71092 Homo sapien
27	984.4	77.6	3488	6	AR202509	AR202509 Sequence
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31	935.6	73.7	1062	4	AY112898	AY112898 Mustela p
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ALIGNMENTS

RESULT 1
AR169785
LOCUS AR169785
DEFINITION Sequence 1 from patent US 6291195.
ACCESSION AR169785
VERSION AR169785.1 GI:17907693
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1269)
AUTHORS Salon,J.A., Laz,T.M., Nagorny,R. and Wilson,A.E.
TITLE DNA encoding a human melanin concentrating hormone receptor (MCH)
and uses thereof
JOURNAL Patent: US 6291195-A 1 18-SEP-2001;

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Best Local Similarity		100.0%;	Pred. No. 8,7e-238;		
Matches 1269;	Conservative	0;	Mismatches	0;	Indels
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QY	121	GGTGGCAGCGCGTGGAGSGCTGCGCGACGCTGGTGGTGGTGGAGGGAGTCACTCGTGG	180		
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QY	181	TGGGAGCAGGCGGACCGGCACTGGCTGTGATGACCTGGAAAGCTTCGCTGCCCCACTGGT	240		
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DEFINITION	Homo sapiens, similar to G protein-coupled receptor 24, clone		PRI 12-JUL-2001
ACCESSION	MG:3221	IMAGE:3503484	mRNA, complete cds.
VERSION	BC001736		
KEYWORDS	BC001736.1	GI:12804624	
SOURCE	MG.		
ORGANISM	Homo sapiens.		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota, Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE	Mammalia: Eutheria: Primates; Catarrhini; Hominiidae; Homo.		
JOURNAL	1 (bases 1 to 2042)		
	Strausberg, R.		
	Direct Submission		
	Submitted (16-JAN-2001) National Institutes of Health, Mammalian		
	Gene Collection (MGC), Cancer Genomics Office, National Cancer		
	Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,		
	USA		
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov		
COMMENT	Contact: MGC help desk		
	Email: cgapbs-remail.nih.gov		
	Tissue Procurement: ATCC		
	CDNA Library Preparation: Rubin Laboratory		
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)		
	DNA Sequencing by: Genome Sequence Centre,		
	BC Cancer Agency, Vancouver, BC, Canada		
	info@bcsc.bc.ca		
	Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,		
	Susana Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,		
	Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo		
	Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven		
	Ness, Pawan Pandoh, Anna-Lisa Prabhu, Parvaneh Saeedi, Jacqueline		
	Schlein, Duane Smalins, Michael Smith, Lorraine Spence, Jeff Stott,		
	Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,		
	George Yang, Scott Zuyderduyn, Marco Mairra.		
	Clone distribution: MGC clone distribution information can be found		
	through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov		
	Series: IRAL Plate: 6 Row: 1 Column: 16.		
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BASE COUNT      454 a      600 c      565 g      423 t
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Best Local Similarity 99.9%   Pred. No. 1.7e-237;
Matches 1268;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

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QY      721  TTTCATCAGATCAACCCCTGTGGGTATATGCCAGACTCATCCCTTCCAGAGAGTGA 780
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QY      1021  TACTATGTCTACAGCTGACGCTTGTTCATCAAGCGGCGGACGCTTGTCTTAC 1080
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QY      1081  TTATACATGCGGCGCATCAGCTTGGGCTATATGCCAAGCTGCTCAACCCCTTGTATAC 1140
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Db      1354 ATCGGCTCTGTGAGAGCGTTTGGCAAGCGTGTGTCTGTGTGTAAGCTTGTAC 1413
QY      1201  GGGCAGCTTGGGCTGTGAGCAAGCTCAGAGCGCTGAGCAAGAGAGAGCAAGAAAGCAAA 1260
Db      1414 GGGCAGCTTGGGCTGTGAGCAAGCTCAGAGCGCTGAGCAAGAGAGAGCAAGAAAGCAAA 1473
QY      1261  GGCACCTGA 1269
Db      1474 GGCACCTGA 1482

RESULT 3
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BC021146      Homo sapiens, clone MGC:32129 IMAGE:4890530, mRNA, complete cds.
VERSION      BC021146.1 GI:18088973
KEYWORDS      MGC.
SOURCE      Homo sapiens.
ORGANISM      Homo sapiens.
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2042)
TITLE      Strausberg, R.
JOURNAL      Direct Submission
Submitted (03-JAN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK      NIH-MGC project URL: http://mgc.nci.nih.gov
COMMENT      Contact: MGC help desk
Email: gcgaps-remail.nih.gov
Tissue Procurement: ATCC
DNA Library Preparation: Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
BC Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@cgsc.bc.ca
Steven Jones, Jennifer Amano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeay, Steven
Ness, Pawan Pandoh, Anna-Liisa Prabhhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smalls, Michael Smith, Lorraine Speed, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.

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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Link at: <http://Image.lim.gov>
Series: IRML Plate: 40 Row: n Column: 6
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.

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Query Match 99.9%; Score 1267.4; DB 9; Length 2042;
Best Local Similarity 99.9%; Pred. No. 1.7e-237;
Matches 1268; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 4
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LOCUS
DEFINITION MCH receptor antagonist.
ACCESSION BD013168
VERSION BD013168.1
KEYWORDS WO 0121169-A/7.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1275)
AUTHORS Kato,K., Mori,M., Suzuki,N., Shimomura,Y., Takekawa,S. and Cho,N.
TITLE MCH receptor antagonist.
JOURNAL Patent: WO 0121169-A 7 29-MAR-2001;
TAKEDA CHEMICAL INDUSTRIES LTD, KANEYOSHI KATO, MASAKI MORI, NOBUHIRO
SUZUKI, YUKIO SHIMOMURA, SHIRO TAKEKAWA, NOBUO CHO
OS Homo sapiens (human)
PN WO 0121169-A/7
PD 29-MAR-2001
PF 19-SEP-2000 WO 2000JP006376

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SHIRO TAKERAMA,
PI NOBU CHO
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Matches 1266; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DEFINITION complete cds.
ACCESSION AB063174
VERSION AB063174.1 GI:14475646
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS
Shimomura, Y., Mori, M., Sugo, T., Ishibashi, Y., Abe, M., Kurokawa, T.,
Onda, H., Nishimura, O., Sumino, Y., and Fujino, M.
Isolation and identification of melanin-concentrating hormone as
the endogenous ligand of the SLC-1 receptor
Biochem. Biophys. Res. Commun. 261 (3), 622-626 (1999)
MEDLINE
JOURNAL
99373129
2. (bases 1 to 1275)
Sugo, T. and Mori, M.
Direct Submission
Submitted (13-JUN-2001) Tsukasa Sugo, Takeda Chemical Industries,
Ltd., Discovery Research Laboratories I, Pharmaceutical Research
Division, Wadai 10, Tsukuba, Ibaraki 300-4247, Japan
(E-mail: Sugo.Tsukasa@takeda.co.jp, Tel: 81-298-64-5010(ex.5010),
Fax: 81-298-64-5000)

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CC	XX	SHIRO TAKEKAWA,	
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DEFINITION	MCH receptor antagonist.	1283 bp	DNA
ACCESSION	BD013174		linear
VERSION	BD013174.1		
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SOURCE	Homo sapiens.		
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REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 1283)		
TITLE	Kato,R., Mori,M., Suzuki,N., Shimomura,Y., Takekawa,S. and Cho,N.		
JOURNAL	MCH receptor antagonist		
COMMENT	Patent: WO 0121169-A 13 29-MAR-2001.		
	TAKEDA CHEMICAL INDUSTRIES LTD, KANEYOSHI KATO, MASAOKI MORI, NOBUHIRO SUZUKI, YUKIO SHIMOMURA, SHIRO TAKEKAWA, NOBUO CHO		
	OS Homo sapiens (human)		
	PN WO 0121169-A/13		
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	PI SHIRO TAKEKAWA,		
	PI NOBUO CHO		
	PC A61K31/137, A61K31/27, A61K31/4035, A61K31/44, A61K31/445, PC		
	A61K31/4453		
	PC A61K31/472, A61P43/00, A61P31/04, C07D211/14, C07D211/18 PC		
	, C07D211/46, C07D211/58,		
	PC C07D211/70, C07D401/12, C07D405/12, C07D409/12, C07D417/12 CC		
FEATURES	Key	Location/Qualifiers	
Source	1..1283	Location/Qualifiers	
BASE COUNT	238 a 423 c 350 g 272 t		
ORIGIN	/organism="Homo sapiens" /db_xref="taxon:9606"		

Db	1028	TACTATGTGCTACAGCTGACCCAGTTGTCTCATATGACGCCGCCCGACCTTACCTTGTCTAC	1087
Qy	1081	TTATACAAATGCGGCGCATACAGCTTTGGGCTATATGCCAACAGCTGACCTTAAACCCCTTTTGTGTAC	1140
Db	1088	TTATACAAATGCGGCGCATACAGCTTTGGGCTATATGCCAACAGCTGACCTTAAACCCCTTTTGTGTAC	1147
Qy	1141	ATGTGCTCTGTGAGACGTTTCCGCAAAAGCCTTGCTCTGCTGTGAGTGAAGCTTGCAGCCGAC	1200
Db	1148	ATGTGCTCTGTGAGACGTTTCCGCAAAAGCCTTGCTCTGCTGTGAGTGAAGCCTTGCAGCCGAC	1207
Qy	1201	GGGACGCTTGGCGCTGTCTGACCAAGCTTCAGACGGGCTGACGAGAGAGACAGCAAAAGCANA	1260
Db	1208	GGGACGCTTGGCGCTGTCTGACCAAGCTTCAGACGGGCTGACGAGAGAGAGACAGCAAAAGCANA	1267
Qy	1261	GGGACCTGA 1269	
Db	1268	GGGACCTGA 1276	
RESULT 9			
AX174768	AX174768	1385 bp	DNA linear PAT 03-JUL-2001
LOCUS	Sequence 1 from Patent WO0143759.		
DEFINITION	AX174768		
ACCESSION	AX174768		
VERSION	AX174768.1	GI:14598289	
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 1385) Campbell, C.A., Haddingham, S.J., Harrison, D.C. and Herliu, G.J. New use Patent: WO 0143759-A 1 21-JUN-2001; SMITHKLINE BEECHAM PLC (GB) FEATURES	Location/Qualifiers	
source	1..1385		
BASE COUNT	255 a 471 c 371 g 288 t		
ORIGIN			
Query Match	97.5%; Score 1237.4; DB 6; Length 1385;		
Best Local Similarity	99.9%; Pred. No. 1.3e-231;		
Matches 1238; Conservative	0; Mismatches 1; Indels 0; Gaps 0;		
Qy	31	GGGAGGCGAGTTGGGCTTGGAGGCGGCGAGCGCTGCCAGCTACGAGAGAACCCCTT	90
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Qy	91	CCCAGCTGCGGGGCTTGGCGCTCCGGGACAAAGTGGCAAGCGCTGAGGCTGCGCAGCT	150
Db	126	CCCAGCTGCGGGGCTTGGCGCTCCGGGACAAAGTGGCAAGCGCTGAGGCTGCGCAGCT	185
Qy	151	GGCGTGGTGGAGGAGAGCTACGCTCGGTTTGGGAGCAGCGGACCGGCACTGGGTGATG	210
Db	186	GGCGTGGTGGAGGAGAGCTACGCTCGGTTTGGGAGCAGCGGACCGGCACTGGGTGATG	245
Qy	211	GACCTGGAGAGCTTGGCTGCTGCCACTGTGTCCAATGCCAGCAACACCTGTGATGGCCC	270
Db	246	GACCTGGAGAGCTTGGCTGCTGCCACTGTGTCCAATGCCAGCAACACCTGTGATGGCCC	305
Qy	271	GATTAACCTCACTTACAGAGATCACGCTCCGTCGACGGGGAGGACATCTCTATCAATCAATC	330
Db	306	GATTAACCTCACTTGGGAGATCACGCTCTCTGCGACGGGGAGGACATCTCTATCAATCAATC	365
Qy	331	ATCAATGCTTTCGTTTGGCGACCATGTGCTTCCGTGGGCAATCAATCGGAATCCAGCGTC	390
Db	366	ATCAATGCTTTCGTTTGGCGACCATGTGCTTCCGTGGGCAATCAATCGGAATCCAGCGTC	425
Qy	391	ATCTTCGCGGTCGGAGAGATCCAAACTGACATCGGTGGCAAAACGTCCTCCGACATCTTC	450

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 Db 486 ATCATACACCTCTCGGTAGTAGATCTCTCTTTCCTCGGGGATGCGCTTCATGATCCAC 545
 QY 511 CAGCTCATGGGCAATGGGCTGTGGGCACTTTGGGGAGACCATGTGACCTCATCCAGGCC 570
 Db 546 CAGCTCATGGGCAATGGGCTGTGGGCACTTTGGGGAGACCATGTGACCTCATCCAGGCC 605
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 Db 606 ATGATGCAATAGTACAGTTCACAGACACCTACATCTGACCCGATGGCCATTGACCGC 665
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 QY 691 CTGGTATGTCGCTCTCTGTTGGGCGCTCTCTTCATGAGCATACCCCTGTGGCTGAT 750
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 Db 906 GTGCTATCAGACCGCATACGTGAGATCTGACAGCATGACGTCTCAGTGGGCCCC 965
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 Db 1206 TTGTTCTGTGTCGTGAGAGCTGAGCCAGGCGAGCTTGGCTGTGACAGAGCTGAC 1265
 QY 1231 ACGGCTGACGAGAGAGAGAGCAAAAGCAAGGCACTGA 1269
 Db 1266 ACGGCTGACGAGAGAGAGAGCAAAAGGCAAGGCACTGA 1304
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 LOCUS Macaca mulatta melanin-concentrating hormone receptor subtype 1
 DEFINITION (MCH1R) mRNA, complete cds.
 ACCESSION AF513988
 VERSION AF513988.1 GI:21361063
 SOURCE rhesus monkey.
 ORGANISM Macaca mulatta
 Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 Cercopithecinae; Macaca.
 REFERENCE 1 (bases 1 to 1444)

AUTHORS Tan, C.P., Sano, H., Iwaasa, H., Pan, J., Sailer, A., Hreniuk, D.L.,
 Feigener, S.D., Palyha, O.C., Figueroa, D.J., Austin, C.P., Jiang, M.M.,
 Yu, H., Ito, J., Ito, M., Guan, X.M., Kanatani, A., Van der
 Ploeg, L.H.T., and Howard, A.D.
 TITLE Melanin-Concentrating Hormone Receptor Subtypes 1 and 2: Species
 Specific Gene Expression
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1444)
 AUTHORS Tan, C.P., Sano, H., Iwaasa, H., Pan, J., Sailer, A., Hreniuk, D.L.,
 Feigener, S.D., Palyha, O.C., Figueroa, D.J., Austin, C.P., Jiang, M.M.,
 Yu, H., Ito, J., Ito, M., Guan, X.M., Kanatani, A., Van der
 Ploeg, L.H.T., and Howard, A.D.
 TITLE Direct Submission
 JOURNAL Submitted (21-MAY-2002) Metabolic Disorders, Merck & Co., Box 2000
 80Y-265, Rahway, NJ 07065, USA
 FEATURES
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 LMNGVHGEFMTLITTDANDANSQFSTYILTLAMDRLATVLRHPISSTKRPESVA
 TLVCLMLASFISITPWLRLARLIPPGAVCGRLRPNPDILKFLIYQEFLLFA
 LPEFVITAAVRLIQRMTSSVAPASQSRILRRKRVTRALICLVEFCMAYVLO
 LPTLSIRPLTLEFYLYNAALISGLYANSCINPVIYLVLETFERRKRLVSVKPAQGL
 RAVNSAQTADEERTSEKGT"
 BASE COUNT 281 a 461 c 393 g 309 t
 ORIGIN
 Query Match 87.9%; Score 1115.2; DB 9; Length 1444;
 Best Local Similarity 97.2%; Pred. No. 9.2e-208;
 Matches 1135; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
 QY 102 GCCTTGGCTCGGAGCAAGGTGGGAGCGCTGAGAGCTGGGAGCGCTGGGTGGGA 161
 Db 1 GCCTTGGCTCGTGTGAGCAAGGTGGGAGCGCTGGGAGCGCTGGGTGGGA 60
 QY 162 GGGAGCTCAGCTCGTGTGTGGAGACAGGCGACCGGCACTGGATGACCTGGAAGC 221
 Db 61 GGGAGCTCAGCTTGTGTGTGGAGACCGGCGACCGGCACTGGATGACCTGGAAGC 120
 QY 222 CTGCTGCTGCGCTGCTGCTCCATGCGACAGCAACCTCTGATGGCCCGCATTAACCTCAC 281
 Db 121 CTGCTGCTGCGCTGCTGCTCCATGCGACAGCAACCTCTGATGGCCCGCATTAACCTCAC 180
 QY 282 TTCAGAGAGTACCTCCCTGCGACGAGGAGCATCTCTACATCAACATCATATGCTTTC 341
 Db 181 CTCGGAGAGTACCTCCCTGCGCTCAGGAGGCTCTCTACATCAACATCATATGCTTTC 240
 QY 342 GGTGTGCGGACCATCTGCTCTCGGCAATCATGCGGAATCTCAGCTATCTTGGCGGT 401
 Db 241 GGTGTGCGGACCATCTGCTCTCGGCAATCATGCGGAATCTCAGCTATCTTGGCGGT 300
 QY 402 CGTGAAGAGTCCAAAGCTCAGTGTGCAACAACTGCCCGCATCTTCAATCAATCAACT 461
 Db 301 CGTGAAGAGTCCAAAGCTCAGTGTGCAACAACTGCCCGCATCTTCAATCAATCAACT 360
 QY 462 CTGGAGTAGATATCTCTCTCTCTGAGCATGCGCTTCATGATCCACCAAGCTCATGGG 521
 Db 361 CTGGAGTAGATATCTCTCTCTCTGAGCATGCGCTTCATGATCCACCAAGCTCATGGG 420
 QY 522 CAATGGGATGTGGCACTTTGGGAGACATGTGACACCTCATACAGCGCATGATGCCAA 581
 Db 421 CAATGGGATGTGGCACTTTGGGAGACATGTGACACCTCATACAGCGCATGATGCCAA 480

QY 388 GTCATCTTCGCGTGTGAGAGTCCAGCTGCACCTGTGTGCAACAACTCCCGACATC 447
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Db 181 GTCATCTTCGCGTGTGAGAGTCCAGCTGCACCTGTGTGCAACAACTCCCGACATC 240
QY 448 TTTCATCATCAACCTCTCGGTAGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 507
241 TTTCATCATCAACCTCTCGGTAGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
QY 508 CACACACATCATGGGAGTGTGGGACCTTGTGGGAGACATGTGTGACCCCTCATCAG 567
301 CACACACATCATGGGAGTGTGGGACCTTGTGGGAGACATGTGTGACCCCTCATCAG 360
QY 568 GCCATGATGCCAATATGTCAGTTCCACAGACCTTACATCTGTGACCGCATGGCATTTGAC 627
361 GCCATGATGCCAATATGTCAGTTCCACAGACCTTACATCTGTGACCGCATGGCATTTGAC 420
QY 628 CGCTACCTGGGACATGTGACCCCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 687
421 CGCTACCTGGGACATGTGACCCCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480
QY 688 ACCCTGTATCTGCT 747
481 ACCCTGTATCTGCT 540
QY 748 TATGACAGATCATCCCT 807
541 TATGACAGATCATCCCT 600
QY 808 CCAGACATGTACCT 867
601 CCAGACATGTACCT 660
QY 868 TTGTGTGATCATCAAGCGCATAGAGATCTGTGAGCGATGAGTGTGAGTGTGAGTGT 927
661 TTGTGTGATCATCAAGCGCATAGAGATCTGTGAGCGATGAGTGTGAGTGTGAGTGT 720
QY 928 CCCGCTCCAGGCGCATCTCGGCTCGGAGACAAAGAGGAGTGTGAGTGTGAGTGT 987
721 CCCGCTCCAGGCGCATCTCGGCTCGGAGACAAAGAGGAGTGTGAGTGTGAGTGT 780
QY 988 ATCTGTCTGTCT 1047
781 ATCTGTCTGTCT 840
QY 1048 TCCATCAGCGCGCGACCTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1107
841 TCCATCAGCGCGCGACCTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 900
QY 1108 TATGCCAAGAGTGTCTCAACCCCTTGTGTATCTGTGTGTGTGTGTGTGTGTGTGT 1167
901 TATGCCAAGAGTGTCTCAACCCCTTGTGTATCTGTGTGTGTGTGTGTGTGTGTGT 960
QY 1168 CGCTGTGCTCTGT 1227
961 CGCTGTGCTCTGT 1020
QY 1228 CAGAGGCTGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1269
1021 CAGAGGCTGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1062

RESULT 14
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LOCUS AX280755
DEFINITION Sequence 378 from Patent WO0177172.
ACCESSION AX280755
VERSION AX280755.1 GI:16608122
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1

AUTHORS Lehmann-Brunnsma, K., Liaw, C. W., and Lin, I. L.
TITLE Non-vendogenous, constitutively activated known g protein-coupled
JOURNAL receptors
Patent: WO 0177172-A 378 18-OCT-2001;
Arena Pharmaceuticals, Inc. (US)
FEATURES
source Location/Qualifiers
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Best Local Similarity 99.8%; Pred. No. 9,7e-197;
Matches 1060; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 208 ATGGAGCTTGGAGAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 267
Db 1 ATGGAGCTTGGAGAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 60
QY 268 CCCGATTAACCTCACTTTCAGAGATCACCTCTCTCTCTCTCTCTCTCTCTCTCTCT 327
Db 61 CCCGATTAACCTCACTTTCAGAGATCACCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
QY 328 ATCATCATGCTCTGT 387
Db 121 ATCATCATGCTCTGT 180
QY 388 GTCATCTTCGCGTGTGAGAGTCCAGCTGCACCTGTGTGCAACAACTCCCGACATC 447
Db 181 GTCATCTTCGCGTGTGAGAGTCCAGCTGCACCTGTGTGCAACAACTCCCGACATC 240
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Db 241 TTTCATCATCAACCTCTCGGTAGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
QY 508 CACACACATCATGGGAGTGTGGGACCTTGTGGGAGACATGTGTGACCCCTCATCAG 567
Db 301 CACACACATCATGGGAGTGTGGGACCTTGTGGGAGACATGTGTGACCCCTCATCAG 360
QY 568 GCCATGATGCCAATATGTCAGTTCCACAGACCTTACATCTGTGACCGCATGGCATTTGAC 627
Db 361 GCCATGATGCCAATATGTCAGTTCCACAGACCTTACATCTGTGACCGCATGGCATTTGAC 420
QY 628 CGCTACCTGGGACATGTGACCCCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 687
Db 421 CGCTACCTGGGACATGTGACCCCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480
QY 688 ACCCTGTATCTGCT 747
Db 481 ACCCTGTATCTGCT 540
QY 748 TATGCCAAGAGTGTCTCAACCCCTTGTGTATCTGTGTGTGTGTGTGTGTGTGTGT 807
Db 748 TATGCCAAGAGTGTCTCAACCCCTTGTGTATCTGTGTGTGTGTGTGTGTGTGTGT 600
QY 808 CAGAGAGCTGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 867
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QY 868 TTGTGTGATCATCAAGCGCATAGAGATCTGTGAGCGATGAGTGTGAGTGTGAGTGT 927
Db 661 TTGTGTGATCATCAAGCGCATAGAGATCTGTGAGCGATGAGTGTGAGTGTGAGTGT 720
QY 928 CCCGCTCCAGGCGCATCTCGGCTCGGAGACAAAGAGGAGTGTGAGTGTGAGTGT 987
Db 721 CCCGCTCCAGGCGCATCTCGGCTCGGAGACAAAGAGGAGTGTGAGTGTGAGTGT 780
QY 988 ATCTGTCTGTCT 1047
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QY 1048 TCCATCAGCGCGCGACCTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1107

PE 30-DEC-1999; 99WO-US31169.
XX
PR 31-DEC-1998; 98US-0224426.
XX
PA (SYNA-) SYNAPTIC PHARM CORP.
XX
PI Salton JA, Laz TM, Nagorny R, Wilson AE;
XX
XX
XX WPI: 2000-548644/50.
DR P-PSDB: AAB13436.
DR
XX
XX Novel nucleic acid encoding human melanin concentrating hormone
PR receptor, useful for treating cardiovascular disorders, hypertension and
PT diabetes, whose mutant form is activated by melanin concentrating
PT hormone -
XX
PS Claim 26; Fig 1; 173pp; English.

Neuroregulators modulate communication in the nervous system. Melanin concentrating hormone I (MCH1) is one such neuroregulator. MCH may serve as an integrative neuropeptide, involved in stress response, feeding regulation and sexual activity. Also, MCH is thought to participate in water balance regulation, energy metabolism, general arousal/attention state, memory and cognitive functions and psychiatric disorders. The present sequence is the coding sequence of human MCH1 receptor. MCH1 receptor is a G-protein coupled receptor. The present sequence may be used in the therapy for a variety of disorders: steroid or pituitary hormone disorder, epinephrine release disorder, gastrointestinal disorder, cardiovascular disorder, electrolyte balance disorder, hypertension, diabetes, respiratory disorder, asthma, reproductive function disorder, immune disorder, endocrine disorder, musculoskeletal disorder, neuroendocrine disorder, cognitive disorder, memory disorder, e.g. Alzheimer's disease, sensory modulation and transmission disorder, motor coordination disorder, sensory integration disorder, dopaminergic function disorder e.g. Parkinson's disease, olfaction disorder, sympathetic innervation disorder, depression, stress, fluid-imbalance disorder, urinary disorder e.g. urinary incontinence, seizure, pain, psychotic behaviour e.g. schizophrenia, morphine tolerance, opiate addiction or migraine. The present sequence is also contained in plasmid pEX1-HR-T1231 (ATCC 203197).

Sequence 1269 BP; 234 A; 419 C; 347 G; 269 T; 0 other;

Query Match	100.0%	Score 1269	DB 21	Length 1269
Similarity	100.0%	Pred. No. 3.4e-285		
Matches 1269	0	Mismatches 0	Indels 0	Gaps 0

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	1	ATGTAGTGGAGCCATGAAGAAGGATGGGAGGGCACTTGGCTTGGAGGCGGCAC	60
Db	1	ATGTAGTGGAGCCATGAAGAAGGATGGGAGGGCACTTGGCTTGGAGGCGGCAC	60
QY	61	GGCTGCCAGGCTAGGAGGAAGACCCCTTCCGACTGCGGGCTTGGCTCCGGACAA	120
Db	61	GGCTGCCAGGCTAGGAGGAAGACCCCTTCCGACTGCGGGCTTGGCTCCGGACAA	120
QY	121	GGTGGCAGGCGCTGGAGGCTGCGGACGCTCGTGGGGGAGGAGCACTCAGCTCGTTG	180
Db	121	GGTGGCAGGCGCTGGAGGCTGCGGACGCTCGTGGGGGAGGAGCACTCAGCTCGTTG	180
QY	181	TGGGAGCAGCAGCCAGCGGCACTGGCTGTATGGACCTGGAAAGCTTGCTGTCCTAGTGT	240
Db	181	TGGGAGCAGCAGCCAGCGGCACTGGCTGTATGGACCTGGAAAGCTTGCTGTCCTAGTGT	240
QY	241	CCCAATGCCAGCAACACTCTGTATGGCCCCGATTAACCTCACTTACAGAGATCAACTCCT	300
Db	241	CCCAATGCCAGCAACACTCTGTATGGCCCCGATTAACCTCACTTACAGAGATCAACTCCT	300
QY	301	CGCAGGGAGGAGATCCTCACTCAATCAATCAATGCTTGCGGTGTGGCACCATTGCG	360
Db	301	CGCAGGGAGGAGATCCTCACTCAATCAATCAATGCTTGCGGTGTGGCACCATTGCG	360
QY	361	CTCTTGGGATCATGGGAACGCCAGGTCACTTTCGCGGTGTGAAGAAGTCCAAAGCTG	420
Db	361	CTCTTGGGATCATGGGAACGCCAGGTCACTTTCGCGGTGTGAAGAAGTCCAAAGCTG	420

Db	361	CTCTGGGGCATCAATCGGGAAGCTCAAGGTCATCTTCGGGGTGTGAGAAAGATCCAAAGCTG	420
Oy	421	CACGTGGTGCAACAACGTCGCCGACATCTTTCATCATCAACCTCTCGGTAGTAGATCTCTC	480
Db	421	CACTGTGGTCAACAACGTCGCCGACATCTTTCATCATCAACCTCTCGGTAGTAGATCTCTC	480
Oy	481	TTTCTCTCGGGCATGCGCTTCATGATCCACAGGTCATGGGCAATGGGGTGTGGCACTTT	540
Db	481	TTTCTCTCGGGCATGCGCTTCATGATCCACAGGTCATGGGCAATGGGGTGTGGCACTTT	540
Oy	541	GGGGAGAACATGTGACACCCCTCATCACGGCCATGGATGCCAATATGTCACTTCAACAGACC	600
Db	541	GGGGAGAACATGTGACACCCCTCATCACGGCCATGGATGCCAATATGTCACTTCAACAGACC	600
Oy	601	TACATCTCGACCGCATGCGGCATTGACGCGTACGCGGCATGCGGCATGCGGCATGCGGC	660
Db	601	TACATCTCGACCGCATGCGGCATTGACGCGTACGCGGCATGCGGCATGCGGCATGCGGC	660
Oy	661	ACGAAGTCTCGGAAGCCCTGTGTGGCCACCTGGTATGTGCTCTCTGTGGGCCCTCTCC	720
Db	661	ACGAAGTCTCGGAAGCCCTGTGTGGCCACCTGGTATGTGCTCTCTGTGGGCCCTCTCC	720
Oy	721	TTTCATCAGCATACACCCCTGTGTGGCTGTATGTCACAGTCATCCCTCCAGAGAGGTGCA	780
Db	721	TTTCATCAGCATACACCCCTGTGTGGCTGTATGTCACAGTCATCCCTCCAGAGAGGTGCA	780
Oy	781	GTGGGCTCGGCGCATACGCTGGGCCCAACCCAGACATGACCTCTACTGTTCACCCCTGTAC	840
Db	781	GTGGGCTCGGCGCATACGCTGGGCCCAACCCAGACATGACCTCTACTGTTCACCCCTGTAC	840
Oy	841	CAGTTTTCCTGGCCCTTGGCCCTGTGTGTGTGTATCAACAGCCGATACAGTGAAGATC	900
Db	841	CAGTTTTCCTGGCCCTTGGCCCTGTGTGTGTGTATCAACAGCCGATACAGTGAAGATC	900
Oy	901	CTGCAGCGCATGACGTCCTCAGTGGCCCCCGCTCCAGAGAGCATCCGAGTCCGGGAGCA	960
Db	901	CTGCAGCGCATGACGTCCTCAGTGGCCCCCGCTCCAGAGAGCATCCGAGTCCGGGAGCA	960
Oy	961	AAGAGGGTGACCCGACAGCCCATCGCCATCTGTCTGTCTTTTGTGTGTGTGGGCACCC	1020
Db	961	AAGAGGGTGACCCGACAGCCCATCGCCATCTGTCTGTCTTTTGTGTGTGTGGGCACCC	1020
Oy	1021	TACGTGTGGCTACAGGTCGACCCAGTTGTTCATCAGCGCGCCGACCTCTCACTTGTCTAC	1080
Db	1021	TACGTGTGGCTACAGGTCGACCCAGTTGTTCATCAGCGCGCCGACCTCTCACTTGTCTAC	1080
Oy	1081	TTATACAATGCGGGCATCAGCTTGGGCTATGCCAACAAGCTGCTCAACCCCTTGTGTATC	1140
Db	1081	TTATACAATGCGGGCATCAGCTTGGGCTATGCCAACAAGCTGCTCAACCCCTTGTGTATC	1140
Oy	1141	ATGCGTCTGTGAGAGTTCGCGAAGAGCGTGGTCTGTGCGTGAAGCTCAGCCGAG	1200
Db	1141	ATGCGTCTGTGAGAGTTCGCGAAGAGCGTGGTCTGTGCGTGAAGCTCAGCCGAG	1200
Oy	1201	GGGCAAGCTTCGCGCTGTGAGCAACGCTCAGACGGCTGACGAGGAGAGGAGCAAGAAACAAA	1260
Db	1201	GGGCAAGCTTCGCGCTGTGAGCAACGCTCAGACGGCTGACGAGGAGAGGAGCAAGAAACAAA	1260
Oy	1261	GGCAGCTGGA 1269	
Db	1261	GGCAGCTGGA 1269	
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ID	ABK14548	standard; cdNA: 1269 BP.	
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XX	AC		
XX	DT	08-MAY-2002 (first entry)	
XX	DE	Human cDNA encoding melanin concentrating hormone receptor, MCH1.	
XX			

RESULT 2
ABK14548
ID ABK14548 standard; cDNA; 1269 BP.

AC	ABK14548;
XX	
XX	08-MAY-2002 (first entry)
DT	
XX	
XX	Human cDNA encoding melanin concentrating hormone receptor, MCH1
XX	

KW Human; ss; gene; melanin concentrating hormone receptor; MCH1;
KW steroid hormone disorder; pituitary hormone disorder;
KW epinephrine release disorder; gastrointestinal disorder;
KW cardiovascular disorder; hypertension; diabetes; respiratory disorder;
KW asthma; reproductive function disorder; immune disorder;
KW musculoskeletal disorder; neuroendocrine disorder; cognitive disorder;
KW memory disorder; motor coordination disorder; obesity; eating disorder;
KW dopaminergic function disorder; pain; psychosis; opiate addiction;
KW affective disorder; migraine; transgenic.

OS Homo sapiens.

Key Location/Qualifiers
FT CDS 1..1269
FT /tag= a
FT /product= "MCH1"

PN MO200202744-A2.

PD 10-JAN-2002.

PF 05-JUL-2001; 2001WO-US21350.

PR 05-JUL-2000; 2000US-0610635.

PA (SYNA-) SYNAPTIC PHARM CORP.

PI Salon JA, Laz TM, Nagorny R, Wilson AE.

DR WPI: 2002-164532/21.

DR P-PSDB; AAU735833.

PT Purified human melanin concentrating hormone receptor protein and
PT polynucleotides for screening modulator useful for treating memory
PT disorder, sensory modulation and transmission disorder, motor
PT coordination disorder

PS Claim 2; Fig 1; 524pp; English.

CC The invention relates to a purified human melanin concentrating hormone
CC (MCH1) receptor protein and its encoding nucleic acid (or mutant
CC activated by MCH or its analogue or homologue). Also included are
CC expression vectors, probes, transformed insect cells, antisense
CC oligonucleotides, anti-MCH1 antibodies, an agent capable of inhibiting
CC the binding of the antibody to MCH1, a transgenic animal expressing the
CC protein, or a homologous knockout or antisense complementary to the MCH1
CC nucleic acid, anti/agonists of MCH1, and methods of isolating chemical
CC compounds which activate MCH1. The protein, nucleic acid, antibody,
CC anti/agonists and compound are useful for diagnosing and treating a
CC steroid or pituitary hormone disorder, an epinephrine release disorder, a
CC gastrointestinal disorder, cardiovascular disorder, electrolyte balance
CC disorder, hypertension, diabetes, respiratory disorder, asthma,
CC reproductive function disorder, immune disorder, endocrine disorder,
CC musculoskeletal disorder, neuroendocrine disorder, cognitive disorder,
CC memory disorder, sensory modulation and transmission disorder, motor
CC coordination disorder, sensory integration disorder, motor integration
CC disorder, dopaminergic function disorder, sensory transmission disorder,
CC olfaction disorder, sympathetic innervation disorder, pain, psychotic
CC behaviour, morphine tolerance, opiate addiction, affective disorder,
CC stress-related disorder, fluid-balance disorder, seizure disorder or
CC migraine, an eating disorder or obesity. The present sequence
CC encodes human MCH1.

XX Sequence 1269 BP; 234 A; 419 C; 347 G; 269 T; 0 other;

Query Match 100.0%; Score 1269; DB 24; Length 1269;
Best Local Similarity 100.0%; Pred. No. 3.4e-285;
Matches 1269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGAGTGGGAGCCATGAAGAGGAGTGGGAGGCGAGTTGGCTTGGAGCGCGCAGC 60
Db 1 ATGTGAGTGGGAGCCATGAAGAGGAGTGGGAGGCGAGTTGGCTTGGAGCGCGCAGC 60

QY 61 GGCTGCAGAGGCTACGAGGAAGACCCCTTCCGACTCGGGGCTTGGCTCCGGGACAA 120
Db 61 GGCTGCAGAGGCTACGAGGAAGACCCCTTCCGACTCGGGGCTTGGCTCCGGGACAA 120
QY 121 GGTGGCAGGCGGTGAGAGGCTGGCGAGCTGCTGGTGGAGGAGAGCTGAGCTGGTTG 180
Db 121 GGTGGCAGGCGGTGAGAGGCTGGCGAGCTGCTGGTGGAGGAGAGCTGAGCTGGTTG 180
QY 181 TGGGACGAGGCGACCGGACATGCTGATGAGACCTGGAAGCCTGCTGCCACTGGT 240
Db 181 TGGGACGAGGCGACCGGACATGCTGATGAGACCTGGAAGCCTGCTGCCACTGGT 240
QY 241 CCCAATGCGAGCAACACCTGATGAGCCCGCATACCTGACTTACAGAGATACCTTCT 300
Db 241 CCCAATGCGAGCAACACCTGATGAGCCCGCATACCTGACTTACAGAGATACCTTCT 300
QY 301 CGCAGGGGAGACATCTCTACATCAACATCAATGCTTGGTGGTGGCAGCATCTGC 360
Db 301 CGCAGGGGAGACATCTCTACATCAACATCAATGCTTGGTGGTGGCAGCATCTGC 360
QY 361 CTCCTGGGATCATGAGGAACTCCAGGTCATCTTCCGGTGGTGGAGAGTCCAACTG 420
Db 361 CTCCTGGGATCATGAGGAACTCCAGGTCATCTTCCGGTGGTGGAGAGTCCAACTG 420
QY 421 CACTGTGCACAAACGTCCTCCGACATCTTCATCAACCTCTGGTAGTAGATCTCTC 480
Db 421 CACTGTGCACAAACGTCCTCCGACATCTTCATCAACCTCTGGTAGTAGATCTCTC 480
QY 481 TTTCTCTGGGATGACCTTTCATGATCCAGCAGTCAATGAGGCAATGGGATGGTGG 540
Db 481 TTTCTCTGGGATGACCTTTCATGATCCAGCAGTCAATGAGGCAATGGGATGGTGG 540
QY 541 GGGGAGACATGTGACACCTTATACAGGCACTGATGATGATGATGATGATGATGATG 600
Db 541 GGGGAGACATGTGACACCTTATACAGGCACTGATGATGATGATGATGATGATGATG 600
QY 601 TACATCTGACGACGATGACGCTGACCTGACCTGACCTGACCTGACCTGACCTGAC 660
Db 601 TACATCTGACGACGATGACGCTGACCTGACCTGACCTGACCTGACCTGACCTGAC 660
QY 661 ACGAAGTTCGGAAGCCCTGTTGGCCACCTGATGATGATGATGATGATGATGATGAT 720
Db 661 ACGAAGTTCGGAAGCCCTGTTGGCCACCTGATGATGATGATGATGATGATGATGAT 720
QY 721 TTTACACATACACCCCTGTTGGCTGATGATGATGATGATGATGATGATGATGATG 780
Db 721 TTTACACATACACCCCTGTTGGCTGATGATGATGATGATGATGATGATGATGATG 780
QY 781 GTGGCTGCGGACATACGCTGCTCCCAACACGACGACGACGACGACGACGACGACG 840
Db 781 GTGGCTGCGGACATACGCTGCTCCCAACACGACGACGACGACGACGACGACGACG 840
QY 841 CAGTTTTTCTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTT 900
Db 841 CAGTTTTTCTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTT 900
QY 901 CTGAGGCGCATGAGCTGCTGAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 960
Db 901 CTGAGGCGCATGAGCTGCTGAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 960
QY 961 AAGAGGTGACCCGACAGACGATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
Db 961 AAGAGGTGACCCGACAGACGATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
QY 1021 TACTATGTGCTACAGCTGACCACTTGTCAATACGCGCGGACCTGACCTTGTCTAC 1080
Db 1021 TACTATGTGCTACAGCTGACCACTTGTCAATACGCGCGGACCTGACCTTGTCTAC 1080
QY 1081 TTATACATGAGGCGCATGAGCTTGGCTGATGATGATGATGATGATGATGATGATG 1140
Db 1081 TTATACATGAGGCGCATGAGCTTGGCTGATGATGATGATGATGATGATGATGATG 1140
QY 1141 ATGTGCTCTGTGAGACGTTCCGCAACGCTTGTGCTGTGTGTGTGTGTGTGTGTGT 1200

|||||
Db 1141 ATGTGCTCTGTAGAGCTTCGCAACGGTTGTCTCTCGTGTGAAGCTGAGCCAG 1200
Qy 1201 GGGCAGCTTGGCGCTGTACGAACGCTCAGACGGCTGAGAGAGAGACAGAAACAA 1260
Db 1201 GGGCAGCTTGGCGCTGTACGAACGCTCAGACGGCTGAGAGAGAGAGAAAGCAA 1260
Qy 1261 GGCACCTGA 1269
Db 1261 GGCACCTGA 1269
RESULT 3
AAD13654
ID AAD13654 standard; cDNA; 1269 BP.
AC AAD13654;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human melanin-concentrating hormone receptor variant #3 cDNA.
XX
KW Human; melanin-concentrating hormone; MCH analogue; signal transduction;
KW appetite; therapy; anorexia; acquired immune deficiency syndrome; AIDS;
KW wasting; cachexia; frail elderly; weight maintenance; cancer; anorectic;
KW pain reduction; stress reduction; sexual dysfunction; variant; ss.
XX
OS Homo sapiens.
XX
OS synthetic.
XX
FH Key Location/Qualifiers
FT CDS 1..1269
FT /tag= a
FT /product= "Human MCH receptor protein variant #3"
XX
PN W0200157070-A1.
XX
PD 09-AUG-2001.
XX
PF 01-FEB-2001; 2001MO-US03293.
XX
PR 03-FEB-2000; 2000US-0179967.
XX
PA (MERI) MERCK & CO INC.
XX
PI Bednarek M;
XX
DR WPI; 2001-463416/52.
DR P-PSDB; AAE07330.
XX
PT Novel peptide encoding a melanin-concentrating hormone analog useful
PT for increasing weight or appetite -
XX
XX
PS Disclosure; Page 33; 66pp; English.
XX
CC The present invention relates to truncated melanin-concentrating hormone
CC (MCH) analogues active at the MCH receptor. The truncated MCH analogues
CC are optionally modified peptide derivatives of mammalian MCH. The MCH
CC analogues can bind to the MCH receptor and bring about signal
CC transduction. The MCH agonists can be used to facilitate a weight gain,
CC maintenance of weight and/or an appetite increase. The MCH agonists can
CC also be used to treat disorders such as anorexia, acquired immune
CC deficiency syndrome (AIDS), wasting, cachexia and frail elderly. The MCH
CC antagonists can be used to facilitate weight loss, appetite decrease,
CC weight maintenance, cancer treatment, pain reduction, stress reduction
CC and/or treatment of sexual dysfunction. The present sequence is a human
CC MCH receptor variant cDNA.
XX
SQ Sequence 1269 BP; 234 A; 420 C; 347 G; 268 T; 0 other;

Query Match 99.68; Score 1264.2; DB 22; Length 1269;
Best Local Similarity 99.88; Pred. No. 4,4e-284;
Matches 1266; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATGTGAGTGGAGCCATGAAAGAGATGGAGAGGAGTGGGCTTGGAGGCGGAGC 60
Db 1 ATGTGAGTGGAGCCATGAAAGAGAGTGGAGAGGAGTGGGCTTGGAGGCGGAGC 60
Qy 61 GCGTCGACGGCTACGAGAGAACCCCTTCCGACATCGGGGGCTTGCTCCGGACAA 120
Db 61 GCGTCGACGGCTACGAGAGAACCCCTTCCGACATCGGGGGCTTGCTCCGGACAA 120
Qy 121 GGTGGCAGGCGCTGGAGGCTCCGACGCTCGTGGGTGGAGGGAGCTACGCTGGTTG 180
Db 121 GGTGGCAGGCGCTGGAGGCTCCGACGCTCGTGGGTGGAGGGAGCTACGCTGGTTG 180
Qy 181 TGGAGCAGGCGGACGCGACATGGCTGATGAGACCTGGAACCTCGCTGTCGCCACTGGT 240
Db 181 TGGAGCAGGCGGACGCGGACATGGCTGATGAGACCTGGAACCTCGCTGTCGCCACTGGT 240
Qy 241 CCCAATGCCAGCAACACCTGTGATGGCCCGATAAACCTCACTTACAGACATCACTTCCT 300
Db 241 CCCAATGCCAGCAACACCTGTGATGGCCCGATAAACCTCACTTGGCAGGATCACTTCCT 300
Qy 301 CGCAGGGGAGCATCTCTACATCAACATCAATCAATGCTTGGGTGGGACCATGTCG 360
Db 301 CGCAGGGGAGCATCTCTACATCAACATCAATCAATGCTTGGGTGGGACCATGTCG 360
Qy 361 CTCTGGGCGATCATGGGAACTCCACGGCTCATCTTCGCGGTGCTGAAAGAACTCCAACTG 420
Db 361 CTCTGGGCGATCATGGGAACTCCACGGCTCATCTTCGCGGTGCTGAAAGAACTCCAACTG 420
Qy 421 CACTGGTGCACACACGTCCTCCGACATCTTCAATCAATCAACCTCTCGGTAGTATCTCTC 480
Db 421 CACTGGTGCACACACGTCCTCCGACATCTTCAATCAATCAACCTCTCGGTAGTATCTCTC 480
Qy 481 TTTCTCTGGGATGCGCTTATGATGATCCACAGGCTCATGGGCAATGGGTTGGCACTTT 540
Db 481 TTTCTCTGGGATGCGCTTATGATGATCCACAGGCTCATGGGCAATGGGTTGGCACTTT 540
Qy 541 GGGAGACCATGTGCACCTCATCAGGCGCATGTGACCAATAGTCACTTACACGACAC 600
Db 541 GGGAGACCATGTGCACCTCATCAGGCGCATGTGACCAATAGTCACTTACACGACAC 600
Qy 601 TACATCTGACCGCATGACCGCTTATGACCGCTTATGACCGCTTATGACCGCTTATG 660
Db 601 TACATCTGACCGCATGACCGCTTATGACCGCTTATGACCGCTTATGACCGCTTATG 660
Qy 661 ACGAAGTCCGGAAGCCCTGTGGCCACCGTGGATCTGCTCTGTGGCCCTCTCC 720
Db 661 ACGAAGTCCGGAAGCCCTGTGGCCACCGTGGATCTGCTCTGTGGCCCTCTCC 720
Qy 721 TTTATCAGCATACCCCTGTGTGCTGTATGACAGACTCATCCCTTCCAGAGAGTGA 780
Db 721 TTTATCAGCATACCCCTGTGTGCTGTATGACAGACTCATCCCTTCCAGAGAGTGA 780
Qy 781 GTGGGCTGGCGATACGCGCTGCGCCCAACCAAGACACTGACTCTTACTGTTACCTGTAC 840
Db 781 GTGGGCTGGCGATACGCGCTGCGCCCAACCAAGACACTGACTCTTACTGTTACCTGTAC 840
Qy 841 CAGTTTTCCTGGGCTTGGCCCTGCTTGTGGTATCAACAGCGCATAGTGAGATC 900
Db 841 CAGTTTTCCTGGGCTTGGCCCTGCTTGTGGTATCAACAGCGCATAGTGAGATC 900
Qy 901 CTGCAGCGCATAGCTCTCACTGTGCCCCCGGCTTCCAGCGCAGCATCGGCTGGGACA 960
Db 901 CTGCAGCGCATAGCTCTCACTGTGCCCCCGGCTTCCAGCGCAGCATCGGCTGGGACA 960
Qy 961 AAGAGGATACCCGACACAGCATGCTGTGTGCTTCTTGTGTGCTGGGACACC 1020
Db 961 AAGAGGATACCCGACACAGCATGCTGTGTGCTTCTTGTGTGCTGGGACACC 1020
Qy 1021 TACTATGTCTACAGTGCACAGTGTGTCATCAGCCGCGACCCCTACCTTTGTCTAC 1080
Db 1021 TACTATGTCTACAGTGCACAGTGTGTCATCAGCCGCGACCCCTACCTTTGTCTAC 1080

|||||
Db 1021 TACTATGTGGTACAGCTGACGCCAGTGTGTCATGACGGCCGACCCCTACCTTTGTCTAC 1080
QY 1081 TTATACATGCGCGCATCAGCTTGGCTATGCCAACAGCTGCTCAACCCCTTTGTGTAC 1140
Db 1081 TTATACATGCGCGCATCAGCTTGGCTATGCCAACAGCTGCTCAACCCCTTTGTGTAC 1140
QY 1141 ATCTGCTGCTGTAGAGCTTCCGCAACGCTTGGTCTGTGCTGGTGAAGCCTGACGCCAG 1200
Db 1141 ATCTGCTGCTGTAGAGCTTCCGCAACGCTTGGTCTGTGCTGGTGAAGCCTGACGCCAG 1200
QY 1201 GGGCAGCTTGGCGCTGTACAGAACGCTCAGACGGCTGACGAGGAGAGACAGAAAGCAA 1260
Db 1201 GGGCAGCTTGGCGCTGTACAGAACGCTCAGACGGCTGACGAGGAGAGACAGAAAGCAA 1260
QY 1261 GGCACCTGA 1269
Db 1261 GGCACCTGA 1269

RESULT 5

AAH47297 standard; cDNA: 1269 BP.

AAH47297;

30-NOV-2001 (first entry)

Human long form MCHIR cDNA.

Melanin concentrating hormone receptor; MCHIR; MCH; chimeric; fusion;

fluorescent polypeptide; orexigenic; anabolic; food intake; MCHIR; ss.

Homo sapiens.

Location/Qualifiers

1..1269

/*tag= a

WO200168706-A1.

20-SEP-2001.

14-MAR-2001; 2001WO-US08071.

15-MAR-2000; 2000US-0189698.

(MERI) MERCK & CO INC.

Marsh DJ;

WPI: 2001-565791/63.

P-PSDB: AAB85894.

Fusion proteins comprising melanin concentrating hormone receptor

peptides and fluorescent proteins, useful for identifying appetite

stimulants -

Example 1; Page 17-18; 71pp; English.

The invention provides melanin concentrating hormone (MCH) receptor

(MCHIR) chimeric and fusion proteins. The MCHIR chimeric proteins comprise

MCHIR polypeptide regions from different species. The MCHIR fusion protein

comprise MCHIR polypeptide region and a fluorescent polypeptide region

joined directly, or via a linker, to the carboxy side of the MCHIR

polypeptide region. The MCHIR fusion proteins can be expressed by standard

recombinant methodology. MCH action promotes feeding (orexigenic) and up

regulation of MCH activity stimulates food intake. The present sequence

Best Local Similarity 99.8%; Pred. No. 4,4e-284;
Matches 1266; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGTAGTGGGAGCCATGAGAGAGGAGTGGGGAGAGTGGCTTGGAGGGGGAGC 60
Db 1 ATGTAGTGGGAGCCATGAGAGAGGAGTGGGGAGAGTGGCTTGGAGGGGGAGC 60
QY 61 GGTCTGCAGAGCTACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
Db 61 GGTCTGCAGAGCTACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
QY 121 GGTGAGGAGGCTGAGAGAGCTGCGCAGCTGCGTGGTGGAGAGAGTCAAGCTTG 180
Db 121 GGTGAGGAGGCTGAGAGAGCTGCGCAGCTGCGTGGTGGAGAGAGTCAAGCTTG 180
QY 181 TGGGAGCAGGAGCAGGAGCAGCTGCGTGGAGAGCTGGAAGCCTGCTGCGCAGTGGT 240
Db 181 TGGGAGCAGGAGCAGGAGCAGCTGCGTGGAGAGCTGGAAGCCTGCTGCGCAGTGGT 240
QY 241 CCCAATGCGCAGCAGACCTGTGATGAGCCCGATACCTCATTGACAGAGATCACTTCT 300
Db 241 CCCAATGCGCAGCAGACCTGTGATGAGCCCGATACCTCATTGACAGAGATCACTTCT 300
QY 301 GGCAGGGGAGCATCTCTACATCAACATCATATGCTTGGTGTGGACCATCTGC 360
Db 301 GGCAGGGGAGCATCTCTACATCAACATCATATGCTTGGTGTGGACCATCTGC 360
QY 361 CTCCTGGGATATGGGAGAGCTCCAGGGATCTTGGGGTGGAGAGAGAGAGAGAG 420
Db 361 CTCCTGGGATATGGGAGAGCTCCAGGGATCTTGGGGTGGAGAGAGAGAGAGAG 420
QY 421 CACTGTGTGACAGACGCTCCCGCAGCATCTTCAATCAACCTCTCGTGTAGATCTCTC 480
Db 421 CACTGTGTGACAGACGCTCCCGCAGCATCTTCAATCAACCTCTCGTGTAGATCTCTC 480
QY 481 TTTTCTCTGGCATGCTCTTCAATGATCCAGCAGCTCATAGGGGATGGGAGTCTT 540
Db 481 TTTTCTCTGGCATGCTCTTCAATGATCCAGCAGCTCATAGGGGATGGGAGTCTT 540
QY 541 GGGGAGACCATGAGACCTCTCATGAGGAGCATGAGTGCATATGTCATTCACAGCAGC 600
Db 541 GGGGAGACCATGAGACCTCTCATGAGGAGCATGAGTGCATATGTCATTCACAGCAGC 600
QY 601 TACATCTGACCGCATGAGCGCATGACGCTACCTGAGCAGCTGACACCCATCTCTCC 660
Db 601 TACATCTGACCGCATGAGCGCATGACGCTACCTGAGCAGCTGACACCCATCTCTCC 660
QY 661 ACGAAGTTCGGAGAGCCCTGTGGGAGACCTGAGATGCTGCTCTGTGGGCTCTCC 720
Db 661 ACGAAGTTCGGAGAGCCCTGTGGGAGACCTGAGATGCTGCTCTGTGGGCTCTCC 720
QY 721 TTTCATGAGCATACCCCTGTGGTGTATGTCAGACTCATCCCTTCCAGAGAGTGA 780
Db 721 TTTCATGAGCATACCCCTGTGGTGTATGTCAGACTCATCCCTTCCAGAGAGTGA 780
QY 781 GTGGGCTGCGGATACGCTTGGGAGACCTGAGAGTGTGCTGCTGCTGCTGCTG 840
Db 781 GTGGGCTGCGGATACGCTTGGGAGACCTGAGAGTGTGCTGCTGCTGCTGCTG 840
QY 841 CAGTTTCTGAGCCTTGGGAGCCTTGTGGTGTATGTCAGAGCGCATAGTGAAGATC 900
Db 841 CAGTTTCTGAGCCTTGGGAGCCTTGTGGTGTATGTCAGAGCGCATAGTGAAGATC 900
QY 901 CTGACGAGATGACGCTCAGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
Db 901 CTGACGAGATGACGCTCAGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
QY 961 AAGAGGATGACCGCAG 1020
Db 961 AAGAGGATGACCGCAG 1020
QY 1021 TACTATGTGCTACAGTGAAGAGAGTGTGTCATGAGCGCGCAGACCTGCTGTAC 1080
Db 1021 TACTATGTGCTACAGTGAAGAGAGTGTGTCATGAGCGCGCAGACCTGCTGTAC 1080

XX
CC
XX

which is used in an example from the present invention.

Db 967 AAGAGGTTGACCCGACAGCCATCGCCATCTGTCTGTTTGTGTGCTGGCACC 10

Db	607	TACATCCTGACCGGCAATGAGCCATTTGACCGCTTACCTGGCCACTGTCCACCCCATCTCTTCC	666
QY	661	ACGAAGTTCGGGAAGCCCTCTGTGGCCACCCCTGGTATCTGCCTCTGTGGGCCCTCTCC	720
Db	667	ACGAAGTTCGGGAAGCCCTCTGTGGCCACCCCTGGTATCTGCCTCTGTGGGCCCTCTCC	726
QY	721	TTTCATCAGCATCACCCCGTGTGGCTGTATGGCAGACTATCCCTTTGCCAGAGAGTGA	780
Db	727	TTTCATCAGCATCACCCCGTGTGGCTGTATGGCAGACTATCCCTTTGCCAGAGAGTGA	786
QY	781	GTGGGCTCGGGCATACGCTCTGTGCCCAACCCAGACACTGACCTTACTGCTTCAACCTGTAC	840
Db	787	GTGGGCTCGGGCATACGCTCTGTGCCCAACCCAGACACTGACCTTACTGCTTCAACCTGTAC	846
QY	841	CAGTTTTTCTTCGCGCTTTTGCCCTGTCTTTTGTGTGTCATCACAGCCGATACGTAGAGATC	900
Db	847	CAGTTTTTCTTCGCGCTTTTGCCCTGTCTTTTGTGTGTCATCACAGCCGATACGTAGAGATC	906
QY	901	CTGCAGCGCATGACGTCTCTAGTGGGCCCGGCTCCGACGGAGACATCCGGCTGGGGACA	960
Db	907	CTGCAGCGCATGACGTCTCTAGTGGGCCCGGCTCCGACGGAGACATCCGGCTGGGGACA	966
QY	961	AAGAGGGTGAACCCGACACAGCCATGCGCATCTGTCTGTCTTTTGTGTGGGACACC	1020
Db	967	AAGAGGGTGAACCCGACACAGCCATGCGCATCTGTCTGTCTTTTGTGTGGGACACC	1026
QY	1021	TACTATGTGCTACAGCTGAGCCAGATTGTCCATGACGGCGCCGACCCCTACCTTTGTCTAC	1086
Db	1027	TACTATGTGCTACAGCTGAGCCAGATTGTCCATGAGCGCGCCGACCCCTACCTTTGTCTAC	1086
QY	1081	TTTATACAAATGCGGCGCATCAGCTTTGGGCTATGCCCAAGCTGCTCAACCCCTTTGTCTAC	1140
Db	1087	TTTATACAAATGCGGCGCATCAGCTTTGGGCTATGCCCAAGCTGCTCAACCCCTTTGTCTAC	1146
QY	1141	ATCGGCTGTGTGAGAGCTTCCGCAAAAGCTTGTGTCTGTGCTGTGAAGCTTCAACCCAG	1200
Db	1147	ATCGGCTGTGTGAGAGCTTCCGCAAAAGCTTGTGTCTGTGCTGTGAAGCTTCAACCCAG	1206
QY	1201	GGGAGGCTTCCGCGCTGTACAGCAACGCTCAGACGCTGACGAGGAGAGGACAGAAAGCAAA	1260
Db	1207	GGGAGGCTTCCGCGCTGTACAGCAACGCTCAGACGCTGACGAGGAGAGGACAGAAAGCAAA	1266
QY	1261	GGCACCCTGA 1269	
Db	1267	GGCACCCTGA 1275	
RESULT 12			
AAA72924			
ID	AAA72924	standard; cDNA: 1283 BP.	
XX	AAA72924:		
AC			
XX	22-NOV-2000	(first entry)	
DT			
XX			
DE			
XX	Human SLC-1 (L) cDNA sequence SEQ ID NO:17.		
XX			
KW	SLC-1; MHC; melanin concentrating hormone; screening; eating;		
KW	appetite stimulant; appetite regulator; period pain; atonic bleeding;		
KW	cesarean section; milk congestion; antibiotic agent; drug;		
KW	fetal asphyxia; cervical rupture; premature birth; uterine rupture;		
KW	Prader-Willi syndrome; anorectic; gynaecological; abortifaciant;		
KW	antonaemia; anabolic; orphan G protein-couple receptor protein; ss.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200040725-A1.		
XX			
PD	13-JUL-2000.		
XX			
FP	27-DEC-1999;	99MO-JP07336.	
XX			
PR	28-DEC-1998;	98JP-0374454.	

PR 28-APR-1999; 99JP-0122688.
PR 02-SEP-1999; 99JP-0249300.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
XX Mori M, Shimomura Y, Takekawa S, Sugo T, Ishibashi Y, Kltada C,
PI Suzuki N;
XX WPI; 2000-475832/41.
DR

PS Example 11, Page 115-116; 123pp; Japanese.

CC The present invention describes method for screening components (1) or
CC their salts that can alter the binding properties of melanin-
CC concentrating hormone (MCH) or its derivative or salt to SLC-1 or its
CC salt. Compounds identified by (1) are useful as SLC-1 (antagonists in
CC eating disorders and as preventives and remedies for e.g. period pains,
CC uterine recovery failure, caesarean section, artificial interruption of
CC pregnancy, galactosistosis, tonic uterine contraction, foetal asphyxia,
CC rupture of uterus, cervical rupture, premature birth and Prader-Willi
CC syndrome. The present sequence represents a human SLC-1 cDNA sequence,
CC which is used in an example from the present invention.

50 Sequence 1283 BP; 238 A; 423 C; 350 G; 272 T; 0 other;

Query Match	99.6%	Score 1264.2	DB 21	Length 1283

Matches 1266; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY	1	ATATGACATGGGGAGGCGCATTAACAAGAAGAGTGGGGAGGGGACAGTGGGCTTGGAGCGGCGAGC	60
Db	8	ATGTGATAGTGGGAGGCGCATTAACAAGAAGAGTGGGGAGGGGACAGTGGGCTTGGAGCGGCGAGC	67
OY	61	GGCTGCGCAGGGCTACGAGAGGAAGACCCCTTCTCCACACTGCGGGGGCTTCGCTCCGGGACAA	120
Db	68	GGCTGCGCAGGGCTACGAGAGGAAGACCCCTTCTCCACACTGCGGGGGCTTCGCTCCGGGACAA	127
OY	121	GGTGGCAGGCGCTGGAGGCTGCCGACACTGCGTGGGTGGAGGGAGCACTGCTCGTTG	180
Db	128	GGTGGCAGGCGCTGGAGGCTGCCGACAGCTCGTGGGTGGAGGGAGCACTGAGCTCGGTTG	187
OY	181	TGGGAGCAGAGGCGACCGGCACTGCTGGATGAGCACTGGAAGCTTCGCTGCGCCACTGGT	240
Db	188	TGGGAGCAGAGGCGACCGGCACTGCTGGATGAGCACTGGAAGCTTCGCTGCGCCACTGGT	247
OY	241	CCCAATGCGCACCAACACCTTGATGGGGCCCGATTAACCTCACTCAGAGGATACACCTCT	300
Db	248	CCCAATGCGCACCAACACCTTGATGGGGCCCGATTAACCTCACTTGGAGGATACACCTCT	307
OY	301	CGCACGGGGAGACATCTCTCAATCAACATCATCATGCTTCGGGTTCGGGACACATCTGC	360
Db	308	CGCACGGGGAGACATCTCTCAATCAACATCATCATGCTTCGGGTTCGGGACACATCTGC	367
OY	361	CTCTCTGGGCATCATCGGGAACTCCAGGCTCATCTTCGGGTCGTGAAGAATCCAAGCTG	420
Db	368	CTCTCTGGGCATCATCGGGAAATCCACGCTCATCTTCGGGTCGTGAAGAATCCAAGCTG	427
OY	421	CACATGATCAACACAGTCCCGCAATTTATCATCAACCTCTCGGATGAGATATCTCTC	480
Db	428	CACATGATCAACACAGTCCCGCAATTTATCATCAACCTCTCGGATGAGATATCTCTC	487
OY	481	TTTCTCTCGGGGCATGCCCTTTCATGATCACCAGCTCATTGGGCAATGGGGTGTGGACATT	540
Db	488	TTTCTCTCGGGGCATGCCCTTTCATGATCACCAGCTCATTGGGCAATGGGGTGTGGACATT	547
OY	541	GGGAGAGACATGTGACACCTTCATCAGGGCATGGATGCCAATAGTAGTTCACACAGCACCC	600
Db	548	GGGAGAGACATGTGACACCTTCATCAGGGCATGGATGCCAATAGTAGTTCACACAGCACCC	607


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QY 721 TTCATCAGCATCACCCCTGTGTGCTGTATGCCAGACTATCCCTTCCAGAGGTGCA 780
    |||||||
Db 728 TTCTACAGCATCACCCCTGTGTGCTGTATGCCAGACTATCCCTTCCAGAGGTGCA 787
    |||||||
QY 781 GTGGGCTGGGGCATACGCTGCCCCAACCCAGACACTGACCTGTACTGTTACCCCTGTAC 840
    |||||||
Db 788 GTGGGCTGGGGCATACGCTGCCCCAACCCAGACACTGACCTGTACTGTTACCCCTGTAC 847
    |||||||
QY 841 CAGTTTTCCTGGCCTTGGCCCTTGTGTGTGTCATCAGCCGATACGTAGAGATC 900
    |||||||
Db 848 CAGTTTTCCTGGCCTTGGCCCTTGTGTGTGTCATCAGCCGATACGTAGAGATC 907
    |||||||
QY 901 CTGCAGCGCATGACGTCTGAGTGCCGCCCTCCAGCGCATCCGGCTGCGGACA 960
    |||||||
Db 908 CTGCAGCGCATGACGTCTGAGTGCCGCCCTCCAGCGCATCCGGCTGCGGACA 967
    |||||||
QY 961 AAGAGGGTGACCCGCAACGCAATCGCCATCTGTGTCTTCTTGTGTGCTGGGACCC 1020
    |||||||
Db 968 AAGAGGGTGACCCGCAACGCAATCGCCATCTGTGTCTTCTTGTGTGCTGGGACCC 1027
    |||||||
QY 1021 TACTATGTGTAGAGTGANCCAGTTGTCTATAGCCGCCGACCTCACCCTTGTCTAC 1080
    |||||||
Db 1028 TACTATGTGTAGAGTGANCCAGTTGTCTATAGCCGCCGACCTCACCCTTGTCTAC 1087
    |||||||
QY 1081 TTATACATGCGGSCATACGCTGGGCTATGCCAACAGCTGCCCAACCCCTTGTGTAC 1140
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Db 1088 TTATACATGCGGSCATACGCTGGGCTATGCCAACAGCTGCCCAACCCCTTGTGTAC 1147
    |||||||
QY 1141 ATCGTCTCTGTGAGAGTTCGCCAAACGCTTGTCTGTGCTGTAAGCCTGCAGCCAG 1200
    |||||||
Db 1148 ATCGTCTCTGTGAGAGTTCGCCAAACGCTTGTCTGTGCTGTAAGCCTGCAGCCAG 1207
    |||||||
QY 1201 GGGCAGCTTGGCCTGTGAGCAAGCTCAGACGGCTGACGAGAGAGAGCAAGCAAA 1260
    |||||||
Db 1208 GGGCAGCTTGGCCTGTGAGCAAGCTCAGACGGCTGACGAGAGAGAGCAAGCAAA 1267
    |||||||
QY 1261 GGCACCTGA 1269
    |||||||
Db 1268 GGCACCTGA 1276
    |||||||

```

Search completed: February 19, 2003, 09:33:07
 Job time : 299 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 19, 2003, 09:23:11 ; Search time 2090 Seconds
(without alignments)
9833.528 Million cell updates/sec

Title: US-09-885-478-1
Perfect score: 1269
Sequence: 1 atgtcagtcggcgccatgaa.....cagaagcaagcaccctga 1269

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gd_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	973.8	76.7	1114	14	BM805549
2	886.4	69.9	958	13	BM805549
3	811.8	64.0	872	13	BM805549
4	773.4	60.9	921	13	BM805549
5	769.8	60.7	797	13	BM805549
6	625.2	49.3	834	12	BM805549

7	609.4	48.0	845	12	BM805549
8	590.2	46.5	869	13	BM805549
9	566.2	44.6	885	13	BM805549
10	489	38.5	859	10	BM805549
11	386.4	30.4	600	10	BM805549
12	344	27.1	345	14	BM805549
13	289.2	22.8	387	10	BM805549
14	272.8	21.5	1086	12	BM805549
15	270.6	21.3	313	13	BM805549
16	246	19.4	497	12	BM805549
17	209	16.5	440	12	BM805549
18	201.4	15.9	264	10	BM805549
19	157.4	12.4	288	10	BM805549
20	153.8	12.1	260	10	BM805549
21	152.8	12.0	284	10	BM805549
22	139	11.0	274	10	BM805549
23	116.8	9.2	642	10	BM805549
24	116.4	9.2	904	12	BM805549
25	113.4	8.9	995	17	BM805549
26	105.4	8.3	720	13	BM805549
27	104.6	8.2	794	17	BM805549
28	104.4	8.2	937	17	BM805549
29	103.6	8.2	656	9	BM805549
30	100.2	7.9	1029	17	BM805549
31	95.8	7.5	852	9	BM805549
32	92.2	7.3	1141	17	BM805549
33	91.2	7.2	741	13	BM805549
34	84.8	6.7	836	17	BM805549
35	84.6	6.7	980	13	BM805549
36	83.4	6.6	529	9	BM805549
37	83.2	6.6	877	17	BM805549
38	82.4	6.5	2146	11	BM805549
39	80.8	6.4	785	13	BM805549
40	79.2	6.2	960	13	BM805549
41	79	6.2	908	17	BM805549
42	78.2	6.2	730	9	BM805549
43	78	6.1	834	9	BM805549
44	78	6.1	878	9	BM805549
45	6.1	938	9	AL543359	

ALIGNMENTS

RESULT 1
BM805549
LOCUS
DEFINITION
AGENCOURT_6498483 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:5729087
5', mRNA sequence.
ACCESSION
BM805549
VERSION
BM805549.1 GI:19122372
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1114)
AUTHORS
NIH-MGC http://mgc.nci.nih.gov/
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
CONTACT
Contact: Robert Strausberg, Ph.D.
COMMENT
Email: cgabs-remail.nih.gov
Tissue Procurement: Invitrogen
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMNL at:
http://image.llnl.gov
Plate: L1AM12725 row: m column: 24
High quality sequence start: 52
High quality sequence stop: 684.
Location/Qualifiers

FEATURES

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source
1. 1114
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5729087"
/clone_1lb="NIH_MGC_114"
/issue_type="hippocampus"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMV-SPORT6; Site: 1: EcoRV
(destroyed); Site 2: NotI: RNA source male hippocampus,
age 27. Library is oligo-dT primed and directionally
cloned (EcoRV site is destroyed upon cloning). Average
insert size 1.4 kb, insert size range 0.9-4 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 012."

BASE COUNT      198 a      375 c      299 g      241 t      1 others
ORIGIN

Query Match      76.7%; Score 973.8; DB 14; Length 1114;
Best Local Similarity 95.7%; Pred. No. 1.3e-208;
Matches 1043; Conservative 0; Mismatches 43; Indels 4; Gaps 4;

QY 29 TGGGAGGAGGAGTTGGGCTTGAGAGCGGACCGCTGCCAGGCTACGAGAGAACACCCCC 88
Db 23 TGGGAGGAGGAGTTGGGCTTGAGAGCGGCTTCGGTTGGCACTACGAGAGAACACCCCC 82
QY 89 TTCCCGACTGGGAGGCTTGCCTCCGGGACAAAGGTGCGAGCGCTGGAGGCTGCCGAGC 148
Db 83 TTCCCGACTGGGAGGCTTGCCTCCGGGACAAAGGTGCGAGCGCTGGAGGCTGCCGAGC 142
QY 149 CTGCGTGGGTGGAGGAGGCTCAGCTGGTGTGGAGACAGCGACCGGCACTGGCTGA 208
Db 143 CTGCGTGGGTGGAGGAGGCTCAGCTGGTGTGGAGACAGCGACCGGCACTGGCTGA 202
QY 209 TGGACCTGGAAGCCCTGCTGCTGGCCACTGGTCCCAATGCCAGAAACACCTCTATGGCC 268
Db 203 TGGACCTGGAAGCCCTGCTGCTGGCCACTGGTCCCAATGCCAGAAACACCTCTATGGCC 262
QY 269 CCGATTAACCTCACTTCACAGAGATCACCTCTCCGACAGGAGGAGCATCTCTACATCAACA 328
Db 263 CCGATTAACCTCACTTCGCGAGAGATCACCTCTCCGACAGGAGGAGCATCTCTACATCAACA 322
QY 329 TCATCATCCCTTGGGTGTTGGGACACATCTGCTCTGGGACATATCGGGAATCCACGG 388
Db 323 TCATCATCCCTTGGGTGTTGGGACACATCTGCTCTGGGACATATCGGGAATCCACGG 382
QY 389 TCATTTGGCGGTGGTGAAGAAGTCCAAAGTGCACCTGGTGAACAAGTCCCGCAACTCT 448
Db 383 TCATTTGGCGGTGGTGAAGAAGTGCACCTGGTGAACAAGTCCCGCAACTCT 442
QY 449 TCATCATCAACCTCTCGGTAGTATCTCTCTCTCTCTGGGACATCCCTTCATGTATCC 508
Db 443 TCATCATCAACCTCTCGGTAGTATCTCTCTCTCTCTGGGACATCCCTTCATGTATCC 502
QY 509 ACCAGCTATGGGCAATGGGCTGTGGCACTTGGGAGAGACATATGCAACCTCATACAGG 568
Db 503 ACCAGCTATGGGCAATGGGCTGTGGCACTTGGGAGAGACATATGCAACCTCATACAGG 562
QY 569 CCATGATGCAATAGTTCAGTTCACACGACCTACATCTGACCGCATGGCCATTTGACC 628
Db 563 CCATGATGCAATAGTTCAGTTCACACGACCTACATCTGACCGCATGGCCATTTGACC 622
QY 629 GCTACCTGGGCACTGTCCACCCCATCTCTTCACAGAAAGTTCGGGAAGCCCTCTGTGGCCA 688
Db 623 GCTACCTGGGCACTGTCCACCCCATCTCTTCACAGAAAGTTCGGGAAGCCCTCTGTGGCCA 682
QY 689 CCTGGGATGCTGCTCTGTGGGCTCTCTCTTCATCAGCATACCCCTGTGGCTGT 748
Db 683 CCTGGGATGCTGCTCTGTGGGCTCTCTCTTCATCAGCATACCCCTGTGGCTGT 742
QY 749 ATGCGACACTATCCCTTCCCA-GAAGTCACTGGGCTCGGCAATAGGCTGCCAAC 808
Db 743 ATGCGACACTATCCCTTCCCA-GAAGTCACTGGGCTCGGCAATAGGCTGCCAAC 801

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QY 809 CAGACACTGACCTTACTGSGTTCACCCCTGACACAGTTTTTCTGSGCTTCCCTGCTT 868
Db 802 CAGACACTGACCTTACTGSGTTCACCCCTGACACAGTTTTTCTGSGCTTCCCTGCTT 861
QY 869 TTGTGTCATCACAGCGCATACGATGATCTCTGACAGCGCATGATGATGATGATGATG 928
Db 862 TTGTGTCATCACAGCGCATACGATGATGATCTCTGACAGCGCATGATGATGATGATG 921
QY 929 CCGGCTTCCAGCGCAGCATCGGCTCGGACAAAGAGGCTGACCGGACAGCCATCGCA 988
Db 922 CCGGCTTCCAGCGCAGCATCGGCTCGGACAAAGAGGCTGACCGGACAGCCATCGCA 980
QY 989 TCTGTGTCGCTTCTTTGTCGTGGGACACCTACTATGCTGTACAGTGCACAGTTG 1047
Db 981 TCTGTGTCGCTTCTTTGTCGTGGGACACCTACTATGCTGTACAGTGCACAGTTG 1040
QY 1048 TCCATCAGCC-GCCGACCCCTCACCCTTGTCTACTTATACATGCGCCATCAGCTTGG 1106
Db 1041 TCCATTAACCGCGCGGACCCCTCACCCTTGTGCAACATTAACACGCGCATACCTGG 1100
QY 1107 CTATGCCAAC 1116
Db 1101 CTATGCCAAC 1110

RESULT 2
B1754621 958 bp mRNA linear EST 25-SEP-2001
603025173F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5195443 5',
mRNA sequence.
B1754621
B1754621.1 GI:15746199
EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 958)
REFERENCE NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgrabs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/MLNC at:
http://image.llnl.gov
Plate: L14M11489 row: b column: 20
High quality sequence stop: 862.
Location/Qualifiers
1. 958
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5195443"
/clone_1lb="NIH_MGC_114"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMV-SPORT6; Site: 1: NotI;
Site: 2: EcoRV (destroyed); RNA source anonymous pool of 6
male brains, age range 23-27 yo. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.5 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 019. Note:
this is a NIH_MGC Library."

BASE COUNT      168 a      329 c      256 g      205 t
ORIGIN

Query Match      69.9%; Score 886.4; DB 13; Length 958;

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us-09-885-478-1.rst

BI757659
LOCUS
BI757659
872 bp
mpna
linear
ecm 35-sep-2001

DEFINITION
005027991f1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5198231 5',
mRNA sequence.

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1.0.0.0
VERSION
BI757659.1
GI:15749237

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SOURCE ORGANISM	human.
-----------------	--------

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NIH-MGC <http://mgc.nci.nih.gov/>.

JOURNAL COMMENT
Unpublished (1999)
Contact: Robert Strauch, PhD

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

Clone distribution: MGC clone distribution information can be found through the MGC Database.

http://image.llnl.gov
Plate: LLAM11496 row: 5 column: 24

FEATURES
high quality sequence stop: 829.
Location/Qualifiers

/organism="Homo sapiens"

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/clone="IMAGE:5198231"  
/clone 11b="NTH MGC 114"
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/lab_host="DH10B"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;

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male brains, age range 23-27 yo. Library is oligo-dT

upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb. Library is normalized and enriched for

full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note:

BASE COUNT	156	a	306	c	208	g	202	t
BASE COUNT	156	a	306	c	208	g	202	t

Query Match 64 0%: Score 811 8: DB 13: Length 873:

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Best LocalSimilarity 98.7%; Pred. No. 3.2e-172;
Matches 860; Conservative 0; Mismatches 7; Indels 4; Gaps 4;

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191 CGACCGCACTGGCTGGATGGACCTGGAAGCCTGCTGCTGCCACTGGTCCCATGCCA 250

Db 1 CGACCGCACTGGCTGATGGACCTGGAAGCCTCGCTGCTGCCACTGTGTCCCAATGCCA 60

251 GCACACCTCTGATGGCCCCGATAACCTCACTCAGCAGGATCACCTCCTCGCACGGGA 310

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[illegible]

371 TCATCG-GGAACCTCCACGGTCATCTTCGCGGTCGTGAAGAGTCCAAGCTGCACTGGTGC 429

Db 181 TCATCGGGAACCTCACGGTCTTCGGGTGCTGAGAAGTCCCAAGCTGCACCTGTTGC 240

430 AACACGTCGCCGACATCTTCATCATCAACCTCTCGGTAGTAGATCTCCTCTTCTCCTG 489

DB 241 AACACGTCCTCCGACATCTTCATCATCAACCTCTCGGTAGTAGATCTCCTTTTCTCCTG 300

[illegible]

Db 301 GGCATGCCCTTCATGATCCACCAGCTCATGGGCAATGGGGTGTGGCACTTTGGGAGACC 360

QY	550	ATGTGCACCCCTCATACACGGCCATGGATGCCAATAAGTACGTTACACAGACACTACATCCGTG	609
Db	361	ATGTGCACCCCTCATACACGGCCATGGATGCCAATAAGTACGTTACACAGACACTACATCCGTG	420
QY	610	ACCGGCATGGCCATTTGACCGCTACCTGGCCACTGTGCCACCCCATCTCTTCCACGAAGTTC	669
Db	421	ACCGGCATGGCCATTTGACCGCTACCTGGCCACTGTGCCACCCCATCTCTTCCACGAAGTTC	480
QY	670	CGGAAGCCCTCTGTGGCCACCCCTGGTGTATGCTCTGTGGGCCCTCTCTTCATCAGC	729
Db	481	CGGAAGCCCTCTGTGGCCACCCCTGGTGTATGCTCTGTGGGCCCTCTCTTCATCAGC	540
QY	730	ATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCTTCCAGAGAGTGTAGTGGGCTGC	789
Db	541	ATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCTTCCAGAGAGTGTAGTGGGCTGC	600
QY	790	GGCATACGCTGTGCCCAACCCAGACACTGACCTCTACTGCTTACCCCTTACAGATTTTTC	849
Db	601	GGCATACGCTGTGCCCAACCCAGACACTGACCTCTACTGCTTACCCCTTACAGATTTTTC	660
QY	850	CTGGCCTTTGGCCCTGCTCTTTTGTGTGTCATCAAGCCGCGATACGTGAGGATCCTCGACGCG	909
Db	661	CTGGCCTTTGGCCCTGCTCTTTTGTGTGTCATCAAGCCGCGATACGTGAGGATCCTCGACGCG	720
QY	910	ATGACGCTCTCATGTGTGCCCCCGGCTCTCCAGCGACAGCATTCGGCTCTCGGACAAAGAGGTG	969
Db	721	ATGACGCTCTCATGTGTGCCCCCGGCTCTCCAGCGACAGCATTCGGCTCTCGGACAAAGAGGTG	779
QY	970	ACCCGACAGCCATGACCATCTGTGTGGCTCTTGTGTGTGCTGGGCAACCCACTATATGTG	1029
Db	780	ACCCGCTACAG-CATGGCCATCTGTGTGGCTCTTGTGTGTGCTGGGCA-CCTACTATGTG	837
QY	1030	CTACAGCTGACCCAGCTGTGCCATTCACGCCGC	1060
Db	838	CTACAGTGTACCCAGCTGTGCCATTCACGCCGC	868
RESULT 4			
LOCUS	Bg913631		
DEFINITION	Bg913631	921 bp mRNA linear EST 05-JUN-2001	
ACCESSION	602811509P1	NCI CGAP_Brn67 Homo sapiens cdna clone IMAGE:4943498	
VERSION	5', mRNA sequence.		
KEYWORDS	Bg913631		
SOURCE	Bg913631.1	GI:14294107	
ORGANISM	human.		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
JOURNAL	1 (bases 1 to 921)		
COMMENT	NIH-MGC http://mgc.nci.nih.gov/ .		
	National Institutes of Health, Mammalian Gene Collection (MGC)		
	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgabbs-remail.nih.gov		
	Tissue Procurement: David N. Louis, M.D.		
	cDNA Library Preparation: Life Technologies, Inc.		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)		
	DNA Sequencing by: Incyte Genomics, Inc.		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LLNL at:		
	http://image.llnl.gov		
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FEATURES	High quality sequence stop: 731.		
source	location/Qualifiers		
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	/clone="IMAGE:4943498"		
	/clone_lib="NCI CGAP_Brn67"		
	/tissue_type="anaplastic oligodendroglioma with 1p/19q		
	loss"		
	/lab_host="DH10B (T1 phage-resistant)"		

			/note="Organ: brain; Vector: PCMV-SPORT6; Site: 1; NotI: Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.3 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP library."	
BASE COUNT	174 a	309 c	247 g	191 t
ORIGIN				
Query Match	60.9%;	Score 773.4;	DB 13;	Length 921;
Best Local Similarity	93.8%;	Pred. No. 1.4e-163;		
Matches 860;	Conservative 0;	Mismatches 15;	Indels 6;	Gaps 5;
OY	55	GGCAGCGGTGCACAGCTACGAGGAAGAACCCTTCGCCAGCTGGCGGGCTTGCCCTCG	114	
Db	1	GGCACGGGTGCACAGCTACGAGGAAGAACCCTTCGCCAGCTGGCGGGCTTGCCCTCG	60	
OY	115	GGACAAGGTGCAGGCGCTGGAAGGCTGCCGACGCTGCGTGGGTGAGGGAGACTCACT	174	
Db	61	GGACAAGGTGCAGGCGCTGGAAGGCTGCCGACGCTGCGTGGGTGAGGGAGACTCACT	120	
OY	175	CGGTGTGGGAGACAGCGCAGCGGCACTAGGCTGGATGACCTTGAAACCTTCGCTGCC	234	
Db	121	CGGTGTGGGAGACAGCGCAGCGGCACTAGGCTGGATGAGACTTGAAGCCCTGCTGTCGC	180	
OY	235	ACTGATCCCAATGCCCAGCAACACCTGATGGGCCCGAATACCTCACTACACAGATCA	294	
Db	181	ACTGATCCCAATGCCCAGCAACACCTGATGGGCCCGAATACCTCACTACACAGATCA	240	
OY	295	CCTCCGCGAGGGGAGCATCTCTCAACATCAACATCATCATCCTTTGGTTCGGCACC	354	
Db	241	CCTCCGCGAGGGGAGCATCTCTCAACATCAACATCATCATCCTTTGGTTCGGCACC	300	
OY	355	ATCTGCTCTCTGGGCAATCATGGGAACTCCACGGTCACTTTGGCGGTGTAAGAAGTCC	414	
Db	301	ATCTGCTCTCTGGGCAATCATGGGAACTCCACGGTCACTTTGGCGGTGTAAGAAGTCC	360	
OY	415	AAGCTGCATGTGTGAACAACAGTCCCGACATCTTCATATCACTCAACCTTCGGTAGAT	474	
Db	361	AAGCTGCATGTGTGAACAACAGTCCCGACATCTTCATATCACTCAACCTTCGGTAGAT	420	
OY	475	CTCTCTCTCTCTCTGGGCAATGGCTTTCATGATTCACACAGCTCATGGGCAANTGGGTGTG	534	
Db	421	CTCTCTCTCTCTCTGGGCAATGGCTTTCATGATTCACACAGCTCATGGGCAANTGGGTGTG	480	
OY	535	CACATTGGGAGAACCATGTGCAACCTCATACAGGCGCATGATGCCAATAGTCAAGTTCACC	594	
Db	481	CACATTGGGAGAACCATGTGCAACCTCATACAGGCGCATGATGCCAATAGTCAAGTTCACC	540	
OY	595	AGCACTACATCTCTGACCCGCATGGCATTTGAACCGGTACTCTGGCCATCTCCACCCCATC	654	
Db	541	AGCACTACATCTCTGACCCGCATGGCATTTGAACCGGTACTCTGGCCATCTCTCCACCCCATC	600	
OY	655	TCTTCACGAAGTTCGGAAGCCCTGTGGGCAACCCCTGATATGCAATGCACTCCGTTGGGCG	714	
Db	601	TCTTCACGAAGTTCGGAAGCCCTGTGGGCAACCCCTGATATGCAATGCACTCCGTTGGGCG	658	
OY	715	CTCTCTCTCATGACATCAACCCCTGTGTGGCTGTATGCCAGACTCAATCCCTTCCAGGA	774	
Db	659	CTCTCTCTCATGACATCAACCCCTGTGTGGCTGTATGCCAGACTCAATCCCTTCCAGGA	718	
OY	775	GGTGCAGTGGGCTGGGCGCATAGCGCTGCCCAACCCGACACATGACTCTACTATGTTCAAC	834	
Db	719	GGTGCAGTGGGCTGGGCGCATAGCGCTGCCCAACCAACCAACATGAGCTCACTATGTTCAAC	778	
OY	835	-CTGTACCAAGTTTTTCTCTGGCCCTTGGCCCGCTTTGTGGTCAATAC--AGGCGATAC	891	
Db	779	ACTGTACCAAGTATTTCTCTGGCCCTTGGCCCGCTTTGTGGTCAATACAGCCGCAATCC	838	
OY	892	GTAGAGAT-CTTGACAGCATGACGTCCTCAAGTGGCCCCCGCTCCAGCGCAGCATCCG	950	
Db	839	GTAGAGATCCCTTGACAGCATGACGTCCTCAAGTGGCCCCCGCTCCAGCGCAGCATCCG	898	
OY	951	GCTGCGGACAAAGGG 967		

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High quality sequence stop: 774.

	Query Match	Best Local Similarity	99.58	Score 769.8	DB 13	Length 797
	Matches 793	Conservative	0	Mismatches 2	Indels 2	Gaps 2
QY	17	TGAAGAAGGAGTGGGGAGGGGCACTTGGGCTTGGAGGCGGACGCGCTGCAGGCTACGG	76			
Db	1	TGAAGAAGGAGTGGGGAGGGGCACTTGGGCTTGGAGGCGGACGCGCTGCAGGCTACGG	60			
QY	77	AGGAAGACCCCTTCCCGACTGGGGGGCTTCCGCTCCGGGACAAAGTGTGGAGGCGCTTGA	136			
Db	61	AGGAAGACCCCTTCCCGACTGGGGGGCTTCCGCTCCGGGACAAAGTGTGGAGGCGCTTGA	120			
QY	137	GCGTGGCCGACGCTGGCGTGGGTGGAGGGAGCTCAGCTCGGTTTGTGGAGCAGGCGACCG	196			
Db	121	GCGTGGCCGACGCTGGCGTGGGTGGAGGGAGCTCAGCTCGGTTTGTGGAGCAGGCGACCG	180			
QY	197	GCACCTGGCTGATGAGCACTGGAAGCCGCGTGGTGGCCACTGGTCCCAATGCCAGACACA	256			
Db	181	GCACCTGGCTGATGAGCACTGGAAGCCGCGTGGTGGCCACTGGTCCCAATGCCAGACACA	240			
QY	257	CCCTCTGATGGCCCGGATTAACCTCACTTCAAGACAGATACCTCTCTGACAGGGAGCATCT	316			
Db	241	CCCTCTGATGGCCCGGATTAACCTCACTTGGCAGAGTACCTCTCTGACAGGGAGCATCT	300			

RESULT	6
LOCUS	BF342364
DEFINITION	BF342364 834 bp mRNA linear EST 22-NOV-2000
ACCESSION	602013155F1 NCL.CGAP-Brn64 Homo sapiens cDNA clone IMAGE:4148940
VERSION	5, mRNA sequence.
KEYWORDS	BF342364
SOURCE	BF342364.1 GI:11289365
ORGANISM	EST.
	human.
	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE	1 (bases 1 to 834)
AUTHORS	NH-MGC http://mgc.nci.nih.gov/ .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4148940"
/clone_lib="NCI CGAP Brn64"
/tissue_type="glioblastoma with EGFR amplification"

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QY 514 CTCATGAGGCAATGGGGTGTGGCACTTTGGGAGACATGTGCACCCATCATCAGCGCATG 573
Db 481 CTCATGAGGCAATGGGGTGTGGCACTTTGGGAGACATGTGCACCCATCATCAGCG -CATG 539
QY 574 GATGCCAATAGTCACTTACACGACACCTACATCTGACCCGATGGCATTTGACCGGTAC 633
Db 540 GATGCCAATAGTCACTTACACGACACCTACATCTGACCG -CATGGGCAATGACCGGTAC 538
QY 634 CTGG-CCAGTGTCCAGCCCATCTCTCCAGAGT---CCGGAAGCCCTGTGGCCAC 689
Db 599 CTGGCCCACTGTCCAGCCCATCTCTCCAGAGT---CCGGAAGCCCTGTGGCCAC 638
QY 690 CCTGGTGAATGCTCCTCTGTG-GGCCCTCTCTTCATCATGACATCCCTGTGTGGCT-- 746
Db 659 CTGGTTGAATCTCTCTGTGTGGCCCTCTCTTCATTCAGTTTACCCCTGTGTGGTTG 718
QY 747 GATGCCAGACATCACTCCCTTCCAGAGGTGCAGTGGCT 787
Db 719 GTTTCGCAATTCATCTTCCGAGGGGCTGGGCTGGGT 759

RESULT 8
BG519797 869 bp mRNA linear EST 02-APR-2001
LOCUS BG519797
DEFINITION 602578956F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503484 5',
mRNA sequence.

ACCESSION BG519797
VERSION BG519797.1 GI:13515559
KEYWORDS EST.

SOURCE human.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 869)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov

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High quality sequence stop: 780.

Location/Qualifiers

1..869

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:3503484"

/clone_lib="NIH_MGC_19"

/tissue_type="neuroblastoma"

/lab_host="DH10B (phage-resistant)"

/note="Organ: brain; Vector: pOT81; Site: 1; XhoI; Site: 2;

ECORI; cDNA made by oligo-dT priming, directionally

cloned into EcoRI/XhoI sites using the following 5'

adaptor: GGCACGAG(G). Library constructed by Ling Hong

in the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NIH_MGC library."

BASE COUNT 175 a 259 c 258 g 177 t

ORIGIN

Query Match 46.5%; Score 590.2; DB 12; Length 869;
Best Local Similarity 98.5%; Pred. No. 2.2e-122;
Matches 606; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

QY 1 ATGTAGTGGGAGCCATGAAGAGGAGTGGGAGGGCAGTTGGGCTTGCAGCGGACG 60
Db 215 ATGTAGTGGGAGCCATGAAGAGGAGTGGGAGGGCAGTTGGGCTTGCAGCGGAGC 274
QY 61 GGGTCGAGGGCTAGGAGGAGAGAGCCCTTCCGACATGGCGGGGTTGGCTCCGGGACAA 120
Db 275 GGGTCGAGGGCTAGGAGGAGAGAGAGCCCTTCCGACATGGCGGGGTTGGCTCCGGGACAA 334
QY 121 GGTGGAGGCGCTGGAGGCTCCGCGAGCTCGTGGGTGGAGGGAGCTCAGTCGGTTG 180
Db 335 GGTGGAGGCGCTGGAGGCTCCGCGAGCTCGTGGGTGGAGGGAGCTCAGTCGGTTG 394
QY 181 TGGGAGGAGGCGAGCGGAGCTGGGTGGATGGAGCTGGAGGCTGGCTGGCTGGCTGGCT 240
Db 395 TGGGAGGAGGCGAGCGGAGCTGGGTGGATGGAGCTGGAGGCTGGCTGGCTGGCTGGCT 454
QY 241 CCCAATGCGAGCAACACCTGTGATGGCCCGATTAACCTCAGTACAGATGACCTCCT 300
Db 455 CCCAATGCGAGCAACACCTGTGATGGCCCGATTAACCTCAGTACAGATGACCTCCT 514
QY 301 CGCAGGCGGAGCATCTCTCTACATCAATCATGCTCTGGTGTGGCAGCATCTGC 360
Db 515 CGCAGGCGGAGCATCTCTCTACATCAATCATGCTCTGGTGTGGCAGCATCTGC 574
QY 361 CTCTGGGAGCATGCGGAGCACTCCAGCTCATCTTCGCGGTGGTGGAGAGTCCAGCTG 420
Db 575 CTCTGGGAGCATGCGGAGCACTCCAGCTCATCTTCGCGGTGGTGGAGAGTCCAGCTG 634
QY 421 C-ACGTGTGCAACAACGTCCTCCGAGCATCTTCATCAACCTCGGTAGTAGATCTCT 479
Db 635 CAACGTGTGCAACAACGTCCTCCGAGCATCTTCATCAACCTCGGTAGTAGATCTCT 694
QY 480 CTCTCTCTGGGAGCATGCGGAGCACTCCAGCTCATCTTCGCGGTGGTGGAGAGTCCAGCTT 539
Db 695 CTCTCTCTGGGAGCATGCGGAGCACTCCAGCTCATCTTCGCGGTGGTGGAGAGTCCAGCTT 754
QY 540 TGGGAGGAGCATGTCACCCCTCATCAGCGGAGTGGATGCCAATAGTCAATCAGCAGAC 599
Db 755 TGGGAGGAGCATGTCACCCCTCATCAGCGGAGTGGATGCCAATAGTCAATCAGCAGAC 814
QY 600 CTACATCTGACCGC 614
Db 815 CTACATCTGACCGC 829

RESULT 9
B1818110 685 bp mRNA linear EST 04-OCT-2001
LOCUS B1818110
DEFINITION 603032524F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5173852 5',
mRNA sequence.

ACCESSION B1818110
VERSION B1818110.1 GI:15928318
KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 685)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

<http://image.lnl.gov>

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High quality sequence stop: 679.

Location/Qualifiers

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/db_xref="taxon:9606"
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/lab_host="DH10B"
/Note="Organ: pooled brain, lung, testis; Vector:
pcmv-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."

BASE COUNT      132 a      205 c      212 g      136 t
ORIGIN

Query Match      44.6%; Score 566.2; DB 13; Length 685;
Best Local Similarity 99.5%; Pred. No. 5.1e-117;
Matches 568; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGTCACTGGAGGAGCATGAAGAAGGAGTGGGAGGCACTTGGCTTGGAGCGCGCAGC 60
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Db 115 ATGTCACTGGAGGAGCATGAAGAAGGAGTGGGAGGCACTTGGCTTGGAGCGCGCAGC 174

QY 61 GCGTCCAGGCTACGAGAGAACCCCTTCCGACTGCGGGGCTTGGCTCCGGAGCAA 120
    |||||||
Db 175 GCGTCCAGGCTACGAGAGAACCCCTTCCGACTGCGGGGCTTGGCTCCGGAGCAA 234

QY 121 GGTGCGAGGGGCTGGAGGCTGGCGGACGTCGCGGGTGGAGGGAGCTAGCTCGGTTG 180
    |||||||
Db 235 GGTGCGAGGGGCTGGAGGCTGGCGGACGTCGCGGGTGGAGGGAGCTAGCTCGGTTG 294

QY 181 TGGGAGCAGGCGGACGTCGCTGGATGACCTGGAAAGCTCGCTGCGCCACTGTG 240
    |||||||
Db 295 TGGGAGCAGGCGGACGTCGCTGGATGACCTGGAAAGCTCGCTGCGCCACTGTG 354

QY 241 CCCAATGCGCAACACCTCTGATGGCCCGGATTAACCTCACTCAGAGATCAACCTCT 300
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Db 355 CCCAATGCGCAACACCTCTGATGGCCCGGATTAACCTCACTCAGAGATCAACCTCT 414

QY 301 CGCAGGGGAGCATCTCTTACATCAATCATATGCTTCGCTGGTTCGGCACCATTCTGC 360
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Db 415 CGCAGGGGAGCATCTCTTACATCAATCATATGCTTCGCTGGTTCGGCACCATTCTGC 474

QY 361 CTCTGGGAGCATTCGGGAGACTCCAGGTCATCTTCCGGGTGCGTGAAGAACTCCAGCTG 420
    |||||||
Db 475 CTCTGGGAGCATTCGGGAGACTCCAGGTCATCTTCCGGGTGCGTGAAGAACTCCAGCTG 534

QY 421 CACTGGTGCACAACGTCCTCCGACATCTTCATCACTCAACCTCTGGGATAGATCTCTCTC 480
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Db 535 CACTGGTGCACAACGTCCTCCGACATCTTCATCACTCAACCTCTGGGATAGATCTCTCTC 594

QY 481 TTTCCTCTGGGAGCATTCCTTCATGATCCACAGCTCATTTGGGCAATTTGGGCTT 540
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Db 595 TTTCCTCTGGGAGCATTCCTTCATGATCCACAGCTCATTTGGGCAATTTGGGCTT 654

QY 541 GGGGAGACCATGTGCACCTTCATCAAGGCA 571
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Db 655 GGGGAGACCATGTGCACCTTCATCAAGGCA 685

RESULT 10
BS12747 859 bp mRNA linear EST 26-OCT-2000
LOCUS 601150756p1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503484 5',
DEFINITION mRNA sequence.
ACCESSION BS12747
VERSION BS12747.1 GI:9131846
KEYWORDS EST.
SOURCE human.
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 859)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov
Plate: L16M16 row: P column: 13
High quality sequence start: 3.
High quality sequence stop: 733.
Location/Qualifiers

source
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/clone="IMAGE:3503484"
/clone_lib="NIH_MGC_19"
/tissue_type="neuroblastoma"
/lab_host="DH10B (phage-resistant)"
/Note="Organ: brain; Vector: pORF7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

BASE COUNT      151 a      267 c      254 g      186 t      1 others
ORIGIN

Query Match      38.5%; Score 489; DB 10; Length 859;
Best Local Similarity 94.0%; Pred. No. 1.2e-99;
Matches 553; Conservative 0; Mismatches 26; Indels 9; Gaps 4;

QY 1 ATGTCACTGGAGGAGCATGAAGAAGGAGTGGGAGGCACTTGGGCTTGGAGCGCGCAGC 60
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Db 194 ATGTCACTGGAGGAGCATGAAGAAGGAGTGGGAGGCACTTGGGCTTGGAGCGCGCAGC 253

QY 61 GCGTCCAGGCTACGAGAGAACCCCTTCCGACTGCGGGGCTTGGCTCCGGAGCAA 120
    |||||||
Db 254 GCGTCCAGGCTACGAGAGAACCCCTTCCGACTGCGGGGCTTGGCTCCGGAGCAA 313

QY 121 GGTGCGAGGCGCTGGAGGCTGCCGACGCTCGTGGTGGAGGGAGCTCAGCTGGTTG 180
    |||||||
Db 314 GGTGCGAGGCGCTGGAGGCTGCCGACGCTCGTGGTGGAGGGAGCTCAGCTGGTTG 373

QY 181 TGGGAGCAGGCGGACGTCGCTGGATGACCTGGAAAGCTCGCTGCGCCACT--G 238
    |||||||
Db 374 TGGGAGCAGGCGGACGTCGCTGGATGACCTGGAAAGCTCGCTGCGCCACTGG 433

QY 239 GTTCCAATGCGCAACACCTCTGATGGCCCGGATTAACCTCACTCAGAGATCACTC 298
    |||||||
Db 434 GTTCCAATGCGCAACACCTCTGATGGCCCGGATTAACCTCACTCAGAGATCACTC 493

QY 299 CTGCGACGGGAGCATCTCTTACATCAATCATATGCTTCGCTGGGTGGCAGCATCT 358
    |||||||
Db 494 CTGCGACGGGAGCATCTCTTACATCAATCATATGCTTCGCTGGGTGGCAGCATCT 553

QY 359 GCGTCCCTGGGAGCATTCGGGAATCTCCAGGTCATCTTCCGGGTGCGTGAAGAACTCCAAAC 418
    |||||||
Db 554 GCGTCCCTGGGAGCATTCGGGAATCTCCAGGTCATCTTCCGGGTGCGTGAAGAACTCCAAAC 613

QY 419 TGCACCTGTGCAACAACGTCCTCCGACATC--TTCATCATCAACCTCTCGGTAG-----TAG 472
    |||||||
Db 614 TGCACCTGTGCAACAACGTCCTCCGACATCTTTCATCATCAACCTCTCGGTAGTGAATCT 673
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QY 473 ATCTCTCTTCTCCTGGGATGACCTTCATGATCCACACAGCTTCATGGGATGGGTGT 532
 Db 674 CCTTCTTCTTCCTGCTGGCATTTGNCCTCATGATCCACACAGCTTCATGGGATGGGTGT 723
 QY 533 GGCAC-TTTGGGAGAACCATGTGACCTCTCATACAGGCCCATGATGCC 579
 Db 734 GGCACCTTTGGGAGAACCTTGTGCCCTCATACAGGCATGGGTGCC 781
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 DEFINITION 601150023F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503020 5',
 mRNA sequence.
 ACCESSION BE312542
 VERSION BE312542.1 GI:9131383
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE 1 (bases 1 to 600)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov
 Plate: LCM175 row: m column: 05
 High quality sequence start: 7
 High quality sequence stop: 574.
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 /clone="IMAGE:3503020"
 /clone_lib="NIH_MGC_19"
 /tissue_type="neuroblastoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: brain; Vector: pOTB1; Site_1: XhoI; Site_2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCACGAG(G). Library constructed by Ling Hong
 in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-CDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."
 BASE COUNT 113 a 174 c 197 g 116 t
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 Query Match 30.4%; Score 386.4; DB 10; Length 600;
 Best Local Similarity 99.5%; Pred. No. 1.3e-76;
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 Db 195 ATGTCAGTGGAGCATTGAGAGAGAGTGGGAGGAGGAGTGGGCTTGGAGGCGGAGC 254
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 Db 255 GGTGTCAGGCTACGAGAGAGAACCCCTTCCGACCTCGGGGCTTGGGCTCCGGAGCAA 314
 QY 121 GGTGTCAGGCTGAGAGCTGCCAGAGCTGCTGGTGGAGGAGGAGCTCAGTCGGTTG 180
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 Db 181 TGGGACAGGCGACCGGACCTGGCTGATGAGCTGGAAGCTCGCTCTCCACCTGTGT 240

Db 375 TGGGAGCAGGCGACCGGACCTGGCTGATGAGCCTGGAGACCTTGCTGCCACTGTT 434
 QY 241 CCCAATGCGAGAACACCTTGATGGCCCCGATACCTCACTTCAGGAGATCACTTCT 300
 Db 435 CCCAATGCGAGAACACCTTGATGGCCCCGATACCTCACTTCAGGAGATCACTTCT 494
 QY 301 CGCAGCGGGAGCATCTCTTACATCAACATCAATGCGCTTGGTGGCACCATTCTGC 360
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 LOCUS F07228 345 bp mRNA linear EST 20-FEB-1995
 DEFINITION HSC12F101 normalized infant brain cDNA Homo sapiens cDNA clone
 c-12f10, mRNA sequence.
 ACCESSION F07228
 VERSION F07228.1 GI:672877
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE 1 (bases 1 to 345)
 AUTHORS Aultrey,C., Behar,G., Bois,F., Bouchier,C., da Silva,C., Devignes
 ,M.D., Duprat,S., Houlgatte,R., Juneau,M.N., Lamy,B., Lorenzo,F.,
 Mitchell,H., Mariage-Samson,R., Pletu,G., Pouliot,Y.,
 Sebastiant-Kabaktchis,C. and Tessier,A.
 TITLE IMAGE: molecular integration of the analysis of the human genome
 and its expression
 JOURNAL C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
 MEDLINE 95277534
 COMMENT Contact: Genethon
 Genethon Centre de recherche sur le Genome Humain
 1, rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
 Tel: 33169472800
 Fax: 33160778698
 Email: genexpress@genethon.fr
 Single read.
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 Seq primer: (-21)M13_universal.
 Location/Qualifiers
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 /sex="Female"
 /tissue_type="total brain"
 /dev_stage="3 months old"
 /note="Organ: brain; Vector: lafmid BA; Site_1: HindIII;
 Site_2: NotI; sex:Female; dev_stage=3 months old;
 isolate=muscular atrophy patient; tissue_type=total brain
 ; total mRNA was oligo-(dT) primed and directionally
 cloned 5' -> 3' into the HindIII -> NotI sites of the
 lafmid BA vector. Clone library from B.Souares, Psychiatry
 Dept. Columbia University, USA. Normalization_method:
 Bento Soares, P.N.A.5 in press"
 BASE COUNT 67 a 118 c 79 g 80 t 1 others
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 Best Local Similarity 99.7%; Pred. No. 3.9e-67;
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QY 424 TGGTGACACACGTCGCCGACATCTTCATCATCAACCTCTCGTAGTAGATCTCTTT 483
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 QY 484 CTCCTGGGATGCGCTTCATGATTCACACGATCATGGGCAATGGGATGGGACATTTGGG 543
 DB 121 CTCCTGGGATGCGCTTCATGATTCACACGATCATGGGCAATGGGATGGGACATTTGGG 180
 QY 544 GAGACATGTGACACCTTCATCAAGGCGCATGATGCGCAATAGTCAATTGACAGACCTAC 603
 DB 181 GAGACATGTGACACCTTCATCAAGGCGCATGATGCGCAATAGTCAATTGACAGACCTAC 240
 QY 604 ATCTTACCGCCATGCGCATTTGACCGCTACCTGGCCACTGTCCACCCCATCTTCCAG 663
 DB 241 ATCTTACCGCCATGCGCATTTGACCGCTACCTGGCCACTGTCCACCCCATCTTCCAG 300
 QY 664 AAGTTCGGAAGCCCTCTGTGGCCACCTGTGATCTGCTCTCTG 708
 DB 301 AAGTTCGGAAGCCCTCTGTGGCCACCTGTGATCTGCTCTCTG 345

RESULT 13
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 LOCUS UI-M-BH1-ant-c-04-0-UI-r1 NIH_BMAP_M.S2 Mus musculus cDNA clone
 DEFINITION UI-M-BH1-ant-c-04-0-UI-r1 NIH_BMAP_M.S2 Mus musculus cDNA clone
 ACCESSION BE647763
 VERSION BE647763.1 GI:9973583
 KEYWORDS EST.
 SOURCE house musculus.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
 AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477
 COMMENT Contact: Chih, H
 National Institute of Mental Health
 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
 20892-9643, USA
 Tel: 301 443 1706
 Fax: 301 443 9690
 Email: mestr@mail.nih.gov
 CDNA Library Preparation: M.B. Soares Lab Clone distribution:
 Researchers may obtain BMAP CDNA clones from RESEARCH GENETICS. It
 should be noted that Bento Soares is generating a small number of
 additional specialized non-redundant arrays of BMAP cDNAs whose
 availability will be considered under appropriate and limited
 collaborative arrangements
 Seq primer: M13 Reverse.
 Location/Qualifiers
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 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UI-M-BH1-ant-c-04-0-UI"
 /clone_1ib="NIH_BMAP_M.S2"
 /lab_host="DH10B (Life Technologies)"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker; Site.1: Not I; Site.2: Eco RI; The
 NIH_BMAP_M.S2 library is a subtracted library derived from
 NIH_BMAP_M.S1, which in turn is a subtracted library
 derived from a mixture of normalized libraries from ten
 regions of the mouse brain (cerebellum, brain stems,
 olfactory bulbs, hypothalamus, cortex, amygdala, basal
 ganglia, pineal gland, striatum, hippocampus). The driver
 used for subtraction consisted of a pool of 5,000 clones
 from the NIH_BMAP_M.S1 library and a pool of 2,000 clones

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BASE COUNT 84 a 121 c 102 g 80 t
 ORIGIN
 Query Match 22.8%; Score 289.2; DB 10; Length 387;
 Best Local Similarity 92.9%; Pred. No. 8.4e-55;
 Matches 303; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
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 DB 1 GCATCCGGCTGCGGACAAAGAGGTGACCGGACAGCATGGCATGCTGTGCTCT 60
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 QY 1124 TCAACCCCTTTGTGATACATGCTGCTGTGAGACGTTCCGCAAGCCTGTCTGCG 1183
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 QY 1184 TGAAGCCTGACCCGACGCGAGCTGCGCTGTACACCAAGCTGACAGCGTGCAGG 1243
 DB 241 TGAAGCCTGACCCGACGCGAGCTGCGCTGTACACCAAGCTGACAGCGTGCAGG 300
 QY 1244 AGAGCAGCAAGAAAGCAAGGACCTGCA 1269
 DB 301 AGAGCAGCAAGAAAGCAAGGACCTGCA 326

RESULT 14
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 DEFINITION mRNA sequence.
 ACCESSION BF313837
 VERSION BF313837.1 GI:11261906
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: c9apbs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov
 Plate: LNCMI038 row: c column: 09
 High quality sequence stop: 603.
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 EcoRI; CDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCACAG(G). Library constructed by Ling Hong
 in the laboratory of Gerald M. Rubin (University of

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source

1..1086
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4134848"
 /clone_1ib="NIH_MGC_19"
 /clone_type="neuroblastoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: brain; Vector: pOTB7; Site.1: XhoI; Site.2:
 EcoRI; CDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCACAG(G). Library constructed by Ling Hong
 in the laboratory of Gerald M. Rubin (University of

Contact: Simpson A.U.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP
Brazil
Tel: +55-11-2704922
Tel: +55-11-2707001
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

Search completed: February 19, 2003, 11:05:46
Job time : 2097 secs

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 19, 2003, 12:07:02 ; Search time 56 Seconds

(Without alignments)
2311.028 Million cell updates/sec

Title: US-09-885-478-2

Sequence: 1 MSVGAMKKGVGRAVLGGG.....LRVSNQOTADEERTESKGT 422

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Delop	6.0	,	Delext	7.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
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Command line parameters:

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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

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4	2164	97.8	1385	3	US-08-984-608-1	Sequence 1, Appli
5	2000	90.4	3488	4	US-09-218-6578-1	Sequence 1, Appli
6	1783	80.6	1214	4	US-09-224-426-3	Sequence 3, Appli
7	1783	80.6	1214	4	US-09-478-601-3	Sequence 3, Appli
8	1783	80.6	1214	4	US-09-478-602-3	Sequence 3, Appli
9	1692	76.5	1316	5	US-08-602-602-3	Sequence 1, Appli
10	1692	76.5	1316	5	PCT-US95-16472-1	Sequence 1, Appli
11	1680	75.9	980	4	US-09-218-6578-6	Sequence 6, Appli
12	535.5	24.2	1244	1	US-07-816-283-7	Sequence 7, Appli

13	535.5	24.2	1.244	1	US-08-417-103-7	Sequence 7, Appl 1
14	532	24.1	1.351	1	US-07-816-283-5	Sequence 5, Appl 1
15	532	24.1	1.351	1	US-08-417-103-5	Sequence 5, Appl 1
16	531.3	24.0	1.147	1	US-08-417-103-15	Sequence 15, Appl 1
17	522	23.6	1.634	1	US-07-816-283-1	Sequence 1, Appl 1
18	522	23.6	1.634	1	US-08-417-103-1	Sequence 1, Appl 1
19	516	23.3	1.205	1	US-08-417-103-13	Sequence 13, Appl 1
20	510	23.1	1.265	1	US-07-816-283-3	Sequence 3, Appl 1
21	510	23.1	1.265	1	US-08-417-103-3	Sequence 3, Appl 1
22	504.5	22.8	1.286	1	US-07-816-283-9	Sequence 9, Appl 1
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24	476	21.5	1.796	1	US-07-816-283-11	Sequence 11, Appl 1
25	476	21.5	1.796	1	US-08-417-103-11	Sequence 11, Appl 1
26	464	21.0	1.610	3	US-08-889-108-7	Sequence 7, Appl 1
27	464	21.0	1.610	5	PCT-US94-10358-7	Sequence 7, Appl 1
28	459	20.8	1.618	3	US-08-889-108-1	Sequence 1, Appl 1
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34	456.5	20.6	1.981	4	US-08-387-707-15	Sequence 15, Appl 1
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36	453	20.5	2.160	4	US-08-188-276A-1	Sequence 1, Appl 1
37	453	20.5	2.162	4	US-09-351-198-1	Sequence 1, Appl 1
38	453	20.5	2.162	4	US-09-113-428-1	Sequence 1, Appl 1
39	451.5	20.4	2.135	4	US-08-430-286A-1	Sequence 1, Appl 1
40	444.5	20.1	1.829	2	US-08-411-855-1	Sequence 1, Appl 1
41	444.5	20.1	1.829	4	US-08-387-707-7	Sequence 7, Appl 1
42	444.5	20.1	1.829	4	US-08-405-221A-7	Sequence 7, Appl 1
43	441	19.9	2.272	3	US-08-147-592A-3	Sequence 3, Appl 1
44	441	19.9	2.272	4	US-08-292-592A-3	Sequence 3, Appl 1
45	435.5	19.9	1.142	3	US-08-763-743-1	Sequence 1, Appl 1

ALIGNMENTS

RESULT 1
 US-09-224-426-1
 : Sequence 1, Application US/09224426
 : Patent No. 6221613
 : GENERAL INFORMATION:
 : APPLICANT: Salon, John A
 : APPLICANT: Laz, Thomas M.
 : APPLICANT: Nagorny, Raisa
 : APPLICANT: Wilson, Amy E.
 : TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
 : FILE REFERENCE: 57453/0PM/JHB
 : CURRENT APPLICATION NUMBER: US/09/224,426
 : NUMBER OF SEQ ID NOS: 15
 : SOFTWARE: PatentIn Ver. 2.0 - beta
 : SEQ ID NO 1
 : LENGTH: 1269
 : TYPE: DNA
 : ORGANISM: Homo sapiens
 : US-09-224-426-1

Alignment Scores:	
Pred. No.:	1_1e-206
Score:	2212.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	4
Gaps:	0
Mismatches:	0
Conservative:	422
Matches:	1266
Indels:	0

US-09-885-478-2 (1-422) X US-09-224-426-1 (1-1269)

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QY	41	GLIYLYRGRGRPRRPRGRLeuProGlnProAlaTRPVALIGLUGLYSerSerAlaArgLeu	60
Db	121	GGTGGCAGGGGGCTGGAGGGCTGCCAGCCTGGCTGGTGGAGGGGAGCTCAGCTCGGTTG	180
QY	61	TRPGLGNALATHRGIUGLYTRHGLYTRPMeLaspLeuGJALASerLeuProTHRGLY	80
Db	181	TGGGAGCAGCGACCGGCACTGGCTGGATGGAGACTGGAGAGGCTGGCTGCCACGCT	240
QY	81	PROAsnAlaSerSnrTHRSerAspGLYProAspAsnLeuTHRSerAlaGLYSerProPro	100
Db	241	CCCAATGCCAGCAACACTCTGTATGGCCCCCGAATCTACTCAGCAGATCACTCTCT	300
QY	101	ARGTHRGLYSerIleSerTYRlleAsnIleIleMetProSerValPheGLYTHRleCys	120
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Db	361	CTCCGGGCATCAATCGGGAATCTCCAGGTCATCTTGGGGTGTGAASAASTCCAAAGTG	420
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QY	181	GLYGLYTHRMetCysTYRLeuIleTHRAlaMetAspAlaAsnSerGlnPheTHRSerTHR	200
Db	541	GGGGAGACCATGTGCACCTCATCAAGGCCATGATGCCAATATGACGTACACGACACC	600
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Db	601	TTCATCTCGACCGGCATGGCATGTGACCGCTGGCAGCTGCACCCCATCTCTTCC	660
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QY	241	PheIleSerIleTHRProValTRPLeuTYRAlaArgLeuIleProPheProGLYGLYAla	260
Db	721	TTCATCAACATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCCCTCCAGAGAGTCA	780
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Db	841	CAGTTTTCCTGGCTTGGCCCTGCCTTTGTGGTATCACACCCGACATACGTAGAGATC	900
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QY	381	IleValLeuCysGLYTHRPhenArgLYSArgLeuValLeuSerValLYSProAlaAlaGln	400

Db	1141	ATCTGCTCTGTGTGAGAGTTCGCCAAACGCTTGCTCTCTCGGTAAAGCTTCAGCCACG	1200
Qy	401	GLYGLINLEUARGALVALSERASNLAGLTHRALASPGLUGLARGTHRGLUSERLYS	420
Db	1201	GGGACGCTTCGGCGCTGTACACAAAGCGGTGACAGAGGAGGACAGAAAGCAA	1260
Qy	421	GLYThr 422	
Db	1261	GGCACC 1266	
RESULT 2			
US-09-478-601-1			
; Sequence 1, Application US/09478601			
; Patent No. 6221616			
; GENERAL INFORMATION:			
; APPLICANT: Salton, John A.			
; APPLICANT: Laz, Thomas M.			
; APPLICANT: Nagorny, Raisa			
; APPLICANT: Wilson, Amy E.			
; TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone			
; TITLE OF INVENTION: Receptor (MCHL) And Uses Thereof			
; FILE REFERENCE: 574532/JPM			
; CURRENT APPLICATION NUMBER: US/09/478,601			
; CURRENT FILING DATE: 2000-01-06			
; EARLIER APPLICATION NUMBER: 09/224,426			
; EARLIER FILING DATE: 1998-12-31			
; NUMBER OF SEQ ID NOS: 15			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 1			
; LENGTH: 1269			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-09-478-601-1			
Alignment Scores:			
Pred. No.: 1,1e-206			
Score: 2212.00			
Percent Similarity: 100.00%			
Best Local Similarity: 100.00%			
Query Match: 100.00%			
DB: 4			
Gaps: 0			
US-09-885-478-2 (1-422) x US-09-478-601-1 (1-1269)			
Qy	1	MetSerValGlyAlaMetLysLysGlyAlaGlyArgAlaValGlyLeuGlyGlySer	20
Db	1	ATGTCAGTGTGGAGCCATGAGAGAGGACTGGGGAGGCGAGTGGGCTTGGAGCGGACG	60
Qy	21	GlyCysGlnAlaThrGluGlnAspProLeuProAspCysGlyAlaCysAlaProGlyGln	40
Db	61	GGGTGGCAAGCTACGGAGAGAACCCCTTCCCACTGCGGGGCGTTGCGTCCGGGACAA	120
Qy	41	GlyGlyArgArgTrpArgLeuProGlnProAlaTrpValGlyGlySerSerAlaArgLeu	60
Db	121	GGTGGAGGCGGTGGAGGGGTGCGGACGCTGCTGGTGGAGGAGGAGCACTCAGCTGGTTG	180
Qy	61	TrpGluGlnAlaThrGlyThrGlyTrpMetLysPheGluValAspSerLeuLeuProThrGly	80
Db	181	TGGGACAGGACGACCGGCACTGGCTGGATGACCTGGAAAGCTTGCTGCTGCCACAGGT	240
Qy	81	ProAsnAlaSerAsnThrSerAspCysProAspAsnLeuThrSerAlaGlySerProPro	100
Db	241	CCCAATAGCAGACACCTCTATATGCCCCATACCTCACTTACGACGAGATCAGCTGCT	300
Qy	101	ArgThrGlySerIleSerTrpIleAsnIleIleMetProSerValPheGlyThrIleCys	120
Db	301	CGGACGGGGAGCATCTCTACATCAACATCATCATGCTTGCGGTGTCGGCACCATCTGC	360
Qy	121	LeuLeuGlyIleIleGlyLysSerThrValIlePheAlaValValLysLysSerLysLeu	140
Db	361	CTCTCTGGGATCATCTGCGGAATCTCACGGGTATCTTCGGGTCTGGAAAGATGTCACACTG	420

OY	261	ValIyCsgIyIleatgleuProaSnProaSPthAspleuTytrPhehtrleuYr	280
Db	781	GTGGGCTGGCGGCAATACCCGCGCCAAACGACACATGACCTTACAGGTTCACCCCTGTAC	840
OY	281	GlnPhePheleuAlaPheAlaIeuproPheValValIlethAlaAlaIatyrAlaArgIle	300
Db	841	CAGTTTTCCTGGCCCTTTGCCCTTGCTTTGTGTGATCATCAGCCGCAATACGTGAGATC	900
OY	301	LeuGlnArgMetThrSerSerValAlaProAlaSerGlnArgSerIleArgleuArgThr	320
Db	901	CTGCAGCGCATGACGCTCCTCAGTGGGCCCCCGCTCCAGGCGAGCAWCCGCGTGGGACA	960
OY	321	LysArgValThrArgThrAlaIleAlaIleCysLeuValPhePheValLysTrpAlaPro	340
Db	961	AAGAGGGTACCCCGACAGCATCGGCATCTGTGCTCTTCTTGTGTGGTGGGACCC	1020
OY	341	TytrIyValleuGlnIeuthrGlnIeuSerIleSerArgProthrIeuthrPheValTytr	360
Db	1021	TACTATGTGCTACAGCTGACCAAGTTGTGATCAGCCGCCGACCTTACCTTTGTCTAC	1080
OY	361	LeuYrAsnAlaAlaIleSerIeugIYTytrAlaAsnSerCysLeuAsnProPheValTytr	380
Db	1081	TTATATCATGGGGCCATCAGCTTGCGGTATGCCAACAGCTGCCTCAACCCCTTGTGTGAC	1140
OY	381	IleValIeuCysGluThrPheArgLysArgLeuValIeuSerValLysProAlaAlaGln	400
Db	1141	ATCGTGCTCTGTGAGACGTTCCGCAACGCTTGCTCCTGTGCGGTGAAGCTGCAGCCAG	1200
OY	401	GlyGlnIeuArgAlaValSerAsnAlaGlnThrAlaAspGlnIuArgThrGlnSerLys	420
Db	1201	GGGCGAGCTTCGCGCTGTACGACACGCTCAGACGGCTGACGAGAGAGAGACAGAAACAAA	1260
OY	421	GlyThr 422	
Db	1261	GGCACC 1266	
RESULT 4			
: Sequence 1, Application US/08984288			
: Patent No. 6033872			
: GENERAL INFORMATION:			
: APPLICANT: BERGSM, DEK			
: APPLICANT: ELLIS, CATHERINE			
: TITLE OF INVENTION: NOVEL HUMAN 11CB SPLICE V			
: TITLE OF INVENTION: ARIANT			
: NUMBER OF SEQUENCES: 6			
: CORRESPONDENCE ADDRESS:			
: ADDRESS: RATNER & PRESTIA			
: STREET: P.O. BOX 980			
: CITY: VALLEY FORGE			
: STATE: PA			
: COUNTRY: USA			
: ZIP: 19482			
: COMPUTER READABLE FORM:			
: MEDIUM TYPE: Diskette			
: COMPUTER: IBM Compatible			
: OPERATING SYSTEM: DOS			
: SOFTWARE: FastSeq for Windows Version 2.0			
: CURRENT APPLICATION DATA:			
: APPLICATION NUMBER: US/08/984,288			
: FILING DATE: 03-DEC-1997			
: CLASSIFICATION:			
: PRIOR APPLICATION DATA:			
: APPLICATION NUMBER: 60/032,763			
: FILING DATE: 11-DEC-1996			
: ATTORNEY/AGENT INFORMATION:			
: NAME: PRESTIA, PAUL F			
: REGISTRATION NUMBER: 23,031			
: REFERENCE/DOCKET NUMBER: P5099			
: TELECOMMUNICATION INFORMATION:			
: TELEPHONE: 610-407-0700			
: TELEFAX: 846169			

:	INFORMATION FOR SEQ ID NO: 1:				
:	SEQUENCE CHARACTERISTICS:				
:	LENGTH: 1385 base pairs				
:	TYPE: nucleic acid				
:	STRANDEDNESS: single				
:	TOPOLOGY: linear				
:	MOLECULE TYPE: cDNA				
:	US-08-984-288-1				
Alignment Scores:					
Pred. NO.:	6.16e-202	Length:	1385		
Score:	2164.00	Matches:	412		
Percent Similarity:	100.00%	Conservative:	0		
Best Local Similarity:	100.00%	Mismatches:	0		
Query Match:	97.83%	Indels:	0		
DB:	3	Gaps:	0		
US-09-885-478-2 (1-422) x US-08-984-288-1 (1-1385)					
QY	11	GLYAAGALAAVALGlyLeuNGlyGlySerGlyCysasInLaThrgLugIuaSProLeu	30		
Db	66	GGGAGGGCAAGTTGGCGTGGAGGGCGAGCGGCCTCCAGGCAAGAACCCCCCTT	125		
QY	31	ProASPcysgslValAcysAlaProGlVglVyrgrArTrpaqLeuProGlnPro	50		
Db	126	CCCgcACTCGGGGGCTTGCGCTCCGGGACAAAGTGGCACGGCGCTGGAGAGCTGCCGACGCT	185		
QY	51	AlATrPvAlGIUGlySerSerAlAArgLeuTrpGluGlnAlaThrgLyThrGlyTrpMet	70		
Db	186	GGGTGGGTGGAGGGGAGGAGTCAGTCGGTTGTGGGAGGAGCGAGCGACACTGGCTGGATG	245		
QY	71	AspleuGuAlaSerleuLeuProThGlyProASnaLaserSnThSeraspGlyPro	90		
Db	246	GACCTGGCAAGCTCGCTGCTGCCACTGTGCCAATGCCAGCAACACTCTGATGGCCCC	305		
QY	91	AspaSnuThrSerAlaGlySerProProArghTrhgLySerIleSerTyrlleaSnile	110		
Db	306	GATAACCTCACTCGCGCAGGAATCACTCTCGCACGGGGAGCATCTCTTCATCAACAATC	365		
QY	111	IlemetProserValPhelGlyThrIlEecysleuenglyllellegIyaSnserrThrVal	130		
Db	366	ATCATGCGCTCGGTGTGTGGCACCATCTGCCCTCTGGGCAATCATCGGAACTCCACGGTC	425		
QY	131	IlepheAlaValValLysLysSerLysleuHistrpcySaSnasNvaLProaspIleph	150		
Db	426	ATCTTCGGGGTCGTGMAAGATCCAAAGCTGCACGTGGTCAACAACGTCGCCGACATCTTC	485		
QY	151	IlelleasnleuSerValValAspleuenuheueuenglymetProphemetIleHis	170		
Db	486	ATCATCAACCTTCGGTAGTAGATCTCCTCTTCTCCTGGGCAATGCCCTTCATGATCCAC	545		
QY	171	GInleuMeGlyAsnGlyValTrpHisPheglyleuthrMetCysThrlleuIerhala	190		
Db	546	CAGCTCATGGGCAATGGGGGTGGGCACTTGGGGAGAACATGTCACCCTCATACACGGCC	605		
QY	191	MetaSpAlaAsnSerGlnPhetHrserrThryrlleuThralametalIleaspArg	210		
Db	606	ATGGATGCCAAATAGACATTCAACGACCTCAATCCTCGAGCGGCATGGCATTGACCGC	665		
QY	211	TyrleuAlaThrValHisProIleSerSerThrlhsPheAglyLspProserValAlaThr	230		
Db	666	TACCTGGCCACGTCCACCCCATCTCTTCCACAGAAGTTCGGAAAGCCCTCTGTGGCCACC	725		
QY	231	LeuValIleCySleuLeuTrPralaleuSerPheIleSerIlethrProValTrpIleuTyrr	250		
Db	726	CTGGTATGTGCTCTCTGTGGGCCCTCTTCCTTCATACACATCACACCCTCGTGTGCTGAT	785		
QY	251	AlAArgleuIleProPheProGlyGlyAlaValAlGlyCysGlyIleArgleuProAnPro	270		
Db	786	GCCAGACTCATCCCTCCACAGAGGTCACTAGTGGGCTGGGCAATACGCTGCCAACCCA	845		
QY	271	AspThraspleuTyrrTriphethrleuTyrlGlnPhePheLualaphelialeuproPhe	280		

D	b	846	GACACTGACCCTTACTGGTTACCCCTGTACCAAGTTTTTCCTGGCCTTGCCCTGCCTTT	905
Q	y	291	ValValIIEThraAlaAIAIYrValArgIIeLueGlnArgMetThrSerSerValAlaPro	310
D	b	906	GTGGTCATCACAGCGCATACGTGAGATCTTCACAGCGATGAGTCTCTCAGTGGCCCC	965
Q	y	311	AlaSerGlnArgSerIleArgLeuArgThrLysArgValIThrArgThralIleAlaIle	330
D	b	966	GGCTCCACCGCAGCATCCGGCTCGGACAAGAAGGGTACCCGCCAGCATGCGCATC	1022
Q	y	331	CysLeuValPhePheValCysTrpAlaProTYrTYrValLeuGlnLeuThrGlnLeuSer	350
D	b	1026	TGCTGTGTTCTTTGTGTGTGTGGGACCCCTACTAGTGTCTACAGCTACCCAACTGTCC	108
Q	y	351	IleSerArgProThrLeuThrPheValTYrLeuTYrAsnAlaAlaIleSerLeuGlyTYr	370
D	b	1086	ATCAGCGCGCCCAACCCCTCACTGTGTACTATTACAAGCGGCATCAGCTTGCGGTAT	114
Q	y	371	AlaAsnSerCysLeuAsnProPheValTYrIleValLeuGlyGluThrPheArgLysArg	390
D	b	1146	GCCAACAGCTGCTCAACCCCTTGTGTATCATGTCTCTGTGAACACTTCCGAAAAGC	120
Q	y	391	LeuValLeuSerValLysProAlaAlaGlnGlyGlnLeuArgAlaValSerAsnAlaGln	410
D	b	1206	TTGTCCTCTGTGGTAAACCTGCAGCGCCAGGGGACACTTCGGCTGTAGCAAGCTCAG	126
Q	y	411	ThraAlaSpGlnGluArgThrGlnSerLysGlyThr	422
D	b	1266	ACGGCTTGACGAGAGAGACGAAGAAGCAAAGGCATCC	1301

RESULT 5
US-09-218-467B-1
; Sequence 1, Application US/09218467B

```

1 GENERAL INFORMATION:
2 APPLICANT: SATHE, GANESH
3 APPLICANT: ELLIS, CATHERINE
4 APPLICANT: HALSEY, WENDY
5 APPLICANT: BERGSMÄ DERK
6 TITLE OF INVENTION: 11cby Genomic Sequence
7 FILE REFERENCE: GP-50010
8 CURRENT APPLICATION NUMBER: US/09/218,467B
9 CURRENT FILING DATE: 2001-06-22
10 NUMBER OF SEQ ID NOS: 8
11 SOFTWARE: FastSeq for Windows Version 3.0
12 SEQ ID NO 1
13 LENGTH: 3488
14 TYPE: DNA
15 ORGANISM: HOMO SAPIENS
16 US-09-218-467B-1

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Alignment Scores:		
pred. No.:	2,77e-165	3488
Score:	2000.00	422
Percent Similarity:	51.098	
Best Local Similarity:	51.098	
Query Match:	90.428	
DB:	4	
US-09-885-478-2 (1-422) x US-09-218-467B-1 (1-3488)		

US-09-885-478-2 (1-422) x US-09-218-467B-1 (1-3488)

Qy	1	MesrSeValGIyAlaMetLlyLsgSVaIyAlaAlaValGIyLncGIyGIySer	20
Db	569	ATGTCACTGGAGACCATGACAGAGCACTGGAGGCACTTGGCTTGCAGCCGCAAC	628
Qy	21	GLYCSGlnAlaThngLgLnAspProLeuProAspCysGIyAlaCysAlaProGIyGln	40
Db	629	GGCGCCAGGCTACGAGAGAAACCCCTTCCGACCTGGCGGGCTTGGCTCCGGACAA	688
Qy	41	GLyGIyARgARgTTPArgLneuproGlnProAlaTPValGIyLysSerSerAlaArgLeu	60
Db	689	GGTGGCAGAGGCTCGAGAGCTGGCCGACGCTGGGGGTGGAGGGAGCCTGACGCTGGTG	748

QY	61	TTpctuglnalathrglythrnglytrpmetaspleuqulalaSerLeuLeuProthrgly	80
Db	749	TGGAGCAGGGGACCGGCACTGGCTGATGAGCATGGAAAGCCCTGCTGCTGCCACTGGT	808
QY	81	ProasnaIaSerAsnThrSerAspGlyProaspAsnLeuThrSerAla-----	96
Db	809	CCCAATGCCAGCAACACCTCTGATGGGCCCGATAACTCTACTTGGCAGGTGAGTTGACT	868
QY	96	-----	96
Db	869	GGAGCCCTCCCTCTCTGGGCTGTGGGTGGAAATGGGAAGTTTCCACCCCTGAGCCAA	928
QY	96	-----	96
Db	929	ACTGCTGGCAACTTATATCAGACTTCTTGGGACAGATCTGTGTCTGCTTTGCTCTG	988
QY	96	-----	96
Db	989	AGGGCAGAGAAAAGGGGGCAATGTCGCCAGGGGCGACGGCGAGAGCAGACAGG	1048
QY	96	-----	96
Db	1049	GCGGAGGCATATTTCAGATATGCCAAGGAAGGGGGCCAGCCGTGAGACAGCAGGGGAAG	1108
QY	96	-----	96
Db	1109	CTCGCTGCTGGGTTCCAAAGATGCTTGGCCAGAAAAAATTCAGGGCTGGAAAAAGCAAGCGA	1168
QY	96	-----	96
Db	1169	GAGAGCTGGAGGGGTGATGTGGGAGACAGCTGGGGGGCTCACTCCTGCACATTAGCCT	1228
QY	96	-----	96
Db	1229	CAGCTTTTACTCCCACTTGGATGATGAGGTCTGAGACATCTTACTGCACTGGAGAGA	1288
QY	96	-----	96
Db	1289	GGCCCTGGGAAGGGAAGACATTACAGAGCCATGAGGGGATTAACTTTCTGGTGAATTAA	1348
QY	96	-----	96
Db	1349	GCTTCTGACATTTCCAGAGCTGGGTTGCCCTGGAGTTCCAGCTTTGAAGAGAAAAGAA	1408
QY	96	-----	96
Db	1409	GGAAAGAAAGAAGGAAGGCTTATGTGATAAATTTTCCAGGCTGCTGAGCTCCAAACAGA	1468
QY	96	-----	96
Db	1469	CAGTTTCTGTCTGTCTCACTCAAGAAAGCCAGGCTCAGAAATACCAATCAAGAAAT	1528
QY	96	-----	96
Db	1529	CCCCGCTAGGAAGCTGGGGTAGGGAGAGCTGCTGGCTTGACCAGGGCAGACCGGCAAA	1588
QY	96	-----	96
Db	1589	AGCCTTACAGACAGTCACCCACAGATATGCCAAGAAATCAGTACACAGTTCCAAACA	1648
QY	96	-----	96
Db	1649	GAGATTTCCAAAATGAACACTCAGGGCTACACATAGAAAAAGCAGCAGACACACACAC	1708
QY	96	-----	96
Db	1709	ACACACACAGACACTTACTTTGTGTCTTCTGCTATGCTGACAGATTTTCTGSGTG	1768
QY	96	-----	96
Db	1769	AAGCCGGGCTCACAGAGTAATCTCTGCAGACAACTGTGGTTTGTGCTCTGGTGCTG	1828
QY	96	-----	96

QY 223 PheArgLysProSerValAlaThrLeuValIleCysLeuLeuTyrPalaLeuSerPheIle 242
|||||
Db 482 TTCGGAACCCCTCCATGGCCACCTGGTGAATCCCTCTGTGGGCGCTCTCTTATC 541
QY 243 SerIleThrProValTyrLeuTyrAlaArgLeuIleProPheProGlyGlyAlaValGly 262
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Db 542 AGTATCACCCCTGTGGCTACGCCAGGCTATCCCTCCAGGGGGTGTGGGC 601
QY 263 CysGlyIleArgLeuProAsnProAspThrAspLeuTyrTyrPheThrLeuTyrGlnPhe 282
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Db 602 TGTGGATCCGCTGCCAACCAGCCAGCTGACTCTACTGTGCTTACCTACAGTT 661
QY 283 PheLeuAlaPheAlaLeuProPheValValIleThrAlaAlaTyrValArgIleLeuGln 302
|||||
Db 662 TTCCTGGCTTGGCCCTTCCGTTGTGGCATTACCGCGCATGTGAATAATCTACAG 721
QY 303 ArgMetThrSerSerValAlaProAlaSerGlnArgSerIleArgLeuArgThrLysArg 322
|||||
Db 722 CGCATACGCTCTGGTGGCCCGCCAGCTCCCAACGACATCCGGCTTGGAGAAAGG 781
QY 323 ValThrArgThrAlaIleAlaIleCysLeuValPhePheValCysTyrPalaProTyrTyr 342
|||||
Db 782 GTGACCCGACGCGCATGTCATCTGTCTGTCTTGTGTGGTGGCCACCCCTACTAT 841
QY 343 ValLeuGlnLeuThrGlnLeuSerIleSerArgProThrLeuThrPheValTyrLeuTyr 362
|||||
Db 842 GTCTGTACCTGACCCAGCTGTTCATCACCCCGACCTTCACCTTGTCTACTTGTAC 901
QY 363 AsnAlaAlaIleSerLeuGlyTyrAlaAsnSerCysLeuAsnProPheValTyrIleVal 382
|||||
Db 902 AACGGCGCATCAGCTTGGGCTATGCTAAACAGCTCTCGAACCCTTGTGTACTATGATG 961
QY 383 LeuCysGlnThrPheArgLysArgLeuValLeuSerValLysProAlaIleGlnGlyGln 402
|||||
Db 962 CTCTGTGACACCTTGTGAAACGCTTGTGTCTCAGTGAACCCGACGCGGAGGAG 1021
QY 403 LeuArgAlaValSerAsnAlaGlnThrAlaAspGluArgThrGlnSerLysGlyThr 422
Db 1022 CTCGCGACGGTCAAGACGCTCAGACAGCTGATGAGAGAGACAGAAAGAGCACCC 1081

RESULT 7
US-09-478-601-3
; Sequence 3, Application US/09478601
; Patent No. 6221616
; GENERAL INFORMATION:
; APPLICANT: Salom, John A.
; APPLICANT: Lutz, Thomas M.
; APPLICANT: Nagorny, Ralisa
; APPLICANT: Wilson, Amy E.
; TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
; FILE REFERENCE: 57453Z\JPW
; CURRENT APPLICATION NUMBER: US/09/478,601
; EARLIER FILING DATE: 2000-01-06
; EARLIER APPLICATION NUMBER: 09/224,426
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1214
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-09-478-601-3

Alignment Scores:
Pred. No.: 8, 22e-165
Score: 1783.00
Percent Similarity: 97.22%
Best Local Similarity: 95.56%
Query Match: 80.61%
DB: 4 Gaps: 0

US-09-885-478-2 (1-422) x US-09-478-601-3 (1-1214)

QY 63 GlnAlaThrGlyThrGlyTyrMetAspLeuGluAlaSerLeuLeuProThrGlyProAsn 82
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Db 2 CAGGCGACCTGACCGAGCTGGATGGATGGCAACCTGTGCTGTGCTGACAGGCCCAAT 61
QY 83 AlaSerAsnThrSerAspGlyProAsnLeuThrSerAlaGlySerProProArgThr 102
|||||
Db 62 GCCAGACATCTCCGATGGCCAGATGATATCATATGGCGGGGTACACTCTCGCACA 121
QY 103 GlySerIleSerTyrIleAsnIleIleMetProSerValPheGlyThrIleCysLeuLeu 122
|||||
Db 122 GGGAGTGTCTTACATCAACATTAATGCTTCCGTTGTGGTACCATCTGTCTCTG 181
QY 123 GlyIleIleGlyAsnSerThrValIlePheAlaValValLysLysSerLysLeuIleTyr 142
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Db 182 GGCATGTGGGAACSTCCACGSGTCATCTTGTGTGGTGGTGAAGAAGTCCAAACSTACSTGG 241
QY 143 CysAsnAsnValProAspIlePheIleIleAsnLeuSerValValAspLeuPheLeu 162
|||||
Db 242 TGCAGCAAGTCCCGACATCTTCATCAACACTCTGTGGGATCTGTCTCTCTG 301
QY 163 LeuGlyMetProPheMetIleHisGlnLeuMetGlyAsnGlyValITyrPHisPheGlyGlu 182
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Db 302 CTGGCATGCTTTCATGATCCACAGCTCATGGGGAAGGCGTGTGGCACTTTGGGGAA 361
QY 183 ThrMetCysThrLeuIleThrAlaMetAspAlaAsnSerGlnPheThrSerThrTyrIle 202
|||||
Db 362 ACCATGTGACCCCTCATCAACGATGAGCGCAACACTCATGATCTCATGACCTTACATC 421
QY 203 LeuThrAlaMetAlaIleAspArgTyrLeuAlaThrAlaHisProIleSerSerThrLys 222
|||||
Db 422 CTGACTGCATGACCATTCACGCTACTTGGCCACCGTCCACCCCATCTCTCCACCAAG 481
QY 223 PheArgLysProSerValAlaThrLeuValIleCysLeuLeuTyrPalaLeuSerPheIle 242
|||||
Db 482 TTCGGAACCCCTCCATGACCCCTGTGGATCTCCCTGTGGGCGCTCTCTTATC 541
QY 243 SerIleThrProValTyrLeuTyrAlaArgLeuIleProPheProGlyGlyAlaValGly 262
|||||
Db 542 AGTATCACCCCTGTGGCTACGCCAGGCTATTCCTTCCAGGGGGTGTGGGC 601
QY 263 CysGlyIleArgLeuProAsnProAspThrAspLeuTyrTyrPheThrLeuTyrGlnPhe 282
|||||
Db 602 TGTGGCATCCGCTGCCAACCAGCACTGACCTCTGCTGCTCAGCTGTACCACTT 661
QY 283 PheLeuAlaPheAlaLeuProPheValValIleThrAlaAlaTyrValArgIleLeuGln 302
|||||
Db 662 TTCCTGGCTTGGCCCTTCCGTTGTGGCATTACCGCGCATGTGAATAATCTACAG 721
QY 303 ArgMetThrSerSerValAlaProAlaSerGlnArgSerIleArgLeuArgThrLysArg 322
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Db 722 CGCATACGCTCTGGTGGCCCGCCAGCTCCCAACGACATCCGGCTTGGAGAAAGG 781
QY 323 ValThrArgThrAlaIleAlaIleCysLeuValPhePheValCysTyrPalaProTyrTyr 342
|||||
Db 782 GTGACCGGACGCGCATGTCATCTGTCTGTCTTGTGTGGTGGCCACCCCTACTAT 841
QY 343 ValLeuGlnLeuThrGlnLeuSerIleSerArgProThrLeuThrPheValTyrLeuTyr 362
|||||
Db 842 GTCTGTGACACCTTGTGAAACGCTTGTGTCTCAGTGAACCCGACGCGGAGGAG 901
QY 363 AsnAlaAlaIleSerLeuGlyTyrAlaAsnSerCysLeuAsnProPheValTyrIleVal 382
|||||
Db 902 AACGGCGCATCAGCTTGGGCTATGCTAAACAGCTCTCGAACCCTTGTGTACTATGATG 961
QY 383 LeuCysGlnThrPheArgLysArgLeuValLeuSerValLysProAlaIleGlnGlyGln 402
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Db 962 CTCTGTGACACCTTGTGAAACGCTTGTGTCTCAGTGAACCCGACGCGGAGGAG 1021
QY 403 LeuArgAlaValSerAsnAlaGlnThrAlaAspGluArgThrGlnSerLysGlyThr 422
Db 1022 CTCGCGACGGTCAAGACGCTCAGACAGCTGATGAGAGAGACAGAAAGAGCACCC 1081


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; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1316 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-602-809-1

Alignment Scores:
Pred. No.: 7,23e-156 Length: 1316
Score: 1692.00 Matches: 340
Percent Similarity: 86.82% Conservative: 9
Best Local Similarity: 84.58% Mismatches: 22
Query Match: 76.49% Indels: 31
DB: Gaps: 3

US-09-885-478-2 (1-422) x US-08-602-809-1 (1-1316)
QY 37 AlaProGlyGlnGlyAlaArg----- 44
DB 74 TCACCAAGAACTCATGAGAGGAAAGGACAGATTAGCAACAGTGAAGGAGGA 133
QY 45 -----TTP---ArgLeuProGlnProAlaTrpValGluGlySerSerAlaArgLeuTrp 61
DB 134 GAATGGTGGAGAGGATTCAGAGATGAACGGTGGTGGCTGGAGGCTGAGCATGCGCAGCAG 193
QY 62 GluGlnAlaThrGlyThrGlyTrpMetAspLeuGluAlaSerLeuLeuProThr-GlyPr 81
DB 194 GATGTCAGTTCACAGAGAAAGCCCATGTCAACAGCCACGCTTGTCTCTGTGCTCC 253
QY 81 oasnaIaseAsnThrSerAspGlyProAspAsnLeuThrSerAlaGlySerProProAr 101
DB 254 A-----GATCACCCTCCTCG 268
QY 101 GThrGlySerIleSerTrpIleAsnIleIleMetProSerValPheGlyThrIleCysLe 121
DB 269 CAGGGGAGCATCTCTCATCATCAACATCATCATCTCGGTGCTGCGCAGCATCTGCT 328
QY 121 uleuGlyIleIleGlyAsnSerThrValIlePheAlaValAlaLysIleSerLeuNH 141
DB 329 CCTGGGCATATCGGAACTCCACGCGTATCTTCGCGGCTGTGAAGAGTCCAGCTGCA 388
QY 141 sTrpCysAsnAsnValProAspIlePheIleIleAsnLeuSerValValAspLeuLeuPh 161
DB 389 CTGGTGCAACACGTCCTCCGACATCTCATCATCACTCTCGGTAGATCTCTCT 448
QY 161 eleuGlyMetProPheMetIleHisGlnLeuMetClyAsnGlyValTrpHisPheG 181
DB 449 TCTCCTGGGATGCCCTTCATGATCCACCACTCATGGGCAATGGGCTGTCCTTGG 508
QY 181 yGluThrMetCysThrLeuIleThrAlaMetAspAlaAsnSerGlnPheThrSerTrp 201
DB 509 GGAGACCATGTGACCTCATCATCAGCGCATGATGCCAATGATGAGTTCACACACACT 568
QY 201 rIleLeuThrAlaMetAlaIleAspArgTrpLeuAlaThrValHisProIleSerThr 221
DB 569 CATCTGACCGCATGGCCATTTGACCGCTACCTGCGCATCTCCACCCCATCTTCCAC 628
QY 221 rIlyspheArgIlyProSerValAlaThrLeuValIleCysLeuLeuThrPalalaSerPh 241
DB 629 GAAGTTCCGAGAGCCCTCTGTGGCCACCTGATATCTGCTCTGTGGGCCCTCTCT 688
QY 241 eIleSerIleThrProValTrpLeuTrpAlaArgLeuIleProPheProGlyAlaVala 261
DB 689 CATCAGCATCACCCCTGTGTGCTGTATGCGACACTCATCCCTTCCAGAGAGTGCAGT 748
QY 261 lGlyCysGlyIleArgLeuProAsnProAspThrAspLeuTrpTrpPheThrLeuTrpG 281
DB 749 GGGCTGGGCGATACGCTGCGCCCAACCCAGACACTGACTCTACTGCTTACCCCTGTACA 808
QY 281 nphePheLeuAlaPheAlaLeuProPheValValIleThrAlaAlaTrpValaArgIleLe 301

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DB 809 GTTTTTCCTGGCCTTTGGCCCTTTGTGTCATCAGACCGGCATATCGTAGATCCT 868
QY 301 uGlnArgMetThrSerSerValAlaProAlaSerGlnArgSerIleArgLeuArgTrp 321
DB 869 GCAGCGCATGACGTCTCTAGTGGGCCCGCCGCTCCACGACGACATCGGCTGGGACMAA 928
QY 321 sArgValThrArgThrAlaIleAlaIleCysLeuValPhePheValCysTrpAlaProTy 341
DB 929 GAGGCTGACCCGCACAGCCATCGCCATCTGTCTGTCTTGTGTGGCTGGGCCACCTTA 988
QY 341 rTyValLeuGlnLeuThrGlnLeuSerIleSerArgProThrLeuThrPheValTyLe 361
DB 989 CTATGTCTACAGCTGACCCAGTTGTCTCATTCAGCCGCCACCTTCTTGTCTACTT 1048
QY 361 uTyAsnAlaAlaIleSerLeuGlyTyAlaAsnSerCysLeuAsnProPheValTyTr 381
DB 1049 ATACAATCGCGGCATCAGCTTGGCTATGCCACACAGCTGCCTCAACCCCTTGTGTACAT 1108
QY 381 eValLeuGlyGluThrPheArgIlyArgLeuValLeuSerValLysProAlaIleGln 401
DB 1109 GGTGCTGTGTGAGAGCTTCCGCAACGCTTGTCTGTGTGTGAGAGCTGTAGCCAGGG 1168
QY 401 yGlnLeuArgAlaValAsnAlaGlnThrAlaAspGluGluArgThrGluSerIlysg 421
DB 1169 GCAGCTTGGCGCTGTACAGCAACGCTGACAGCGCTGACAGAGAGAGACAGAAAGG 1228
QY 421 yThr 422
DB 1229 CACG 1232

RESULT 10
PCT-US95-16472-1
; Sequence 1, Application PC/TUS9516472
; GENERAL INFORMATION:
; APPLICANT: Bergema, Derek J
; APPLICANT: Ellis, Catherine E
; TITLE OF INVENTION: Human Somatostatin Receptor
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation/Corporate
; STREET: P. O. Box 1539-0W2220
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/16472
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50277
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610 270 5024
; TELEFAX: 610 270 5090
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1316 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 27..1232
; OTHER INFORMATION: /note= "The coding sequence is from

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OTHER INFORMATION: nucleotides 27 to 1232.
PCT-US95-16472-1

Alignment Scores:

Pred. No.:	7,23e-156	Length:	1316
Score:	1692.00	Matches:	340
Percent Similarity:	86.82%	Conservative:	9
Best Local Similarity:	84.58%	Mismatches:	22
Query Match:	76.49%	Indels:	31
DB:	5	Gaps:	3

US-09-885-478-2 (1-422) x PCT-US95-16472-1 (1-1316)

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QY 37 AlAProGlyGlnGlyGlyArgArg-----
DB 74 TCACCGAGAACTCATGAGAGGAGGACAAAGATTAGACACAGTGAAGGAGGGA 133
QY 45 -----TTP---ArgLeuProGlnProAlaTrpValGluGlySerSerAlaArgLeuTrp 61
DB 134 GAATGGTGGAGAGATTCAGATGAGACGCTGGAGGCTGAGACATGCCAGCAG 193
QY 62 GluGlnAlaTrpGlyTrpMetAspLeuGluAlaSerLeuLeuProThr-GlyPr 81
DB 194 GATGTCACTTCACAGCAAGCAAGCCATGTCAAAAGCCAGTCTGCTGTGCGCC 253
QY 81 oAsnAlaSerAsnThrSerAspGlyProAspAsnLeuThrSerAlaGlySerProAr 101
DB 254 A-----GGATTCACCTCTCG 268
QY 101 gthrglyserllesertrileasnllellemetproserValPheGlyThrileCysle 121
DB 269 CAGGGGAGATCTCTACATCAATCATCTCTGCTGCTGCTGCTGCTGCTGCTGCT 328
QY 121 uleuglylleleGlyAsnSerThrValilePheAlaValValLysLysSerLysLeuH 141
DB 329 CCGGGGATCATCGGAGACCTCCAGCTCATCTCGCGCTGAGAGAAAGTCCAGCTGCA 388
QY 141 sTrpCysAsnAsnValProAspIlePhelelleAsnLeuSerValValAspLeuLeu 161
DB 389 CTGGTGCACAAACGCTCCGACATCTTCATCAACCTCTGCTGCTGCTGCTGCTCT 448
QY 161 elaleuGlyMetProPheMetIleHisGlnLeuMetGlyAsnGlyValTrpHisPheG 181
DB 449 TCTCCTGGGATGCTCTCTATGATCCACAGCTCATGGGCAATGGGCTGGAGACTTGG 508
QY 181 ygiurhMetCysThrLeuIleThrAlaMetAspAlaAsnSerGlnPheThrSerThy 201
DB 509 GGAGACCATGTGCACCTCATTCAGCGGCATGATGCCAATAGTCACAGTCCACGACCTA 568
QY 201 rIleleuThrAlaMetAlaIleAspArgTrpLeuAlaThrValHisProIleSerSerTh 221
DB 569 CATCTTCAGCGCATGGCCATGACGCTACCTGGCCACCTGCTCACCCATCTCTTCCAC 628
QY 221 rIlyPheArgLysProSerValAlaThrLeuValIleCysLeuLeuTrpAlaLeuSerPh 241
DB 629 GAAGTTCGGAGAGCCCTGTGGCACCCTGGATCTGCTCTGGGGCCCTCTCTCT 688
QY 241 eIleSerIleThrProValTrpLeuTrpValAlaArgLeuIleProPheProGlyLysAla 261
DB 689 CATCAGCATCACCCCTGTGGCTGATGCCACAGCTCATCCCTTCCACAGAGCTCAGT 748
QY 261 lGlyCysGlyIleLeuArgLeuProAsnProAspTrpAspLeuTrpTrpPheThrLeuTrp 281
DB 749 GGGGCTGGGAGATTCAGCTGCCCAACCAAGACACTGACCTTACTGCTTACCTGTACCA 808
QY 281 nPhePheLeuAlaPheAlaLeuProPheValValIleThrAlaAlaTrpValArgIlele 301
DB 809 GTTTTCTCTGGCCCTTGGCCCTTGTGGTGCATCAGACGCGCATACGTGAGGATCTCT 868
QY 301 uGlnArgMetThrSerSerValAlaProAlaSerGlnArgSerIleArgLeuArgTrpThy 321
DB 869 GCACGCGATGACGTCTCAGTGGCCCGGCTCCAGCAGCGACATCCGGCTGGGAGCAAA 928

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QY 321 sArGValThrArgThrAlaIleAlaIleCysLeuValPhePheValCysTrpAlaProTy 341
DB 929 GAGGGTGACCCGACAGACCATGCCCATCTGTCTGTCTTGTGTGTGTGGGACCCCTA 988
QY 341 rTyValleuGlnLeuThrGlnLeuSerIleSerArgProThrLeuThrPheValIlyle 361
DB 989 CTATGTCTTACACTGACCCAGTGTGTCATACACCCCGGACCTTCTGTCTACTT 1048
QY 361 uTyAsnAlaAlaIleSerleuGlyTrpAlaAsnSerCysLeuAsnProPheValTrp 381
DB 1049 ATACAAATGCGGCATCAGTCTGGGCTATGCCAACAGCTGCTTAACCCCTTGTGTACT 1108
QY 381 eValleuCysGlyuThrPheArgLysArgLeuValleuSerValLysProAlaIleGln 401
DB 1109 CGTCTCTGTGAGACGCTTCGGCAAGCCTTGCTGCTGTGAGTACGCTGCACCCAGG 1168
QY 401 yGlnLeuArgAlaValSerAsnAlaGlnThrAlaAspGluAlaArgThrGlnSerLys 421
DB 1169 GCACCTTCGCGCTGTCCAGCAAGCTCAGACGCTGAGAGAGAGAGCAAGAAAGG 1228
QY 421 yThr 422
DB 1229 CACC 1232

```

RESULT 11

US-09-218-467B-6
Sequence 6, Application US/09218467B

Patent No. 6362326
GENERAL INFORMATION:

APPLICANT: SATHE, GANESH
APPLICANT: ELIIS, CATHERINE

APPLICANT: HALSEY, WENDY
APPLICANT: BERGSMAN, DEK

TITLE OF INVENTION: 11cby Genomic Sequence
FILE REFERENCE: GP-50010

CURRENT APPLICATION NUMBER: US/09/218,467B
CURRENT FILING DATE: 2001-06-22

NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 6
LENGTH: 980

TYPE: DNA
ORGANISM: HOMO SAPIENS

US-09-218-467B-6

Alignment Scores:

Pred. No.:	6,74e-155	Length:	980
Score:	1680.00	Matches:	325
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	75.95%	Indels:	0
DB:	4	Gaps:	0

US-09-885-478-2 (1-422) x US-09-218-467B-6 (1-980)

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QY 98 SerProProArgTrpGlySerIleSerTrpIleAsnIleleMetProSerValPheGly 117
DB 3 TCACCTCCGCGAGCGGAGCATCTCTACATCAACATCATCATGCTTGGGTGGG 62
QY 118 ThrIleCysLeuLeuGlyIleIleGlyAsnSerThrValilePheAlaValLysLys 137
DB 63 ACCATCTGCTCTGAGATCATCGGAACTCCACGGTCACTTCTGCGGTGTGAAGAG 122
QY 138 SerLysLeuHisTrpCysAsnAsnValProAspIlePheIleleAsnLeuSerVal 157
DB 123 TCCAACTGACATGATGAGCAACAGCTCCCGCATCTTCATCATCAACTCTCGGTAGTA 182
QY 158 AspLeuLeuPheLeuLeuGlyMetProPheMetIleHisGlnLeuMetGlyAsnGly 177
DB 183 GATCTCCTTCTCTGCTGGGATGCGCTTCATGATCCACACCTTCATGGGCAATGGG 242
QY 178 TrpHisPheGlyGluThrMetCysThrLeuIleThrAlaMetAspAlaAsnSerGlnPhe 197

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Db      243  TGGCACTTTGGGGAGAACCATATGCAACCCATCATCAGCCGATGAGAGCCAAATATGTCAGTTC      302
Qy      198  ThSerThrTyrIleLeuThrAlaMetAlaIleAspArgTyrLeuAlaThrValHisPro      217
Db      303  ACCAGACACTTACATATCTTACACGGCATGGCCATTTGGATGACCGGTACTCTGAGCCATGTCACCCC      362
Qy      218  IleSerSerThrLysPheArgLysProSerValAlaThrLeuValIleCysLeuLeuTrp      237
Db      363  ATCTCTTCACAGAAATGTCGGGAACCCCTCTGTGGCCACCCTGGTATCTGGCTCTCTGGG      422
Qy      238  AlaLeuSerPheIleSerIleThrProValTrpLeuTyrAlaArgLeuIleProPhePro      257
Db      423  GCCCTCTCTTACATAGATATACACCCCTGTGTGGCTGTATGCGCAGCATATCCCTTCCCA      482
Qy      258  GlGlyAlaValAlaGlyCysGlyIleArgLeuProAsnProAspPheAspLeuTyrTrpPhe      277
Db      483  GGAAGTGCAGTGGGGCTGGGGCATACAGGCTGCCACACCCAGACATGACTCTACTGGTTC      542
Qy      278  ThrLeuTyrGlnPhePheLeuAlaPheAlaLeuProPheValValIleThrAlaAlaTyr      297
Db      543  ACCCTCTACCAATTTTCTTCTGGCCCTTGGCCCTGCTTTGTGTGATCATCAGACGGCATAC      602
Qy      298  ValArgIleLeuGlnArgMetThrSerSerValAlaProAlaSerGlnArgSerIleArg      317
Db      603  GTGAGGATCTCTGCACAGGATGACGTCCTCAATGGGCCCGCCCTCCACAGGAGCATCCGG      662
Qy      318  LeuArgThrLysArgValThrArgThrAlaIleAlaIleCysLeuValPhePheValCys      337
Db      663  CTCGGACAAAGAGGTATACCCGACAGCCATCGCATCTGTCGTGCTCTTGTGTGTC      722
Qy      338  TrpAlaProTyrTyrValLeuGlnLeuThrGlnLeuSerIleSerArgProThrLeuThr      357
Db      723  TGGGCAACCTTACTATGTGCTACAGTCGACCAAGTGGTCATCAGCGCCGACCCCTCCAC      782
Qy      358  PheValTyrLeuTyrAsnAlaAlaIleSerLeuGlyTyrAlaAsnSerCysLeuAsnPro      377
Db      783  TTGTGTACTTATACATGCGGCGCATCAGCTTGGGCTGTATGCCAACAAGCTCGCTCAACCC      842
Qy      378  PheValTyrIleValLeuLeuCysGluThrPheArgLysArgLeuValLeuSerValLysPro      397
Db      843  TTGTGTACATCATGCTCTCTGTGAGACGTTCCGCAACGCTTGGTCTGTGGTGAAGCT      902
Qy      398  AlaIleGlnGlyGlnLeuArgAlaValSerAsnAlaGlnThrAlaAspGlnGluArgThr      417
Db      903  GCGAGCCAGGGGACGCTCGGCTGTCAGCAACCTCAGACGGCTGACAGAGAGAGACA      962
Qy      418  GluSerLysGlyThr      422
Db      963  GAAAGCAAGAGCAC      977

RESULT 12
US-07-816-283-7
: Sequence 7, Application US/07816283
: Patent No. 5436155
: GENERAL INFORMATION:
: APPLICANT: Bell, Graeme I.
: APPLICANT: Yamada, Yuiichiro
: APPLICANT: Seino, Susumu
: TITLE OF INVENTION: SOMATOSTATIN RECEPTORS
: NUMBER OF SEQUENCES: 12
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Arnold, White & Durkee
: STREET: PO Box 4433
: CITY: Houston
: STATE: Texas
: COUNTRY: USA
: ZIP: 77210
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn release #1.0, Version #1.25
: CURRENT APPLICATION DATA:

```

APPLICATION NUMBER: US/07/816,283
 FILING DATE: 19911231
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: McDaniel, C. Steven
 TELECOMMUNICATIONS INFORMATION:
 TELEPHONE: 713-781-1400
 TELEFAX: 713-789-2679
 TELEX: 79-0924
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1244 base pairs
 TYPE: NUCLEIC ACID
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA

Alignment Scores:	
Pred. No.:	6, 11e-43
Score:	55.5, 50
Percent Similarity:	52.5%
Best Local Similarity:	31.7%8
Query Match:	24.2%8
DB:	1
	Gaps: 8

US-09-885-478-2 (1-4222) x US-07-816-283-7 (1-12444)

Qy TrpGlnGlnAlaThrGly-LThrGlyTrpMetLeuAspLeuGlnAlaSerLeuProThrGln 80
||||| :||| :||| ||||| ||||| |||||

Db TGGGAGCCGAAGTGTGGGTGTCTCTCCATTTGAGCTCAACGGCTCACTGGGCCAACG-- 107
50

Qy yProAsnAlaSerAsnThrSerAspGlyProAspAsnLeuThrSerAlaGlySerProPr 100
||| ||||| :||| :||| |||||

Db 108 ----AATGGCTCCAAACCGACCGAACCCATCACTACAGATGACAAAG----- 149
----AATGGCTCCAAACCGACCGAACCCATCACTACAGATGACAAAG-----

Qy 100 cArgThrGlySerLeuSerTyrlLeasnIleLeuMetProSerValPheGlyThrIleCy 120
||| :||| :||| :||| :||| :|||

Db 150 -----AACGGCGTCTCAGGTTCATCTACTCTCGTGGTGTG 184
-----AACGGCGTCTCAGGTTCATCTACTCTCGTGGTGTG 184

Qy 120 sLeuLeuGlyIleIleGlyAsnSerThrValIlePheAlaValIleLysSerLysIle 140
:||||| :||||| :||||| :||||| :||||| :|||||

Db 185 TGTGTGTGGGCTGTGGGGAACAGCGTGGCATTAATGATATCTCTCGTATGCCAAGAT 244
:||||| :||||| :||||| :||||| :||||| :|||||

Qy 140 uHisTrpCysAsnAsnValProAspIlePheIleIleAsnLeuSerValIalAspLeu 160
: :||| :||| :||| :||| :||| :|||

Db 245 G-----AAGACCATCACAACATCATCACTTAATCTGACCTGGCATTCGAGATGAAT 295
-----AAGACCATCACAACATCATCACTTAATCTGACCTGGCATTCGAGATGAAT 295

Qy 160 uPheLeuLeuGlyMetProPhe-----MetIleAsnIleuMetGln 174
||||| :||||| :||||| :||||| :||||| :|||||

Db 296 CTTCATCTCAAGGAGCTTCCCTCTTGTGGCCATGACAGTGGCGGCTAATGCCA----- 344
CTTCATCTCAAGGAGCTTCCCTCTTGTGGCCATGACAGTGGCGGCTAATGCCA-----

Qy 174 yAsnGlyValTrpHisPheGlyGluThrMetCysThrLeuIleThrAlaMetAspAlaAs 194
-----TGGCCCTTTTGGCAAGGCAACCATCTCGGGGTGGTATGACAGTGAATGGCAT 394
-----TGGCCCTTTTGGCAAGGCAACCATCTCGGGGTGGTATGACAGTGAATGGCAT 394

Qy 194 nSerGlnPheThrSerThrTyrlLeuThrAlaMetAlaIleAspArgTyrlLeuAlaTh 214
:||||| :||| :||| :||| :||| :|||

Db 395 CAATCACTTACACAGATCTCTCTGCTTTCAGCGTATAGACGTGACCGGTACCTGGCGGT 454
CAATCACTTACACAGATCTCTCTGCTTTCAGCGTATAGACGTGACCGGTACCTGGCGGT 454

Qy 214 rValHisProIleSerSerThrLysPheAspLysProSerValAlaThrLeuValIleCy 234
||||| :||| :||| :||| :||| :|||

Db 455 GGTGCAACCCATTAACTCAAGCCAAATGGAGGCAACCCCGACGCCCAACATATCAATGT 514
GGTGAACCCATTAACTCAAGCCAAATGGAGGCAACCCCGACGCCCAACATATCAATGT 514

Qy 234 sLeuIleThrPalaLeuSerPheIleSerIleThrProValTrpLeuTyrlAlaArgLeuI 254
:||||| :||||| :||| :||| :||| :|||

Db 515 AGCGTGTGTGTGTCTCTCTCTGTCATATTTCGCCCATGATGATATAGCGCGGCTCGG 574
AGCGTGTGTGTGTCTCTCTCTGTCATATTTCGCCCATGATGATATAGCGCGGCTCGG 574

Qy 254 eProPheProGlyAlaValGlyCysGlyIleLeuArgLeuProAsnProAspThrAspLe 274
:||| :||| :||| :||| :||| :|||

Db 575 GAGCAACCACTGGGGGAGAGAGACAGCTTGACCATTAACGTGGCCAGGCGAATCCGGGGCTG 634
GAGCAACCACTGGGGGAGAGAGACAGCTTGACCATTAACGTGGCCAGGCGAATCCGGGGCTG 634

Qy 274 uTyr--LTrpPheThrLeuTyrlGlnPhePheLeuAlaPheAlaLeuProPheValIle 293
uTyr--LTrpPheThrLeuTyrlGlnPhePheLeuAlaPheAlaLeuProPheValIle 293

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Db      635  GTRACACAGTTTCATTTATCTACGCCCTTCACTCTGGGGTTCCGGTACCCCTTACATCAT 694
Qy      293  ethralaalaatyvalargilleuqlnargmethrserValAlaproAlaSerGI 313
Db      695  TTGTCTCTGCTACCTGTTTCATCATCAATGAGTGAAGTCCCTGGAAATCCAGTGGATC 754
Qy      313  nArgSerIleArgLeuArgThrLysArgValThrArgThrAlaIleAlaIleCysLeuVa 333
Db      755  ATCCAGAGAGAAAAGTCAGAGAAAAGTGAACCGCATGTGTCACATGAGTGGCTGT 814
Qy      333  lPhepheValCysTrpAlaProTyrTyrValLeuGlnLeuThrGlnLeuSerIleSer-- 352
Db      815  CTTGATCTTCTGCTGCTGCTCCCTTCTACATCTTCAACGCTGTCCTCCGTCTGTGGCCAT 874
Qy      353  -ArgProThrLeuThrPheValTyrLeuTyrAsnAlaAlaIleSerLeuGIYTrAlaAs 372
Db      875  CAGTCCACCCCGCCCGCCGTAAGGATGTTTGACTTGTGGTGAATCCATCACCATTGCCAA 934
Qy      372  nSerCysLeuAsnProPheValTyrIleValLeuCysGlnThrPheArgLysArgLeuVa 392
Db      935  CAGCTCGCCCAACCCCATCTGTACGCTTCTGTCTGACACCTTCAGAG-- 986
Qy      392  lLeuSerValLysProAlaAlaGlnGlnGlnLeuArgAlaIleSerAsnAlaGlnThrAl 412
Db      987  -----AGCTTCCAGAAATGTTCTTCTTGTGTCAGGTGATGTCATCGCA 1030
Qy      412  aAspGluGluArgThrGluSerLys 420
Db      1031  GGATGGGGAGAGAGCAGCAGCTAAG 1055

RESULT 13
US-08-417-103-7
; Sequence 7, Application US/08417103
; Patent No. 5723299
; GENERAL INFORMATION:
; APPLICANT: Bell, Graeme I.
; APPLICANT: Yamada, Yuichiro
; APPLICANT: Saino, Susumu
; TITLE OF INVENTION: SOMATOSTATIN RECEPTORS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/417,103
; FILING DATE: 05-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/816,283
; FILING DATE: 01-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: ARCD:144
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1244 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: 24..1130
US-08-417-103-7

Alignment Scores:
Pred. No.: 6,11e-43 Length: 1244
Score: 535.50 Matches: 117
Percent Similarity: 52.57% Conservative: 77
Best Local Similarity: 31.71% Mismatches: 133
Query Match: 24.21% Indels: 42
Db: 1 Gaps: 8

US-09-885-478-2 (1-422) x US-08-417-103-7 (1-1244)
Qy      61  TrpGluGlnAlaThrGly-ThrGlyTrpMetAspLeuGlnAlaSerLeuProThrGln 80
Db      50  TGGAGGCCAAATGGGGGTGCTCTCCATTGACCTTAACGGCTCACTGGGGCCAAAC-- 107
Qy      80  yProAsnAlaSerAsnThrSerAspGlyProAspAsnLeuThrSerAlaGlySerProPr 100
Db      108  ----AATGGCTCCAAACGACGAGCCATACATGACATGACAGCAAGC----- 149
Qy      100  cArgThrGlySerIleSerTyrIleAsnIleIleMetProSerValPheGlyThrIleCy 120
Db      150  -----AACGCCGTCTCAGCTTCACTTCACTTCTGTTGTG 184
Qy      120  sLeuLeuGlyIleIleGlyAsnSerThrValIlePheAlaValAlaLysSerLysLe 140
Db      185  TGTGTGTGGGCTGTGGCCAAACGCTGTGTCATTATGTCTATCTCCGCTATGCCAAGAT 244
Qy      140  uHisTrpCysAsnAsnValProAspIlePheIleIleAsnLeuSerValValAspLeu 160
Db      245  G-----AAGACCATCACCAACATCATCATCTTACCTGGCCATGCGCATGCACT 295
Qy      160  uPheLeuLeuGlyMetProPhe-----MetIleHisGlnLeuMetGln 174
Db      296  CTTGATGCTAGGGCTCCCTCTGGCCATGCAAGTGGCGCTAGTCCAC----- 344
Qy      174  yAsnGlyValITrPHisPheGlyGlnThrMetCysThrLeuThrAlaMetAspAlaAs 194
Db      345  -----TGGCTTTTGGCAAGCCATCTGCGGGGTGTCATGACTGTAGATGGCAT 394
Qy      194  nSerGlnPheThrSerThrTyrIleLeuThrAlaMetAlaIleAspArgTyrLeuAlaTh 214
Db      395  CAATCAGTTCAACCAATATCTCTGCTGACGGTCAATGACATCGACCCGCTACGGCCGT 454
Qy      214  rValHisProIleSerSerThrLysPheArgLysProSerValAlaThrLeuValIleCy 234
Db      455  GGTGACCCCATTAAGTCAGCCAAATGAGGGGACCCGACAGCCAGACAGATGATCAATGT 514
Qy      234  sLeuLeuTrpAlaLeuSerPheIleSerIleThrProValTrpLeuTyrAlaArgLeuI 254
Db      515  ACGTGTGTGTGTGTCTGCTGTCATTTTGGCCATCATGATATACCGCGGCTCGG 574
Qy      254  eProPheProGlyGlyAlaValAlaGlyCysGlyIleArgLeuProAsnProAspThrAspLe 274
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QY 372 nserCysLeuAsnProPheValTrrIleValLeuGlyuThrPheArgLysArgLeuVa 392
Db 935 CACCTCGGCCAACCCCATCTGTACGCCCTTGTCTGTGACAACTCAAGAG----- 986
QY 392 IleSerValLysProAlaIleGlnGlyGlnLeuArgAlaValSerAsnaIaGlnThrAl 412
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QY 412 aaSPGIuGIuArgThrGluSerLys 420
Db 1031 GGATGGGAGAGGAGGAGCAGCAGTAG 1055
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; Sequence 5, Application US/07816283
; Patent No. 5436155
; GENERAL INFORMATION:
; APPLICANT: Bell, Graeme I.
; APPLICANT: Yamada, Yuichiro
; APPLICANT: Saito, Susumu
; TITLE OF INVENTION: SOKAOSTATIN RECEPTORS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: PO Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/816, 283
; FILING DATE: 19911231
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McDaniel, C. Steven
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-787-1400
; TELEFAX: 713-789-2679
; TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
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; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-07-816-283-5
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Score: 532.00 Matches: 124
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Best Local Similarity: 30.10% Mismatches: 147
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QY 137 LysSerLysLeuHisTrrPcysAsnaIaProAspIlePheIleIleAsnLeuSerVal 156
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QY 231 LeuValIleCysLeuLeuLeuSerPheIleSerThrIleThrProValTrrPLeuTyr 250
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QY 251 AlaArgLeuIleProPheProGlnGlyAlaValGlyCysGlnIleArgLeuProAsnPro 270
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QY 271 AspThrAspLeuTyr--TrrPheThrLeuTrrGlnPhePheLeuAlaPheAlaLeuPro 289
Db 683 TCTGGGGCTTGGTACACAGGTTTCATCATCTTCATCTTGGGGTTCCTGCTGCC 742
QY 290 PheValValIleThrAlaIleValValArgIleLeuGlnArgMetThrSerSerValAla 309
Db 743 CTCACCATCATCTGTCTTGTCTACCTGTTCACTTATCATCAACAGTAAGTCTCTGGAATC 802
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Sequence 5, Application US/08417103
Patent No. 5723299
GENERAL INFORMATION:
APPLICANT: Bell, Graeme I.
APPLICANT: Yamada, Yuchiro
APPLICANT: Sano, Susumu
TITLE OF INVENTION: SOMATOSTATIN RECEPTORS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,103
FILING DATE: 05-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/816,283
FILING DATE: 01-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: ARCD:144
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1351 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 83..1189
US-08-417-103-5
Alignment Scores:
Pred. No.: 1.53e-42 Length: 1351
Score: 532.00 Matches: 124
Percent Similarity: 49.76% Conservative: 81
Best Local Similarity: 30.10% Mismatches: 147
Query Match: 24.05% Indels: 60
DB: 1 Gaps: 12
US-09-885-478-2 (1-422) x US-08-417-103-5 (1-1351)
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Db 2 GATCCTTGCCCT-----CCAGGTCCTATTAGTGAGAAATA 37
Qy 48 ProGlnProAlaTrpValGlu-----GlySerSerAlaArgLeuTrp 61
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Thu Feb 20 11:14:37 2003

us-09-885-478-2.rni

Page 15

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GenCore version 5.1.3
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2755.572 Million cell updates/sec

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Searched: 424239 seqs, 254661826 residues

Total number of hits satisfying chosen parameters: 848478

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	2085	94.3	2138	10	US-09-895-686-8
4	1783	80.6	1214	10	US-09-885-478-3

5	1708	77.2	1478	10	US-09-864-761-9721	Sequence 9721, Ap
6	1224	55.3	720	10	US-09-864-761-21946	Sequence 21946, A
7	886	40.1	519	10	US-09-895-686-25	Sequence 25, Appl
8	777	35.1	459	10	US-09-864-761-10236	Sequence 10236, A
9	565.5	25.6	1023	9	US-09-990-940-1	Sequence 1, Appl1
10	565.5	25.6	1965	9	US-09-791-932-57	Sequence 57, Appl
11	552.5	25.0	336	10	US-09-895-686-22	Sequence 22, Appl
12	539	24.4	575	10	US-09-864-761-9017	Sequence 9017, Ap
13	521	23.6	304	10	US-09-895-686-57	Sequence 57, Appl
14	519	23.5	1427	10	US-09-967-768A-296	Sequence 296, App
15	498	22.5	274	10	US-09-864-761-26601	Sequence 26601, A
16	475	21.5	279	10	US-09-895-686-24	Sequence 24, Appl
17	475	21.5	1773	9	US-10-112-599A-3	Sequence 3, Appl1
18	472	21.3	271	10	US-09-895-686-56	Sequence 56, Appl
19	462	20.9	1610	10	US-09-761-962-16	Sequence 16, Appl1
20	462	20.9	2229	10	US-09-214-904-1	Sequence 1, Appl1
21	456.5	20.6	1981	10	US-09-823-114-15	Sequence 15, Appl
22	455	20.6	1149	10	US-09-993-844-10	Sequence 10, Appl
23	453.5	20.5	1334	10	US-09-761-962-3	Sequence 3, Appl1
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25	453.5	20.5	1423	10	US-09-761-962-1	Sequence 1, Appl1
26	453.5	20.5	1542	10	US-09-761-962-4	Sequence 4, Appl1
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33	421.5	19.1	1408	10	US-09-214-904-5	Sequence 5, Appl1
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41	413	18.7	1805	10	US-09-823-114-18	Sequence 18, Appl
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43	412	18.6	1404	10	US-09-804-551B-9	Sequence 9, Appl1
44	377	17.0	223	10	US-09-895-686-20	Sequence 20, Appl1
45	372	16.8	1238	10	US-09-761-962-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
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; Sequence 1, Application US/09885478
; Patent No. US20020111306A1
; GENERAL INFORMATION:
; APPLICANT: SALON, JOHN A
; APPLICANT: LAZ, THOMAS M
; APPLICANT: NAGORNY, RAISA
; APPLICANT: WILSON, AMY E
; TITLE OF INVENTION: DNA ENCODING A HUMAN MELANIN CONCENTRATING HORMONE RECEPTOR (M
; FILE REFERENCE: 1795/57453-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/885,478
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US99/31169
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1269
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-885-478-1
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Score: 2212.00
Percent Similarity: 100.00%
Length: 1269
Matches: 422
Conservative: 0

Best Local Similarity:	100.00%	Mismatches:	0
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Dp	241	CCCAATGCCAGCAACACCTCTGATGGCCCCGATAACTTACTTACAGAGATCACTCTCT	300
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QY	181	GlyLeuThrMetCysThrLeuIleThrAlaMetAspAlaAsnSerGlnPheThrSerThr	200
Dp	541	GGGAGACCAATGTGCACCTCATACAGGGCAATGGAGCCAAATGACGTACACAGACAC	600
QY	201	TyrIleLeuThrAlaMetAlaIleAspArgTyrLeuAlaThrValHisProIleSerSer	220
Dp	601	TACATCTTGACCGGCATGGCCATTTGACCGCTACTGGCCACATGCCCATCTCTTCC	660
QY	221	ThrIysPheArgIysProSerValAlaThrIleValIleCysLeuLeuTrpAlaLeuSer	240
Dp	661	ACGAGATTCGGAGAGCCCTCTGTGGCACCTGTGTATGTGCTCTCTGTGGCCCTCTCC	720
QY	241	PheIleSerIleThrProValIleTrpLeuTyrAlaArgLeuIleProPheProGlyVala	260
Dp	721	TTTCAATCAGCATCACCCCTGTGGGTGTATGGCAGACATCATCCCTTCCACAGAGGTCA	780
QY	261	ValGlyCysGlyIleArgLeuProAsnProAspThrAspLeuTyrTrpPheThrLeuTyr	280
Dp	781	GTTGGGCTGGCGCATACGCCCTGCCCAACCAAGACACTGACTCTACTGGTCAACCTCTAC	840
QY	281	GlnPhePheLeuAlaPheAlaLeuProPheValValIleThrAlaAlaTyrValArgIle	300
Dp	841	CAGTTTTTCTGGGCTTGGCCCTTGCTTTGTGTGTCATACAGCCGCAATACGTGAGATC	900
QY	301	LeuGlnArgMetThrSerSerValAlaProIaSerGlnArgSerIleArgIleuArgThr	320
Dp	901	CTGCAGCGCATGACGTCTCATGTGGGCCCGCGCTCCACAGCAGCATCGGCTGGGACA	960
QY	321	LysArgValThrArgThrAlaIleAlaIleCysLeuValPhePheValCysTrpAlaPro	340
Dp	961	AAGGGGTGACCCGCACAGCATCGCATCTGTCTGTCTTCTTGTGTGTGGTGGGACCC	1020

OY	361	TYRRYRValLeuGlnLeuThrGlnLeuSerLLeSerArgProThrLeuThrPheValTyr	360
Db	1021	TACTATGTGGCTACAGCGTCAACCGAGTTGTGCATCAGCGCCGCAACCTCACTCTTGTCTAC	1080
OY	361	LeuYrAsnAlaAlaLLeSerLeuGlyTYRrAlaAsnSerCysLeuAsnProPheValTyr	380
Db	1081	TTATACATGTGGGCGCATCACACTTGGGCTATGGCAACAGCTGGCTCAACCCCTTGTGTAC	1140
OY	381	LLeValLeuCysGluThrPheArgLysArgLeuValLeuSerValLysProAlaAlaGln	400
Db	1141	ATCTGCTCTGTGTGAGAGTTCGCCAAACGCTTGGTCTCTGTGGTGAACCTGTCAAGCCAG	1200
OY	401	GlyGlnLeuArgAlaValSerAsnAlaGlnThrAlaAspGluGArgThrGlnSerLys	420
Db	1201	GGCGACGCTCCCGCTGTCAACAACGCTCAAGCGCTGACAGAGAGAGCAAGCAAAAGCAA	1260
OY	421	GlyThr	422
Db	1261	GGCACC	1266

RESULT 2
US-09-92

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000003 2625770 1
; Sequence 1, Application US/09925776
; Patent No. US20020038007A1
; GENERAL INFORMATION:
; APPLICANT: AMES, ROBERT S., JR.
; APPLICANT: SARAU, HENRY M.
; APPLICANT: FOLEY, JAMES J.
; APPLICANT: BERGSMAN, DEBK J.
; APPLICANT: ELLIS, CATHERINE E.
; APPLICANT: CHAMBERS, JON K.
; TITLE OF INVENTION: A METHOD OF FINDING AGONIST AND
; TITLE OF INVENTION: ANTAGONIST*
; FILE REFERENCE: GP-50003-D2
; CURRENT APPLICATION NUMBER: US/09/925,776
; CURRENT FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/032,763
; PRIOR FILING DATE: 1996-12-11
; PRIOR APPLICATION NUMBER: 08/984,288
; PRIOR FILING DATE: 1997-12-03
; PRIOR APPLICATION NUMBER: 60/073,747
; PRIOR FILING DATE: 1998-02-05
; PRIOR APPLICATION NUMBER: 09/060,504
; PRIOR FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1385
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-925-776-1

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Alignment Scores:

Pred. No.:	2,276	194
Score:	2164	412
Percent Similarity:	100.00%	0
Best Local Similarity:	100.00%	0
Query Match:	97.83%	0
DB:	10	0
	Gaps:	0

US-09-885-478-2 (1-422) x US-09-925-776-1 (1-1385)

QY 11 GYAATGAlaValGlyLeuGlyGlySerGlyCysGlnAlaThrGluGluAspProLeu 30
Db 66 GGGAGGGCGATTGGCTTGGAGCGCGACGCTCCACGGCTACGAGAGAACCCCTT 124
QY 31 ProAspCysGlyAlaAcYalaProGlyGlnGlyGlyValArgATTPArgLeuProGlnPro 50
Db 126 CCCGACTGGGGGGCTTGGCTTCGGGACAAAGGTGGCAAGCCGTGGAGGCTGCCAGGCT 188
QY 51 AlATrPValGluGlySerSerAlaArgLeuThrPglGlnAlaThrGlyThrGlyTTPMet 70

Db 186 GCCTGGGTGAGGGAGCTCAGCTCGGTTGTGGAGCAGGCGACCCGACCTGGCTGGATG 245
QY 71 AspleuGluaLaserleuProthrGlyProAsnaLaseranLhseraspGlyPro 90
Db 246 GACCTGGAAAGCCCTGCTGCTGCCACTGGTCCCAATGCCAGCAACACTCTGATGGCCCC 305
QY 91 AspAsnLeuThrSeraLaglySerProProArgThrGlySerLleSerTyrlleasnIle 110
Db 306 GATTAACCTCACTTCGGCAGAGATCACTCCCTCCGACGGGAGCAWCTCTATCATCAACATC 365
QY 111 IleMetProSerValPheGlyThrIleCysLeuLeuGlyIleIleGlyasnSerThrVal 130
Db 366 ATCATGCTCTTCGGTGTGGCACCATCTCCCTCGGATCATCCGGAATCCACGGTCC 425
QY 131 IlePheAlaValAllylsYssSerLysLeuHisTrpCysAsnAsnAlProAspIlePhe 150
Db 426 ATCTTGCGGCTGTGAAGAAGTCCAGCTGCATGGTGCACACAGCTCCCGCATCTTC 485
QY 151 IleIleasnLeuSerValValAspleuLeuPheLeuLeuGlyMetProPheMetIleHis 170
Db 486 ATCATCAACCTCTCGGTAGATGTCCTCTTCCTCGGCAATGCCCTCATGATCCAC 545
QY 171 GlnLeuMetGlyAsnGlyValTrpHisPheGlyGluThrMetCysThrLeuIleThrAla 190
Db 546 CAGCTCATGGCAATGGGGTGTGGCACTTGGGGAGACCATGTGCACCCCTCATCACGGCC 605
QY 191 MetAspAlaAsnSerGlnPheThrSerThrTyrlleLeuThrAlaMetAlaIleAspArg 210
Db 606 ATGGATGCCAATATGATGATTCACACACCTACATCTCTGACCCGCAATGGCATGACCGC 665
QY 211 TyrLeuAlaThrValHisProIleSerSerThrLysPheArgLysProSerValAlaThr 230
Db 666 TACCTGGCACAGTGCACCCCATCTTCACAGAACTTCGGAAAGCCCTGTGGCCACC 725
QY 231 LeuValIleCysLeuLeuTrpAlaLeuSerPheIleSerIleThrProValTrpLeuTyrl 250
Db 726 CTGGTGAATCTGCTCTCTGGGGCCCTCTCTCATCAGATCACCCCTGTGTGGCTGTAT 785
QY 251 AlaArgLeuIleProPheProGlyValAlaValGlyCysGlyIleArgLeuProAsnPro 270
Db 786 GCCAGCTATCCCTTCCAGAGAGTGCAGTGGCTGGGCAATGACCTGGCCCAACCCA 845
QY 271 AspThrAspLeuTyrlTrpPheThrLeuTyrlGlnPhePheLeuAlaPheAlaLeuProPhe 290
Db 846 GACACTGACCTGACTGCTTACACCTGATACAGATTTTCTTGCCCTTGGCCCTGCTTT 905
QY 291 ValValIleThrAlaAlaTyrlValArgIleLeuGlnArgMetThrSerSerValAlaPro 310
Db 906 GTGGTATATCACAGCCCATACGTGAGGATCTGCACGCGATGACGTCTCAGTGGCCCCC 965
QY 311 AlaSerGlnArgSerIleArgLeuArgThrLysArgValThrArgThrAlaIleAlaIle 330
Db 966 GCCTCCACGACGATCCGGCTGGCGGACAAAGAGGTGACCCGCAACGCCATGGCCATC 1025
QY 331 CysLeuValPhePheValCysTrpAlaProTyrlTyrlValLeuGlnLeuThrGlnLeuSer 350
Db 1026 TCGTCTGCTCTTCTTGTGTGGTGGACACCTACTATGTGTACAGTGCACCCAGTTGTCC 1085
QY 351 IleSerArgProThrIleuThrPheValTyrlLeuTyrlAsnAlaAlaIleSerLeuGlyTyrl 370
Db 1086 ATCAGCGCGCCGACCTCACTTGTCTACTATTACATGCGCGCATGACCTTGGGCTAT 1145
QY 371 AlaAsnSerCysLeuAsnProPheValTyrlIleValLeuCysGlnThrPheArgLysArg 390
Db 1146 GCCACAGCTGCTCAACCCCTTTGTGTATCTGCTCTGTGAGACGTTCCGCCAAGCGC 1205
QY 391 LeuValLeuSerValLysProAlaAlaGlnGlyGlnLeuArgAlaValSerAsnAlaGln 410
Db 1206 TTGGTCTCTGCGGTGAAGCTGCAGCCCAAGGGCAGCTTCGCGCTGCAGCAACGGTCAAG 1265
QY 411 ThrAlaAspGlnGluArgThrGlnSerLysGlyThr 422
Db 1266 ACGGTGACGAGAGAGACAAAGCAAGGCAACC 1301

```
RESULT 3
US-09-895-686-8
; Sequence 8, Application US/09895686
; Patent No., US2002010655A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN GPCR PROTEINS
; FILE REFERENCE: PC-0044 CIP
; CURRENT APPLICATION NUMBER: US/09/895,686
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PERL Program
; SEQ ID NO 8
; LENGTH: 2138
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US2002010655A1 145943ZCB1
US-09-895-686-8

Alignment Scores:
Pred. No.: 1,15e-186 Length: 2138
Score: 2085.00 Matches: 400
Percent Similarity: 98.53% Conservative: 3
Best Local Similarity: 97.80% Mismatches: 6
Query Match: 94,264 Indels: 1
DB: Gaps: 0

US-09-885-478-2 (1-422) x US-09-895-686-8 (1-2138)
QY 14 ValGlyLeuGlyGlySerGlyCysGlnAlaThrGluLysProLeuProAspCys 33
Db 21 ATGGGCTTGAGAGCGGACAC -GGCTGGCAGGCTACGAGAGGTAGACCCCTTCCCAACTGC 79
QY 34 GlyAlaCysAlaProGlyGlnGlyArgArgTrpArgLeuProGlnProAlaTrpVal 53
Db 80 GGGGCTTGCCTCCGGGACAGGTGGCAGCGCTGGAGGTGGCGCGAGCTGGGTG 139
QY 54 GlnGlySerSerAlaArgLeuTrpGluGlnAlaThrGlyThrGlyTrpMetAspLeuGlu 73
Db 140 GAGGGAGCTCAGCTCGGTGTGGCAGCATGCGACCGCATGGCTGGATGGACCTGGAA 199
QY 74 AlaSerLeuLeuProThrGlyProAsnAlaSerAsnThrSerAspGlyProAspAsnLeu 93
Db 200 GCCTCGGTGCTGCCACTGCTGCCAATGCCAGCAACACCTGTGATGGCCCGGATTAACCTC 259
QY 94 ThrSerAlaGlySerProProArgThrGlySerIleSerTyrlIleasnIleIleMetPro 113
Db 260 ACTTCGGCAGATCACCTCTCTGCACGGGAGGATCTCTTAATCAACATCATCATATGCC 319
QY 114 SerValPheGlyThrIleCysLeuLeuGlyIleIleGlyasnSerThrValIlePheAla 133
Db 320 TCGGTGTGGCAGCATCTGCTCTTGGGATGATGGGAATCCAGGATCATCTTGGCG 379
QY 134 ValValLysLysSerLysLeuHisTrpCysAsnAsnValProAspIlePheIleIleasn 153
Db 380 GTCTGAGAAAGTCCAAAGTGCACATGGTGCACAAACAGTCCCGCATCTTCATCATCAAC 439
QY 154 LeuSerValValAspleuLeuPheLeuLeuGlyMetProPheMetIleHisGlnLeuMet 173
Db 440 CTCTCGTAAATATCTCTCTTCTCTGGGATGCGCTTCATGATCCACGACTCATG 499
QY 174 GlyAsnGlyValTrpHisPheGlyGluThrMetCysThrLeuIleThrAlaMetAspAla 193
Db 500 GGCATATGGGTGTGGCACTTGGGGAGACCATGTGCACCTTCATCAGCGGCATGGATGCC 559
QY 194 AsnSerGlnPheThrSerThrTyrlleLeuThrAlaMetAlaIleAspArgTyrlleuAla 213
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Db 560 AATAGTCAGTTCACACCACTACATCTGACCGCATGTGACCGCTTACCTGACC 619
Qy 214 ThrValHisProIleSerSerThrIlyPheArgIlyProSerValAlaThrIleValIle 233
Db 620 ACTGTCCACCCCATCTTTCCACGAAGTTCGGAAAGCCCTGTGTGGCCACCTGGTGATC 679
Qy 234 CysLeuLeuTrpAlaLeuSerPheIleSerIleThrProValTrpLeuTrpAlaArgLeu 253
Db 680 TGCCTCTGTGGCCCTCTCTCTCATCATCAGATCACCCTGTGTGGCTGTATGTCAGACATC 739
Qy 254 IleProIleProGlyGlyAlaValAlaGlyCysGlyIleArgLeuProAsnProAspThrAsp 273
Db 740 ATCCCTCTCCAGAGGTGCAAGTGGCTGGCATACGCTGCCCAACCCAGACACTGAC 799
Qy 274 LeuTrpTrpPheThrIleuArgIlnPhePheLeuAlaPheAlaLeuProPheValIle 293
Db 800 CTCACAGTTCACCCCTGTACACAGTTTTCCTGTGGCTTTCCTGCTTGTGGTGATC 859
Qy 294 ThrAlaIleArgValAlaArgIleLeuGlnArgMetThrSerSerValAlaProAlaSerGln 313
Db 860 ACAGCCCATACGATGAGATCTGCAGCCGATGACGCTCAGTGGCCGCCACCTCCAG 319
Qy 314 ArgSerIleArgLeuArgTrpIlyArgValThrArgThrAlaIleAlaIleCysLeuVal 333
Db 920 CGAGCATCCGGCTGGCGAAGAGGGGTACCCGACACCATCCCATCTGTGTGTC 353
Qy 334 PhePheValCysTrpAlaProTyrTyrValIleuGlnLeuThrGlnLeuSerIleSerArg 353
Db 980 TTCTTTGTGTGGGACCTTACTATGTCTACAGTGCATGCCAGTTGTTCATCACCCG 1039
Qy 354 ProThrLeuThrPheValTyrLeuTyrAsnAlaAlaIleSerLeuGlyTyrAlaAsnSer 373
Db 1040 CCGACCCCACTTGTCTACTTATACAAATGCGGCATCAGCTTGGGCTATGCAACAGC 1099
Qy 374 CysLeuAsnProPheValTyrIleValLeuCysGlyThrThrArgIlySarGlyLeuVal 393
Db 1100 TGCCTCAACCGTTTGTGATCATGTGCTGTGAGACGTTCCGCAACGCTTGGTCTG 1159
Qy 394 SerValIlyProAlaIleArgIlnGlyIleuArgAlaValSerAsnIleGlnThrAlaAsp 413
Db 1160 TCGGTGAAGCTGCAGCCGACGGGCACTTCGCGCTGTGCAACGCTCAGGCGGCTGAC 1219
Qy 414 GluGlnArgThrGlnSerIlyGlyThr 422
Db 1220 GAGGAGGACAGAAAGCAAGGACCC 1246

RESULT 4
US-09-885-478-3
; Sequence 3, Application US/09885478
; Patent No. US2002011306A1
; GENERAL INFORMATION:
; APPLICANT: SALON, JOHN A
; APPLICANT: LAZ, THOMAS M
; APPLICANT: NAGORNY, RAISA
; APPLICANT: WILSON, AMY E
; TITLE OF INVENTION: DNA ENCODING A HUMAN MELANIN CONCENTRATING HORMONE RECEPTOR (MCH1
; FILE REFERENCE: 1795/57453-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/885,478
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US99/31169
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1214
; TYPE: DNA
; ORGANISM: RATIUS NORVEGICUS
US-09-885-478-3

Alignment Scores: 1.25e-158 Length: 1214
Pred. No.: 1783.00 Matches: 344

Percent Similarity: 97.22% Conservative: 6
Best Local Similarity: 95.56% Mismatches: 10
Query Match: 80.61% Indels: 0
DB: 10 Gaps: 0

US-09-885-478-2 (1-422) x US-09-885-478-3 (1-1214)

Qy 63 GlnAlaThrGlyThrGlyTrpMetAspLeuGlnAlaSerLeuLeuProThrGlyProAsn 82
Db 2 CAGGGACCTGCACCGGCTGCATGTGCAAACTGTGTGCTGCACCTGACGCCCCAT 61
Qy 83 AlaSerAsnThrSerAspGlyProAspAsnLeuThrSerAlaGlySerProProArgThr 102
Db 62 GCCAGCAACATCTCCGATGGCCAGGATATCATCATTCAGATTCGCGGGTCACTCTCCGACA 121
Qy 103 GlySerIleSerTrpIleAsnIleIleMetProSerValPheGlyThrIleCysLeuLeu 122
Db 122 GGGAGTGTCTCTACATCAATCAATATATGCTTCCGTTGTTGGTATCCATCTGTCTCTG 181
Qy 123 GlyIleIleGlyAsnSerThrValIlePheAlaValAlaIlySlySerIlyLeuHisTrp 142
Db 182 GGCATCGTGGGAACCTCCAGGTCATCTTGTCTGTGGTGAAGATCCAACTACACTGG 241
Qy 143 CysAsnAsnValProAspIlePheIleIleAsnLeuSerValIlyAspLeuPheLeu 162
Db 242 TGCACCAACGTCCTCCGACATCTTCATCAACCTCTCTGTGGATCTGCTCTCTG 301
Qy 163 LeuGlyMetProPheMetIleHisGlnLeuMetGlyAsnGlyValAlaTrpHisPheGlyGlu 182
Db 302 CTGGGCAATGCTTTCATATATCCACGATGAGGGAAGGCGTGTGGCACTTGGGGAA 361
Qy 183 ThrMetCysThrLeuIleThrAlaMetAspAlaAsnSerGlnPheThrSerThrTyrIle 202
Db 362 ACCATGTGCACCTCATATACAGCCATGAGCCCAACATCATGTTCACTACAGCACTTACATC 421
Qy 203 LeuThrAlaMetAlaIleAspArgTyrLeuAlaThrValHisProIleSerSerThrIly 222
Db 422 CTGACTGCCATGACCATTTGACCGGTACTTGGCCACCGTCCACCCCATCTCTCCACCAAG 481
Qy 223 PheArgIlyProSerValAlaThrLeuValIleCysLeuLeuTrpAlaLeuSerPheIle 242
Db 482 TTCGGGAAGCCCTCATATCCACCTGCTGTGATCTGCTCTGTGGGCGCTCTCTCATC 541
Qy 243 SerIleThrProValTrpLeuTrpLeuTyrAlaArgLeuIleProPheProGlyGlyAlaValGly 262
Db 542 AGTATCACCCCTGTGTGGCTCTACGCCAGGCTCATTCCTTCCAGGGGGTGTGTGGGC 601
Qy 263 CysGlyIleArgLeuProAsnProAspThrAspLeuTyrTrpPheThrLeuTyrGlnPhe 282
Db 602 TGTGTCATCCGCTGCCAAACCCGACACTGACCTCTACTGTCTACATCTGTACCAATTT 661
Qy 283 PheLeuAlaPheAlaLeuProPheValValIleThrAlaAlaTyrValArgIleLeuGln 302
Db 662 TTCCTGGCCCTTGGCCCTTCTGTGTGTGTCATTCACCGCGCATTCGTGAATAATCTACAG 721
Qy 303 ArgMetThrSerSerValAlaProAlaSerGlnArgSerIleArgLeuArgTrpIlyArg 322
Db 722 CGCATGAGCTGTGTGGTGGCCCAAGCTCCCAAGCAGACATCCGGCTTGGACAAAGAG 781
Qy 323 ValThrArgThrAlaIleAlaIleCysLeuValPhePheValCysTrpAlaProTyrTyr 342
Db 782 GTGACCCGACGAGCATGATGATGCTGTGTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 841
Qy 343 ValLeuGlnLeuThrGlnLeuSerIleSerArgProThrLeuThrPheValTyrLeuTyr 362
Db 842 GTGTGTCAGCTGACCCACATCTCATTCAGCCGCGCCAGCCCTCAAGTTGTCTACTTATAC 901
Qy 363 AsnAlaAlaIleSerLeuGlyTyrAlaAsnSerCysLeuAsnProPheValTyrIleVal 382
Db 902 AACGGGCGCATCAGCTTGGCTATGCTATACAGCTGCTGGAACCCCTTGTGTATATGTG 961
Qy 383 LeuCysGlnThrPheArgIlyArgLeuValLeuSerValIlyProAlaIleGlnGlyGln 402

Db 962 CTCGTGAGACCTTTCGAAACGCTGATGTGTCTGACTGAAGCCTGCAGCCAGGGGCAG 1021
QY 403 leuATgAlaValSerAspAlaGlnThrAlaAspGlnLugrghrGlnSerlysglyThr 422
Db 1022 CTCGCACGGTCAGACGCTCAGACAGCTGATGAGGAGACAGAAAGCAAGGCACC 1081
RESULT 5
US-09-864-761-9721
; Sequence 9721, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David K.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecolica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 9721
; LENGTH: 1478
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO 286090.10
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.2
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.1
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 5.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.7
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.3
US-09-864-761-9721

Alignment Scores:
Pred. No.: 1,87e-151 Length: 1478
Score: 1708.00 Matches: 346
Percent Similarity: 82.22% Conservative: 10
Best Local Similarity: 79.91% Mismatches: 17
Query Match: 77.22% Indels: 60
DB: 10 Gaps: 6
US-09-885-478-2 (1-422) x US-09-864-761-9721 (1-1478)
QY 32 AspCysGlyAlaCysAlaProGlyGlnGlyAlaArgArgTrpArgLeuProGln----- 49
Db 152 AACTGTGCTCTCTGCTCTC-----TGTGCTCTGCGAGGAGCGGC 190
QY 50 -----ProAlaTrpValGlnGlySer-----SerAlaArgLeuTrpGlnAla 64
Db 191 ATGTTGTGCTCTTCCAGACAGATGCTCAGGGCACTCTGTAGATTCACACAGAAACT 250
QY 65 ThrGlyThrGlyTrpMetAspLeuGlnAlaSerLeuLeuProThrGlyProAsnAspSer 84
Db 251 CATGAGAGAGGAGAAAGGAC-----AAGATTACG 280
QY 85 AsnTrpSerAspGlyProAspAsn----- 92
Db 281 AAC---ACTGAGGAGAGGAGAAATGCTGGAGAGATTCACATGCAACGCTGGCTGCTG 337
QY 92 ----- 92
Db 338 GAGGCTGACATGCCAGCAGATGTCAGTTCTCAGACAAAGCCATGCAACAGCCAA 397
QY 93 -----LeuTrpSerAlaGlySerProProArgTrpGlnGlySerTrpTrpLeuAsn 109
Db 398 CGCTTGCTCTCTGCTCTCCAGATGCTCCTCTGCGACGAGGAGCATCTCTCATCATCACC 457
QY 110 IleIleMetProSerValPheGlyThrIleCysLeuLeuGlyIleIleGlyAsnSerThr 129
Db 458 ATCATCATGCTCTGCTGCTGCTGCGACCATCTGCTCTGCGCATCTGCGGAATCTCCAGC 517
QY 130 ValIlePheAlaValAlaLysSerLysSerLysLeuHisTrpGlyAsnAsnValProAspIle 149
Db 518 GTCATCTTGGGGTGGTGGAGAAAGTCCAGCTGAGGAGCAACAGTCCCGCCGACATC 577
QY 150 PheIleIleAsnLeuSerValValAspLeuLeuPheLeuLeuGlyMetProPheMetIle 169
Db 578 TTCATCATCAACCTCTCGTAGATCTCTCTCTCTGCGCATGCGCTTCATGATGC 637
QY 170 HisGlnLeuMetGlyAsnGlyValTrpHisPheGlyGlnTrpMetGlySerThrLeuIleTrp 189
Db 638 CACCAAGCTCATGGCAATGGGGTGTGGCACTTGGGGAGACATGTGCACCCCTCATCAGC 697
QY 190 AlaMetAspAlaAsnSerGlnPheThrSerThrTrpIleLeuThrAlaMetAlaIleAsp 209
Db 698 GCATGATGATGCCAATAGTACAGTTCCAGCAGCAGCACTCTGACCGCATGGCCATGTGAC 757
QY 210 ArgTrpLeuAlaThrValHisProIleSerSerThrLysPheArgLysProSerValAla 229
Db 758 CGTACCTGGCGCCTGCTCCACCCCATCTCTTCCACGAGATTCGGAGAGCCCTCTGTGGGC 817
QY 230 ThrLeuValIleCysLeuLeuTrpAlaLeuSerPheIleSerIleThrProValTrpLeu 249
Db 818 ACCCGTGTGATCTGCTCTGTGGGCTCTCTCTCTATCAGCATCAACCCCTGTGTGGCG 877
QY 250 TyrAlaIleGlyLeuIleProPheProGlyGlyAlaValAlaGlySerLysIleArgLeuProAsn 269
Db 878 TATGCCAAGCATCAACCCCTCTCCAGAGGAGTCAAGTGGGCTGCGCATGCGCTGCGCAAC 937
QY 270 ProAspTrpAspLeuTrpTrpPheThrLeuTrpGlnPhePheLeuAlaPheAlaLeuPro 289
Db 938 CCAGACATGACCTCTACTGTGTTACCCCTGACAGATTTCTCTGGCCCTTGGCCGCT 997
QY 290 PheValValIleThrAlaAlaIleValAlaGlyIleLeuGlnArgMetThrSerSerValAla 309

?	PRIOR FILLING DATE:	2000-06-30
?	PRIOR APPLICATION NUMBER:	US 09/774,203
?	PRIOR FILLING DATE:	2001-01-29
?	NUMBER OF SEQ ID NOS:	49117
?	SOFTWARE:	Annomax Sequence Listing Engine vers. 1.1
?	SEQ ID NO	21946
?	LENGTH:	720
?	TYPE:	DNA
?	ORGANISM:	Homo sapiens
?	FEATURE:	
?	OTHER INFORMATION:	MAP TO 286090.10
?	OTHER INFORMATION:	EXPRESSED IN BT474, SIGNAL = 0.67
?	OTHER INFORMATION:	EXPRESSED IN FETAL LIVER, SIGNAL = 1
?	OTHER INFORMATION:	EXPRESSED IN LUNG, SIGNAL = 0.78
?	OTHER INFORMATION:	EXPRESSED IN HELA, SIGNAL = 0.74
?	OTHER INFORMATION:	EXPRESSED IN ADULT LIVER, SIGNAL = 1.3
?	OTHER INFORMATION:	EXPRESSED IN BRAIN, SIGNAL = 1.2
?	OTHER INFORMATION:	EXPRESSED IN PLACENTA, SIGNAL = 0.72
?	OTHER INFORMATION:	EXPRESSED IN HEART, SIGNAL = 3.2
?	OTHER INFORMATION:	EXPRESSED IN BONE MARROW, SIGNAL = 3.1
?	OTHER INFORMATION:	SWISSPROT HIT: Q99705, EVALU0.0.0e+00
?	OTHER INFORMATION:	NT HIT: g11418166, EVALU0.0.0e+00
?	OTHER INFORMATION:	EST_HUMAN HIT: BE701073.1, EVALU0.0.0e+00
?	US-09-664-761-21946	
Alignment Scores:		
Pred. No.:	2.1e-106	Length: 720
Score:	1224.00	Matches: 239
Percent Similarity:	100.00%	Conservative: 0
Best local Similarity:	100.00%	Mismatches: 0
Query Match:	55.33%	Indels: 0
DB:	10	Gaps: 0
US-09-885-478-2 (1-422) x US-09-864-761-21946 (1-720)		
OY	184 MetCysThrIleuIleThrAlaMetAspAlaAsnSerGlnPheThrSerThyTyrIleLeu	203
Db	1 ATGGGCAACCTCATCTACGGCCATGGATGGCCATATGTCAGTCCACGACCTACATCTCG	60
OY	204 ThrAlaMetAlaIleAspArgTyrIleuAlaThrValHisProIleSerSerThrIysPhe	223
Db	61 ACCGCCATGGCCATTCAGCCGCTACTGGCCACCTGTCACCCCATCTCTTCCAGAAAGTTC	120
OY	224 ArgIysProSerValAlaThrIleuValIleCysLeuLeuTrpAlaLeuSerPheIleSer	243
Db	121 CGGAGAGCCCTCTGTGGCCACCTGGGTGATCTGCTCTGTGGGCCCTCTCCCTCATCTAGC	180
OY	244 IleThrProValTrpLeuTyrAlaArgIleuIleProPheProGlyValAlaValGlyCys	263
Db	181 ATACCCCGCTGTGGCTGTATGCCAGACTATCCCTCCACGAGAGTGCAGTGGGCTGC	240
OY	264 GlyIleArgLeuProAsnProAspThrAspLeuTyrTrpPheThrIleuTyrGlnPhePhe	283
Db	241 GGCATAGGCTGGCCACACCCAGACACTGACTCTACTGGTTCACCTGTACCAAGTTTTC	300
OY	284 LeuAlaPheAlaLeuProPheValValIleThrAlaAlaTyrAlaArgIleLeuGlnArg	303
Db	301 CTGGCCTTTGGCCCTGCTTTGTGTATCATCAGCCGCACTGAGTGGAGTCTCTGACGGC	360
OY	304 MetThrSerSerValAlaProAlaSerGlnArgSerIleArgIleuArgThrIysArgVal	322
Db	361 ATGACGCTCTCATGGCCCCCGCTCCACGAGCAGCATCCGGGTGGGACAAAGGGGTG	420
OY	324 ThrArgThrAlaIleAlaIleCysLeuValPhePheValCysTrpAlaProTyrTyrVal	343
Db	421 ACCGCGACAGCCATGCGCATCTGTCTGTCTTTGTGTGGCGGACCACTACTATGTG	480
OY	344 LeuGlnIleuThrGlnLeuSerIleSerArgProThrIleuThrPheValTyrIleuTyrAsn	365
Db	481 CTAGAGCTGACCCAGTTGGTCATCAGCGCCGACCTCATCTTTGTCTACTTATACAT	540
OY	364 AlaAlaIleSerLeuGlyTyrAlaAsnSerCysLeuAsnProPheValTyrIleValLeu	383

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DB 541 GCGGCCATCAGCTTGGCTATGCCAACAGCTGCTCAACCCCTTGTGTACATCGTCTC 600
QY 384 CysglturpPhearglyValleuValleuSerVallylProAlaInglyInleu 403
DB 601 TGTGAGAGCTTCGCAAAACGCTTGCTCTGCTGTAAGCTCGAGGCCCGGAGGACCTT 660
QY 404 ArgAlaValSerAsnAlaGlnThrAlaAspGluIuArgThrGlySerlyThr 422
DB 661 CCGCTGTGACAGCAAGCTGACGAGGCTGAGAGAGAGAGCAAGCAAGGACGACC 717

RESULT 7
US-09-895-686-25
; Sequence 25, Application US/09895686
; Patent No. US2002010655A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN GPCR PROTEINS
; FILE REFERENCE: PC-0044 CIP
; CURRENT APPLICATION NUMBER: US/09/895,686
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PERL Program
; SEQ ID NO 25
; LENGTH: 519
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc-feature
; OTHER INFORMATION: Incyte ID No. US2002010655A1 SAB00250R1
US-09-895-686-25

Alignment Scores:
Pred. No.: 7,84e-75 Length: 519
Score: 886.00 Matches: 171
Percent Similarity: 99.42% Conservative: 0
Best Local Similarity: 99.42% Mismatches: 1
Query Match: 40.05% Indels: 0
DB: 10 Gaps: 0

US-09-885-478-2 (1-422) x US-09-895-686-25 (1-519)
QY 179 HispHeGlyGlyThrMetCysThrLeuIleThrAlaMetAspAlaAsnSerGlnPheThr 198
DB 3 CACTTGGGAGACCATGTCACCTCTCATTCAGGCGCATGATGCAATAGTCATTCAC 62
QY 199 SerThrTyrlleuThrAlaMetAlaIleAspArgTyrLeuAlaThrValHisProIle 218
DB 63 AGCACTTACATCTGACCGCCATGGCCATTCACCGCTACCGTCACGTCACCCATC 122
QY 219 SerSerThrIlyPheArgIlyProSerValAlaThrIleuValIleCysLeuLeuTrpAla 238
DB 123 TCTTCACAGAAATCCGGAAGCCCTGTGGGCAACCTGGTGAATCTGCTCTGGGCC 182
QY 239 LeuSerPheIleSerIleThrProValItrPleuTyrlaIaArgLeuIleProPheProGly 258
DB 183 CTCTCTTATCAGATCAACCCCTGTGGCTGTATGGCAACATCATCCCTCCCAAGA 242
QY 259 GlYAlaValAlGlyCysGlyIleArgLeuProAsnProAspTrpAspLeuTyrrPheThr 278
DB 243 GGTGACGTGGGCTGGGCTATGAGCTGCGCAACCGACACTGACCTCTACTGTTAC 302
QY 279 LeuTyrlGlnPhePheLeuAlaPheAlaLeuProPheValIleThrAlaIaItyrVal 298
DB 303 CTGTACCACTTTTCTGCTTTCCTGCTTTCCTGCTTTAGTGTCATACACGCGCATACGTG 362
QY 299 ArgIleLeuGlnArgMetThrSerSerValAlaProAlaSerGlnAspSerIleArgIleu 318
DB 363 AGGATCTCTGACGAGCATGACGTCCTCAGTGGGCGCCGCTCCACGCGAGCATCCGGCTG 422
QY 319 ArgThrLysArgValIthrArgThrAlaIleAlaIleCysLeuValPhePheValCysTrp 338
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DB 423 GCGACAAAGAGGTGACCCGCGACAGCATCGCCATCTGTGTGCTGTCTGTGCTGG 482
QY 339 AlaProTyrrTyrlValleuGlnLeuThrGlnLeuSer 350
DB 483 GCACCTACTATGTGCTACAGCTGACCACTGATTC 518

RESULT 8
US-09-864-761-10236
; Sequence 10236, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE REFERENCE: Acomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 10236
; LENGTH: 459
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO 286090.10
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.67
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.72
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.78
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.74
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2
US-09-864-761-10236
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Alignment Scores:
Pred. No.: 1,16e-64 Length: 459
Score: 777.00 Matches: 152
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 35,13% Indels: 0
DB: 10 Gaps: 0

US-09-885-478-2 (1-422) x US-09-864-761-10236 (1-459)

QY 183 ThrMetysThrLeuIleThrAlaMetAspAlaAsnSerGlnPheThrSerThyTyrIle 202
Db 3 ACCATGGACACCTCATACAGGCGCATGATGCAATAGTCACTTCACCGACCTACATC 62
QY 203 LeuThrAlaMetAlaIleAspArgTyrLeuAlaThrValHisProIleSerSerThrLys 222
Db 63 CTGACCGCATGGCCATGTGACCGCTACCTGGCCACTGTCCACCCCATCTCTCCACGAG 122
QY 223 PheArgLysProSerValAlaThrLeuValIleCysLeuLeuThrPalaLeuSerPheIle 242
Db 123 TTCGGAGGCCCTGTGGCCACCCGTGGATGCTCTCTGGGCCCTCTCCATC 182
QY 243 SerIleThrProValTyrLeuTyrAlaArgLeuIleProPheProGlyAlaValGly 262
Db 183 AGCATACCCCTGTGGGGGTATGCCAGACATCCCTTCCAGGAGGTGAGTGGCC 242
QY 263 CysGlyIleArgLeuProAsnProAspThrAspLeuTyrThrPheThrLeuTyrGlnPhe 282
Db 243 TGGCGGACGCTGTGCCAACCAGACCTGCTACTGTGTACCTGTACCTGACGTTT 302
QY 283 PheLeuAlaPheAlaLeuProPheValIleThrAlaAlaTyrValArgIleLeuGln 302
Db 303 TTCTGGCCTTTGCCCTTGTGGTATCATACAGCGCATAGTAGGATCTCTGAG 362
QY 303 ArgMetThrSerSerValAlaProIleAspGlnArgSerIleArgLeuArgThrLysArg 322
Db 363 CGCATGACGTCCTACGTGGGCCCGGCTCCAGCGCACATCCGGCTCGGAGAAAGAG 422
QY 323 ValThrArgThrAlaIleAlaIleCysLeuValPhe 334
Db 423 GTGACCGGACAGCATCGGCATCTGTGTGCTTC 458

RESULT 9
US-09-990-940-1
; Sequence 1, Application US/09990940
; Publication No. US20030027252A1
; GENERAL INFORMATION:
; APPLICANT: Tian, Hui
; APPLICANT: Zhao, Jiaang
; APPLICANT: Chen, Jin-Long
; APPLICANT: Cutler, Gene
; APPLICANT: An, Songzhu
; APPLICANT: Dai, Kang
; APPLICANT: Gupta, Jamila S.
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: No. US20030027252A1el Receptors
; FILE REFERENCE: 018781-007410US
; CURRENT APPLICATION NUMBER: US/09/990,940
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/252,841
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 60/257,636
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 60/261,377
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/279,554
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/280,696
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1

LENGTH: 1023
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1023)
; OTHER INFORMATION: human G-protein coupled receptor (GPCR) TGR342,
; OTHER INFORMATION: melanin-concentrating hormone receptor 2 (MCHR2)
US-09-990-940-1

Alignment Scores:
Pred. No.: 2,89e-44 Length: 1023
Score: 565.50 Matches: 113
Percent Similarity: 55.95% Conservative: 61
Best Local Similarity: 36.33% Mismatches: 114
Query Match: 36,57% Indels: 23
DB: 9 Gaps: 4

US-09-885-478-2 (1-422) x US-09-990-940-1 (1-1023)

QY 110 IleIleMetProSerValPheGlyThrIleCysLeuLeuGlyIleIleGlyAsnSerThr 129
Db 103 GTCAATCCCTCCCTCCATGATGGGATTAATCTGTCAACAGGCGCTGTGGCAACATCCCTC 162
QY 130 ValIlePheAlaValIleLysSerLysLeuHisTyrCysAsnAsnValProAspIle 149
Db 163 ATGTATTCACTATTAATAGATCCAGGAA-----AAACAGTCCCTTACATC 210
QY 150 PheIleIleAsnLeuSerValAspLeuLeuPheLeuLeuGlyMetProPheMetIle 169
Db 211 TATATCTGCAACCTGGCTGTGGCTGATTTGGTCCACATAGTGGAAATGCTTTCTTATAT 270
QY 170 HisGlnLeuMetGlyAsnGlyValThrPheGlyGlnThrMetCysThrLeuIleThr 189
Db 271 CACCAATGCGCCGAGGAGGAGAGTGGGTGTGGGGGCGCTGTGCACATCATCA 330
QY 190 AlaMetAspAlaAsnSerGlnPheThrSerThrTyrIleLeuThrAlaMetAlaIleAsp 209
Db 331 TCCCTGATCTGTTTACCAATTTGGCTGATGAGCCATATGATACATGATAGTGTGAC 390
QY 210 ArgTyrLeuAlaThrValHisProIleSerSerThrLysPheArgLysProSerValAla 229
Db 391 AGTACTTGGCCCTGCTCCACCATTTTCGACTGACACGTTGGAGAACAGATACAGACC 450
QY 230 ThrLeuValIleCysLeuLeuThrPalaLeuSerPheIleSerIleThrProValIleLeu 249
Db 451 ATCCGATCAATTTGGGCTTTGGGACAGCTTCCTTATTCCTGGCATTCGCTGTGGGTC 510
QY 250 TyrAlaArgLeuIleProPheProGlyAlaValGlyCysGlyIleArgLeuProAsn 269
Db 511 TACTCGAAGGTCATCAATTAAGACGGTGTGAGAGTGTGCTTTGATTTGACATCC 570
QY 270 ProAspThrAspLeuTyrThrPheThrLeuTyrGlnPhePheLeuAlaPheAlaLeuPro 289
Db 571 CCGTAC--GATGTACTCTGTGTATACATTTATTTACAGATAACAATTTTTTTTCCCT 627
QY 290 PheValValIleThrAlaIleThrAlaTyrValArgIleLeu----- 301
Db 628 CTACCCCTGATTTGGTGTGCTGTATATTTATTTATTTATTTGCTATACCTTGGAGATGATCA 687
QY 302 -----GlnArgMetThrSerSerValAlaProIleAspGlnArgSerIleArg 317
Db 688 CAGATAAGATGATCCAGATGCTGCATCCAGTGACCA-----AAA 729
QY 318 LeuArgThrLysArgValThrArgThrAlaIleAlaIleCysLeuValPhePheValCys 337
Db 730 CAGAGAGTGATGAGGTGACAAAGATGGTGTGCTGTGCTGTATATCTGTAGT 789
QY 338 TrpAlaProTyrTyrValLeuGlnLeuThrGlnLeuSerIleSerArgProThrLeuThr 357
Db 790 GCTGCCCTTATCATGTGATACAACTGTGTGATACATGATGAGACAGCCACACTGGCC 849
QY 358 PheValTyrLeuTyrAsnAlaIleAlaIleSerLeuGlyTyrAlaAsnSerCysLeuAsnPro 377

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Db      850  TTCTATGTGGGTATTACCTTCCTCATCTGCTCAGTATGCGACGACGACATTAAACCT 909
Qy      378  pheValTyrIleValIleuGysGIuThrPheArgIysArgIeuValIleuSerValIysPro 397
Db      910  TTCTCTACATCCGCTGCTGAGTGGAAATTTCCAGAAACGCTGCTCCATAATCCAAAGAAAGA 969
Qy      398  AlaIaGInGInGInLeuArgAlaIaIaSerAsn 408
Db      970  GCGACTGAGAGGAATATCAACAATATGGGAAC 1002

RESULT 10
US-09-791-932-57
; Sequence 57, Application US/09791932
; Publication No. US20030003451A1
; GENERAL INFORMATION:
; APPLICANT: Vogel, Gabriel
; APPLICANT: Parodi, Luis A.
; APPLICANT: Hiedsch, Ronald R.
; APPLICANT: Lind, Peter
; APPLICANT: Kaytes, Paul S.
; APPLICANT: Ruff, Valerie
; APPLICANT: Huff, Rita M.
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: No. US20030003451A1el G Protein-Coupled Receptors Cross-Referen
; FILE REFERENCE: 00325.0S1
; CURRENT APPLICATION NUMBER: US/09/791,932
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/184,305
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,304
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,303
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,397
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,247
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/188,880
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/217,369
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/217,370
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/218,492
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: 60/186,810
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/188,064
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: 60/186,457
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: 60/213,861
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/194,344
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: 60/218,337
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 57
; LENGTH: 1965
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-791-932-57

Alignment Scores:
Pred. No.: 7.51e-44 Length: 1965
Score: 565.50 Matches: 113
Percent Similarity: 55.95% Conservative: 61
Best Local Similarity: 36.33% Mismatches: 114
Query Match: 25.57% Indels: 23
DB: 9 Gaps: 4
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US-09-885-478-2 (1-422) x US-09-791-932-57 (1-1965)
Qy      110  IleIleMetProSerValIlePheGlyThrIleCysLeuLeuGlyIleIleIleIysAsnSerThr 129
Db      160  GTCAATCCCTCCCTCCATGATGATGGATTTATGTTTCAACAGAGGGCTGGTGCAACATCCTC 219
Qy      130  ValIlePheAlaValIalIysSerIysLeuHisTrpCysAsnAsnAlaProAspIle 149
Db      220  ATTGATTTCCATATAATATAGATCCAGSAA-----AAACATCTCCCTGACATC 267
Qy      150  PheIleIleAsnLeuSerValIalAspLeuLeuPheLeuLeuGlyMetProPheMetIle 169
Db      268  TATATCTGCAACCTGGCTGGCTGATTTGTCACATAGTTGGATGGATGCTTTCTTAT 327
Qy      170  HisGInLeuMetGlyAsnGlyValTyrPheIlePheGlyGluThrMetCysThrLeuIleThr 189
Db      328  CACCAATGGGCGCCGAGGGGGAGAGCTGGCTTTGGGGGCGCTCTGCAACATCATCA 387
Qy      190  AlaMetAspAlaAsnSerGlnPheThrSerThrTyrIleLeuThrAlaMetAlaIleAsp 209
Db      388  TCCCTGATCTGTATACCAATTTGCTGTAGGCATCATGACTGTATGATGTGGAC 447
Qy      210  ArgTyrLeuAlaThrValHisProIleSerSerThrIysPheArgIysProSerValAla 229
Db      448  AGGTACTTGGCTCGTCACCACTTTCCACTGACACGTTGGAGAACAGTACAAAGACC 507
Qy      230  ThrLeuValIleCysLeuLeuTyrPalaIleuSerPheIleSerIleThrProValTyrLeu 249
Db      508  ATCGGATCAATTTGGCGCTTTGGGAGCTTCCTTATCTGTCATTTGCTGTGGTGC 567
Qy      250  TyrAlaIatGlyLeuIleProPheProGlyValAlaValGlyCysGlyIleArgLeuProAsn 269
Db      568  TACTCGAAGTCATCAATTTAAAGACGGTGGAGAGTTCCTTTGATTTGATGACATC 627
Qy      270  ProAspThrAspLeuTyrTrpPheThrLeuTyrGlnPhePheLeuAlaPheAlaLeuPro 289
Db      628  CCTGAC---GATGTACTCTGTATACACTTTATTTGACGATACCACTTTTTCCT 684
Qy      290  PheValValIleThrAlaAlaIleTyrValArgIleLeu----- 301
Db      685  CTACCCCTGATTTGGTGTCTATATTTTAAATTAAGTATGCTATGAGATGTATCA 744
Qy      302  -----GlnArgMetThrSerSerValAlaProAlaSerGlnArgSerIleArg 317
Db      745  CAGATTAAGATGCAATGCTGCAATCCAGCTATCA-----AAA 786
Qy      318  LeuArgThrIysArgValIleThrArgThrAlaIleAlaIleCysLeuValPhePheValCys 337
Db      787  CAGAGATGATGACAGCTTGACAAAGATGGTGTGCTGTGTACTTTATTCCTGACT 846
Qy      338  TrpAlaProTyrTyrValLeuGlnLeuThrGlnLeuSerIleSerArgProThrLeuThr 357
Db      847  GCTGCCCTTATCATGATGATGATACACTGTGATACATAGTACAGACGCCACAGGGCC 906
Qy      358  PheValTyrLeuTyrAsnAlaAlaIleSerLeuGlyTyrAlaAsnSerCysLeuAsnPro 377
Db      907  TTCTATGTGGGTATTACCTCTCCATCTGCTCAGCATGCTCAGCAGCAGCATTAACCT 966
Qy      378  pheValTyrIleValIleuGysGIuThrPheArgIysArgIeuValIleuSerValIysPro 397
Db      967  TTCTCTACATCCGCTGCTGAGTGGAAATTTCCAGAAACGCTGCTCCATAATCCAAAGAAAGA 1026
Qy      398  AlaIaGInGInGInLeuArgAlaIaIaSerAsn 408
Db      1027  GCGACTGAGAGGAATATCAACAATATGGGAAC 1059

RESULT 11
US-09-895-686-22
; Sequence 22, Application US/09895686
; Patent No. US2002010655A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
```

```
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN PCR PROTEINS
; FILE REFERENCE: PC-0044 CIP
; CURRENT APPLICATION NUMBER: US/09/895,686
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PERL Program
; SEQ ID NO 22
; LENGTH: 336
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID NO. US20020106655A1 1459432X12
US-09-895-686-22

Alignment Scores:
Pred. No.: 9,436-44 Length: 336
Score: 552.50 Matches: 106
Percent Similarity: 94.83% Conservative: 4
Best Local Similarity: 91.38% Mismatches: 1
Query Match: 24.98% Indels: 5
DB: 10 Gaps: 1

US-09-885-478-2 (1-422) x US-09-895-686-22 (1-336).
QY 65 ThGcGlyTTrpMetAspLeuGlAlaSerLeuLeuProThrGlyProAsnAlaSer 84
Db 2 TCCTGGACATCGA-----ACCTCGCTGCTGCCACCTGGTCCCAACGCCAGC 46
QY 85 AsnThrSerAspGlyProAsnLeuThrSerAlaGlySerProProAlaGlySer 104
Db 47 AACACCTCGATGAGCCGCCGATACCTCACTCGGAGAGATACCTCTCCAGCGGAGC 106
QY 105 TlSerTylTlAsnTlTlMetProSerValPheGlyThrTlCysLeuLeuGlyTl 124
Db 107 ATCTCTACATCGACATCATCATGCTTCGGTTCGGCACCATCTCCCTCGGGCATC 166
QY 125 TlGcYAsnSerThrValTlPheAlaValTlYsYSerTlYsLeuHlSTpCysAsn 144
Db 167 ATGGGAACTCCACGGCTCATCTTCGGGGTGTGAAGAAGTCCAAAGCTGCACTGGTGCAAC 226
QY 145 AsnValProAspTlPheTlTlLeuAsnLeuSerValTlAlaAspLeuLeuPheLeuGly 164
Db 227 AACGTCCCGACATCTTCATCATCAACCTTCGGTAGAGATCTCTTCCTCGGGGC 286
QY 165 MetProPheMetTlTlHlSglLeuMetSlyAsnGlyValTTrpHlSphE 180
Db 287 ATGCCCTTGTATTCACCAAGCTCATGGGCAATGGGGTGTGGCACTTT 334

RESULT 12
US-09-864-761-9017
; Sequence 9017, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeonica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
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; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 9017
; LENGTH: 575
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO Z66090.10
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 6.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.5
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.9
US-09-864-761-9017

Alignment Scores:
Pred. No.: 3,856-42 Length: 575
Score: 539.00 Matches: 100
Percent Similarity: 95.33% Conservative: 2
Best Local Similarity: 93.46% Mismatches: 1
Query Match: 24.37% Indels: 4
DB: 10 Gaps: 1

US-09-885-478-2 (1-422) x US-09-864-761-9017 (1-575)
QY 1 MetSerValGlyAlaMetYsYsGlyValGlyAlaValGlyLeuGlyGlySer 20
Db 156 ATGTCACTGGGACCATGAAGAAGGAGTGGGAGGACGATGGGCTTGGAGGGGACG 215
QY 21 GtYcSglAlaThrGluGluAspProLeuProAspCysGlyAlaCysAlaProGlyGln 40
Db 216 GCGTGCACAGCTCAGGAGGAGACCCCTCCCACTCGGGGGCTTGGCGTCCGGGACAA 275
QY 41 GtGlyTArGArGTrPArGLeuProGlnProAlaTPrValGluGlySerSerAlaArgLeu 60
Db 276 GGTGGAGGGGGGAGGGCTGCGGACGCTGGTGGTGGAGGGAGGCTCAGCTGGGTGG 335
QY 61 TrpGluGlnAlaThrGlyThrGlyTTrpMetAspLeuGlAlaSerLeuLeuProThrGly 80
Db 336 TGGGAGGAGGCGACGCGCACTGGCTGGATGACCTGGAAGCCTGCTGCTCCCACTGCT 395
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QY      81  ProximalSerThrSerArglyProAspAsnLeuThrSerAla----- 96
Db      396  CCCAACCCGACACACCTCTGTATGGCCCGATACCTTCATTCGGACGGTGAATTGACT 455
QY      97  GlySerProArgThrGly 103
Db      456  GGGAGCCCTCCCTCCTCTGGG 476

RESULT 13
US-09-895-686-57
; Sequence 57, Application US/09895686
; Patent No. US20020106655A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN GPCR PROTEINS
; FILE REFERENCE: PC-0044 CIP
; CURRENT APPLICATION NUMBER: US/09/895,686
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PERL Program
; SEQ ID NO 57
; LENGTH: 304
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. US20020106655A1 70189983H1
US-09-895-686-57

Alignment Scores:
Pred. No.: 7,46e-41      Length: 304
Score: 521.00           Matches: 99
Percent Similarity: 100.00%      Conservative: 2
Best Local Similarity: 98.02%      Mismatches: 0
Query Match: 23.55%      Indels: 0
DB: 10                  Gaps: 0

US-09-885-478-2 (1-422) x US-09-895-686-57 (1-304)
QY      216  HistHoleSerThrIlePheArglyProSerValAlaThrLeuValIleCysLeu 235
Db      2  CACCCATCTCTCCACCAAGTTCGGAAGCCCTCCATGCGCACCCGTGATCTGCGCTC 61
QY      236  LeuThrAlaLeuSerPheIleSerIleThrProValThrLeuThrAlaArgLeuIlePro 255
Db      62  CTGGGCGCTCTCTCATCATCATACACCCCTGTGTGGCTCTACGGCCAGGCTCATTTCCC 121
QY      256  PheProGlyGlyAlaValGlyCysGlyIleArgLeuProAspProAspThrAspLeuTyr 275
Db      122  TTCCCAAGGGGTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCTGT 181
QY      276  TrpPheThrLeuTyrGlnPhePheLeuAlaPheAlaLeuProPheValIleThrAla 295
Db      182  TGGTTCACTGTACACGGTTTTCCTGGCCCTTCCCTTCCCTTGGTGTCAATTACCCGCC 241
QY      296  AlaTyrValArgIleLeuGlnArgMetThrSerSerValAlaProAlaSerIleArgSer 315
Db      242  GCATACCTGAATACTACAGCCATGACGTCTTCGGTGGCTCCAGCCTCCCAACGCCAGC 301
QY      316  Ile 316
Db      302  ATC 304

RESULT 14
US-09-967-768A-296
; Sequence 296, Application US/09967768A
; Patent No. US20020150877A1
; GENERAL INFORMATION:
; APPLICANT: Augustus, Meena
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
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; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-72
; CURRENT APPLICATION NUMBER: US/09/967,768A
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/60/236,109
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,034
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,111
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 325
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 296
; LENGTH: 1427
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-967-768A-296

Alignment Scores:
Pred. No.: 1.11e-39      Length: 1427
Score: 519.00           Matches: 115
Percent Similarity: 50.40%      Conservative: 74
Best Local Similarity: 30.67%      Mismatches: 124
Query Match: 23.46%      Indels: 62
DB: 10                  Gaps: 11

US-09-885-478-2 (1-422) x US-09-967-768A-296 (1-1427)
QY      48  ProGlnProAla-----"TrpValGluGlySerSerAlaArgLeu----- 60
Db      21  CTTGGGCGCCGCGCGCGCGCTCTGTGGCGCAGCGCTACCTCCGCGCGCTACGCTGCCT 80
QY      61  -----"TrpGluGlnAla 64
Db      81  GCGCGCGACCCCTGTGTCATGACGCCCTCTGACGCTGCCCGCGCGCGCGCGCGCGAGG 140
QY      65  ThrGlyThrGlyThrPheMetAspLeuGlnAlaSerLeuLeuProThrGlyProAsnAlaSer 84
Db      141  CTTGGGCGCGCTGTG-----CCCTCGCGAGCC 167
QY      85  AsnThrSerAspGlyProAspAsnLeuThrSerAlaGlySerProProAlaThrGlySer 104
Db      168  AATGCCAGTACGCGCTCCGCGGAGCGGAGGAGGCGGCGGCGCGCGCGCGCGCGCGCGG 227
QY      105  IleSerThrIleAsnIleLeuMetProSerValPheGlyThrIleCysLeuLeuGlyIle 124
Db      228  GCGGCGGCGCATG---GTGCTATCCAGTCATCTACGCGCTGTGTGCTGTGTGTGTGTG 284
QY      125  IleGlyAsnSerThrValIlePheAlaValAlaValIleCysSerIleCysLeuIleAsn 144
Db      285  GTGGGCAACGCCCTGTGCTATCTTCTGTGATCTTGTGCTACGCCAAGATGAAGAGCGCTAC 344
QY      145  AsnValProAspIlePheIleIleAsnLeuSerValAlaAspLeuLeuPheLeuGly 164
Db      345  AAC-----ATCTACCTGCTCAACCTGGCCGCGCGCGCGCGCTTCTCATGTGTAGC 395
QY      165  MetProPheMetIle-----"HisGlnLeuMetGlyAsnGlyValTyr 178
Db      396  GTGCCCTTGTGTGGCCCTCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 444
QY      179  HisPheGlyGluThrMetCysThrLeuIleThrAlaLeuMetAspAlaAsnSerGlnPheThr 198
Db      435  CCCTTGGCTCGCTGTGCGCGCGCGGCTGTGCTGACGCTGACGCGCGCGCGCGCGCGCG 494
QY      199  SerThrThrIleLeuThrAlaMetAlaIleAspArgTyrIleAlaThrValHisProIle 218
Db      495  AGCGTCTCTGTGTCACCGTGTCTAGCGTGGACCGGTACGCGCGCGCGCGCGCGCGCG 554
QY      219  SerSerThrIlePheArgIleProSerValAlaThrLeuValIleCysLeuLeuThrAla 238
Db      555  CCGCGCGCGACCTTACCGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 614
QY      239  LeuSerPheIleSerIleThrProValThrLeuThrAlaArgLeuIleProPheProGly 258
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RESULT 15
US-09-864-761-26601
Sequence 26601, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecmca-x-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIORITY APPLICATION NUMBER: US 60/180,312
PRIORITY FILING DATE: 2000-02-04
PRIORITY APPLICATION NUMBER: US 60/207,456
PRIORITY FILING DATE: 2000-05-26
PRIORITY APPLICATION NUMBER: US 09/632,366
PRIORITY FILING DATE: 2000-08-03
PRIORITY APPLICATION NUMBER: GB 24263.6
PRIORITY FILING DATE: 2000-10-04
PRIORITY APPLICATION NUMBER: US 60/236,359
PRIORITY FILING DATE: 2000-09-27
PRIORITY APPLICATION NUMBER: PCT/US01/00666
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00667
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00664
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00669
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00665
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00668
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00663
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00662
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00661
PRIORITY FILING DATE: 2001-01-30

Alignment Scores:	
Pred. No.:	9.32e-39
Score:	498.00
Percent Similarity:	100.00%
Best Local Similarity:	98.90%
Query Match:	22.51%
DB:	10
Length:	274
Matches:	90
Conservative:	1
Mismatches:	0
Indels:	0
Gaps:	0

Qy	6	MeLLySLySLyG1VAlG1VAlrAlG1VAlG1VLeuG1VSLyG1VSeSLyCYSLySLnAlaThr	25
Db	1	ATGAAACAAGGAGATGGGAGGSCAGATTGGCTTGGAGGCGGCAAGCGGCTGCAGGCTACG	60
Qy	26	GLGLSLASPLeuProSLProSLCYSLyAlAcSLySLaProG1VGLnG1VSLyVArqRrtrp	45
Db	61	GAGGAGAACCCCCCTTCCCACTGGCGGGGCTTGGGCTCGGGAACAAGTGGCAAGCGCTGG	120
Qy	46	ArGLnProGLnProSLaTrPrVAlGLyGLySeSLaSLArGLnPrGSLnGLnAlaThr	65
Db	121	AGGCTGCCCGACCTGGCTGGTGGTGAAGGAGACCTCACTCGTTGGTGGAGCAGGCGACC	180
Qy	66	GLyThrGLyTYPrMetASPLeuGLnAlaSerLeuLeuProThyGLyProSLnAlaSerAsn	85
Db	181	GGACATGGCTGGATGGACCTGGAAAGCCCTGGCTGGCCCACTGGTCCCAACGCCAGCAAC	240
Qy	86	ThrSerASPLyProASPLnLeuThrSerAla	96
Db	241	ACCTTCGATGGCCCGGATTAACCTCACTTGGCA	273

Search completed: February 19, 2003, 14:50:23
Job time : 85 secs

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

(without alignments)
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3329.028 Million cell updates/sec

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Total number of hits satisfying chosen parameters: 32308132

Listing first 45 summaries

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EST: *

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8:  em_hc:*
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11: gb_hc:*
12: gb_est1:*
13: gb_est4:*
14: gb_est5:*
15: em_estun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hun:*
19: em_gss_inv:*
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21: em_gss_vtc:*
22: em_gss_fun:*
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24: em_gss_mas:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

Query No.	Score	Query	Match Length	DB	ID	Description
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2	1578.5	71.4	958	13	BI754621	BI754621 603025173
3	1369	63.1	872	13	BI757659	BI757659 603027991
4	1395	61.9	797	13	BI818742	BI818742 603037572
5	1368.5	61.9	921	13	BG913631	BG913631 602811509
6	1097.5	49.6	834	12	BF342364	BF342364 602011355
7	1086	49.1	845	12	BF966511	BF966511 602286863
8	1057	47.8	869	12	BG519797	BG519797 602578956
9	1014	45.8	865	13	BI818110	BI818110 603032324
10	880.5	39.8	859	10	BE312747	BE312747 601150756
11	691	31.2	600	10	BE132542	BE132542 601150023
12	591	26.7	387	14	F072728	F072728 HSC1CF101 n
13	539	22.4	387	14	BE647763	BE647763 UT-M-BH1-
14	491.5	22.2	1086	12	BF313837	BF313837 601902234
15	484	20.3	497	12	BF600078	BF600078 26455 MA
16	449	20.3	313	12	BE701073	BE701073 CMO -NN013
17	400	18.2	440	12	BF600064	BF600064 264640 MA
18	402	18.1	264	10	BB586291	BB586291 BB586291
19	391.5	17.7	794	17	CNS01WC1	AI170218 Teltraadon
20	370	16.7	642	10	BE252309	BE252309 601114162
21	362.5	16.4	937	17	CNS03GS6	AI243385 Teltraadon
22	357.5	16.2	720	13	BI753905	BI753905 603022907
23	355	16.0	904	12	BG329444	BG329444 602429002
24	349	15.8	901	17	CNS01SK5	AI155326 Teltraadon
25	347	15.7	1029	17	CNS03S02	AI258812 Teltraadon
26	330	14.9	960	13	BI914562	BI914562 603179505
27	327	14.8	1141	17	CNS04CF7	BI914562 603179505
28	325.5	14.7	2702	11	AK004730	AI284380 Teltraadon
29	320.5	14.5	995	17	CNS04ROE	AK004730 Mus muscu
30	316	14.3	1053	17	CNS04C2T	AI304223 Teltraadon
31	311.5	14.1	1377	11	AK010895	AI283934 Teltraadon
32	304.5	13.8	916	17	CNS02EZK	AK010895 Mus muscu
33	300	13.6	1026	17	CNS04NI4	AI194406 Teltraadon
34	297	13.4	2402	11	AK018203	AI296151 Teltraadon
35	295	13.3	755	13	BI772443	AK018203 Mus muscu
36	295	13.3	1051	13	BM545259	BI772443 603058608
37	294	13.3	2020	11	BM013202	BM545259 AGENCOURT
38	292	13.2	741	13	BI224313	BM013202 Homo sapi
39	291	13.2	656	9	AI119185	BI224313 602940621
40	291	13.2	3336	11	AK018543	AI119185 DKFP761IN
41	290.5	13.1	848	13	BI908815	AK018543 Mus muscu
42	289.5	13.1	3005	11	AK019478	BI908815 603066279
43	287.5	13.0	1082	13	BM922776	AK019478 Mus muscu
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						A0091121 A0091121

ALIGNMENTS

RESULT	1
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LOCUS	
DEFINITION	BM805549 1114 bp mRNA linear EST 05-MAR-2007
ACCESSION	AF620007.6498483 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:572908
VERSION	5 , mRNA sequence.
KEYWORDS	BM805549 BM805549.1 GI:19122372
SOURCE	EST.
ORGANISM	human.
REFERENCE	Homo sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
	1 (bases 1 to 1114)
	NIH-MGC http://mgc.nci.nih.gov/ .
	National Institutes of Health, Mammalian Gene Collection (MGC)

US-09-885-478-2 (1-422) x B1757659 (1-872)

QY 65 ThrGlyThrGlyTyrPmetAspLeuGluAlaSerLeuLeuProThrGlyProAsnAlaSer 84
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Db 3 ACCGGCAGCTGGTGGATGAGACCTGGAGACCTGGCTGGCCACAGTGGCCAAATGGCCAGC 62

QY 85 AsnThrSerAspGlyProAspAsnLeuThrSerAlaGlySerProPArgThrGlySer 104
|||||
Db 63 AACACCTCTGATGGCCCGCATACCTCACTTGGAGAGATCACTCCCTCCGACGGGGAGC 122

QY 105 IleSerTyrIleAsnIleIleMetProSerValPheGlyThrIleCysLeuLeuGlyIle 124
|||||
Db 123 ACTCTCATCATCAATCATCATGCTTCGGTGGTGGCAGCATCTGCTCTGGGAGCATTC 182

QY 125 IleGly-AanserThrValIlePheAlaValValIleCysSerIleuHisTrpCysAs 144
|||||
Db 183 ATCGCGCAACTCCAGCTCATCTTGGGCTGGTGAAGAAGTCCAAAGCTGCACATGGTGCNA 242

QY 144 nasnValProAspIlePheIleIleAsnLeuSerValValAspLeuLeuPheLeuLeuG 164
|||||
Db 243 CAACGCTCCCGACATCTTATCATCACTCTCGGTAGATGATCTCTTTCTCTCGG 302

QY 164 YmetProPmetIleHisGlnLeuMetGlyAsnGlyValITrPHisPheGlyGluThme 184
|||||
Db 303 CATGCCCTTCATGATCCACACACTCATGGGCAATGGGGTGGTGGCACTTGGGGAGACCAT 362

QY 184 TcysThrIleuIleThrAlaMetAspAlaAsnSerGlnPheThrSerThrTyrIleLeuTh 204
|||||
Db 363 GTCCACCTCATACGCGCATGGATGCAATAGTCAGTTCACAGACCATCATCTGAC 422

QY 204 rAlaMetAlaIleAspArgTyrLeuAlaThrValHisProIleSerSerThrLysPheAr 224
|||||
Db 423 CGCGCATGGCATGACCGGTACCTGGCCACTGGCCACCCCATCTCTCCACGAAAGTTCGG 482

QY 224 GlySProSerValAlaThrLeuValIleCysLeuLeuThrPalalaSerPheIleSerI 244
|||||
Db 483 GAAGCCCTCTGTGGCCACCTGTGTGATCTGCCCTGTGGGCCCTCTCTCATCAGCAT 542

QY 244 eThrProValITrPLeuTyrAlaArgLeuLeuPheProPArgIleGlyAlaValAGI-CysG 264
|||||
Db 543 CACCCCTGTGGCTGTATGGCCAGACTCATCCCTTCCAGAGGTGGCGTGGCTGGCG 602

QY 264 YIleArgLeuProAsnProAspThrAspLeuTyrTrpPheThrLeuThrGlnPhePhe 284
|||||
Db 603 CATACGCGTCCCAACCCAGACACATGACCTCTACTGTTACCCCTGACAGTTTTCCT 662

QY 284 uAlaPheAlaLeuProPheValValIleThrAlaIaIaTyrValArgIleLeuGlnArg 304
|||||
Db 663 GGGCTTGGCCCTCTTGTGTGTGATCACAGCCGATACGTGAGATCTCTCAGCGCAT 722

QY 304 tThrSerSerValAlaProAlaSerGlnArgSerIleArgLeuArgThrLysArgValTh 324
|||||
Db 723 GAGCTCTCATGTGGCCCCCTCCAGGGCCAGCATCCGGCTCGGAC-AAAGAGGTGAC 781

QY 324 rArgThrAlaIleAlaIleCysLeuValPhePheValCysTrpAlaProTyrTyrValle 344
|||||
Db 782 CCGTACAGC-ATCGCATCTGTCTGTCTTGTGTGTGGTGGCACC-TACTATGTGT 839

QY 344 uGlnLeuThrGlnLeuSerIleSerArg 353
|||||
Db 840 ACAGTTGACCCAGTTGTTCATCAGGGCG 867

RESULT 4
B1818742 797 bp mRNA linear EST 04-OCT-2001
LOCUS B1818742
DEFINITION 603037572F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5178856 5',
mRNA sequence.
ACCESSION B1818742
VERSION B1818742.1 GI:15930292
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
1 (Bases 1 to 797)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM1445 row: 0 column: 17
High quality sequence stop: 774.
Location/Qualifiers
1..797
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5178856"
/clone.lib="NIH_MGC_115"
/lab.host="DH10B"
/note="Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age 69. Library is male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research genetics tracking code 021. Note: this is a NIH_MGC Library."

BASE COUNT 144 a 262 c 228 g 163 t
ORIGIN

Alignment Scores:
Pred. No.: 1,15e-130 Length: 797
Score: 1369.00 Matches: 262
Percent Similarity: 98.87% Conservative: 1
Best Local Similarity: 98.50% Mismatches: 2
Query Match: 61.89% Indels: 2
Gaps: 0

US-09-885-478-2 (1-422) x B1818742 (1-797)

QY 7 LysIleGlyValAGIArgAlaValAGIleuGlyGlySerGlyCysGlnAlaThrGlu 26
|||||
Db 3 AAGAAGGAGATGGGAGGAGCGATTGGCTTGAGGCGGACAGCGCTCAGAGTACGAG 62

QY 27 GluAspProLeuProAspCysGlyAlaCysAlaProGlyGlnGlyGlyArgArgTyrArg 46
|||||
Db 63 GAAGACCCCTTCCGACTGGCGGGGCTTGGCTCGGAGCAAGGTGGCAGCGCTGAGG 122

QY 47 LeuProGlnProAlaITrValGluGlySerSerAlaArgLeuTrpGluAlaThrGly 66
|||||
Db 123 CTGCCGACCGCTGGCTGGGTGAGGAGGAGCTCACCTCGTGTGGAGGAGGACAGCGGC 182

QY 67 ThrGlyTrpMetAspLeuGluAlaSerLeuLeuProThrGlyProAsnAlaSerAsnThr 86
|||||
Db 183 ACTGCTGGATGGACCTGGAAGCCCTGCTGCCACATGTGTCCCATGCGAGCAACACC 242

QY 87 SerAspGlyProAspAsnLeuThrSerAlaGlySerProPArgThrGlySerIleSer 106
|||||
Db 243 TCTGATGGCCCGATTAACCTCATCTCGGACAGATACCTCTCCAGGGAGCATCTCC 302

QY 107 TyrIleAsnIleIleMetProSerValPheGlyThrIleCysLeuLeuGlyIleIleGly 126
|||||
Db 303 TACATCAACATCATCATCTCTTGGTGGTGGCAGCATCTCTCTGGGATATCGGG 362

QY 127 AsnSerThrValIlePheAlaValValIleCysSerIleuHisTrpCysAsnAsnVal 146
|||||
Db 363 AACCTCAGGTCATCTTGGCGGTGCTGAAGAAGTCCAAAGTGCACATGGTGCACACAGCTC 422

QY 147 Proaspiellepellelleleasleuservalvalaspleuleupheleuleuglymetpro 166
 |||
 Db 423 CCGGACATCTTCATCATCAACCTCTCGGTAGATGTCCTCTTCCGGGACATGCC 482
 QY 167 PheMetIleHISGlnLeuMetClyAsnGlyValTrpHisPheGlyGlnTrpMetCysThr 186
 |||
 Db 483 TTCAGATCCCAACAGCTCATGGGCAATGGGGTGTGGGCACTTGGGGAGACATGTGCACC 542
 QY 187 LeuIleThrAlaMetAspAlaAsnSerGlnPheThrSerThrTrpIleLeuThrAlaMet 206
 |||
 Db 543 CTCACACAGGGCCATGGATGGCAATAAGTCACATCCAGCACATCACATCCAGCCGACATG 602
 QY 207 AlaIleAspArgTrpLeuAlaThrValHisProIleSerSerThrLysPheArgLysPro 226
 |||
 Db 603 GCCATTCACCGGTACTGTGGCAGTGTCCACCCCATCTCTCCAGAAAGTCCGGAAGCC 662
 QY 227 SerValAlaThrLeuValIleCysLeuLeuTrpAlaLeuSerPheIleSerIleThrPro 246
 |||
 Db 663 TCTGTGGCCACCTGTGTATCTGCTCTGTGGCCCTCTCCATCATCACATCAC 721
 QY 247 ValTrpLeuTrpAlaArgLeuIleProPheProGlyAlaValAlaGlyCysGlyIleArg 266
 |||
 Db 722 GTGTGGGTATGGCAGACTCATCCCTCCAGAGGTGATGTGGGTGGGCAATAG 781
 QY 266 GLeuProAsnProAsp 271
 |||
 Db 782 CCTGCCAAGCCAGAG 797
 RESULT 5
 BG913631 921 bp mRNA linear EST 05-JUN-2001
 LOCUS BG913631
 DEFINITION 602811509P1 NCL_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4943498
 5' mRNA sequence.
 ACCESSION BG913631
 VERSION BG913631.1 GI:14294107
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 921)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaaps-remail.nih.gov
 Tissue Procurement: David N. Louis, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L1AM10887 row: a column: 03
 High quality sequence stop: 731.
 Location/Qualifiers
 source 1..921
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4943498"
 /clone_lib="NCL_CGAP_Brn67"
 /tissue_type="anaplastic oligodendroglioma with 1p/19q
 loss"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: brain; Vector: pCMV-SPOK6; Site_1: NCI;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 2.3 kb. Constructed by Life
 Technologies. Note: this is a NCL_CGAP Library."
 BASE COUNT 174 a 309 c 247 g 191 t
 ORIGIN

Pred. No.: 1 59e-130 Length: 921
 Score: 1368.50 Matches: 273
 Percent Similarity: 90.76% Conservative: 2
 Best Local Similarity: 90.10% Mismatches: 26
 Query Match: 61.87% Indels: 4
 DB: 13 Gaps: 1
 US-09-885-478-2 (1-422) x BG913631 (1-921)
 QY 19 GlySerGlyCysGlnAlaThrGlnGluAspProLeuProAspCysGlyAlaPro 38
 |||
 Db 1 GGCACGGGCTCCAGGCTACGAGAGAACCCCTTCCACATCGCGGCTTGGCTCGC 60
 QY 39 GlnGlnGlyGlyArgArgTrpArgLeuProGlnProAlaTrpValGlnGlySerAla 58
 |||
 Db 61 GGACAGGTGGCAGGCGCTGGAGGCTCCGACGCTCCGTGGGTGGAGGGAGCTAGCT 120
 QY 59 ArgLeuTrpGlnGlnAlaThrGlyThrGlyTrpMetAspLeuGlnAlaSerLeuLeuPro 78
 |||
 Db 121 CGGTGTGGAGAGGAGGAGCCGACCTGCTGATGACCTGGAACTCCGCTGCTGCC 180
 QY 79 ThrGlyProAsnAlaSerAsnThrSerAspGlyProAspAsnLeuThrSerAlaGlySer 98
 |||
 Db 181 ACTGTCCCATGGCAGACACACCTCTGATGGCCCATTAACCTCACTTCCGAGATCA 240
 QY 99 ProProArgThrGlySerIleSerTrpIleAsnIleIleMetProSerValPheGlyThr 118
 |||
 Db 241 CCTCTCCACAGGGGAGACATCTCTACATCAACATCATCATCTGCTGGGTCCGAC 300
 QY 119 IleCysLeuLeuGlyIleIleGlyAsnSerThrValIlePheAlaValIlySlySer 138
 |||
 Db 301 ATCTGCCCTCCGCGGACATCATCGGGAACCTCCAGCTCATCTCCGCGGTGGAAGATCC 360
 QY 139 LysLeuHisTrpCysAsnAsnValProAspIlePheIleIleAsnLeuSerValIAsp 158
 |||
 Db 361 AAGCTGCACTGTGCAACACAGCTCCCGACATCTTCATCAACCTCCGAGTAGAT 420
 QY 159 LeuLeuPheLeuLeuGlyMetProPheMetIleHisGlnLeuMetGlyAsnGlyValIAsp 178
 |||
 Db 421 CTCCTCTTCTCCCTGGGATGCCCTTATGATCATCCAGCTCATCTGGGCAATGGGCTGG 480
 QY 179 HisPheGlyGlnTrpMetCysThrLeuIleThrAlaMetAspAlaAsnSerGlnPheThr 198
 |||
 Db 481 CACTTGGGAGACCATATGTCACCCCTCATCAGCATGCAATAGTCAGTTCCACC 540
 QY 199 SerTrpTrpIleLeuThrAlaMetAlaIleAspArgTrpLeuAlaThrValHisProIle 218
 |||
 Db 541 AGCACTACATCTCGACCGCCATGGCCATGACCGCTACCTGACCTGTCACCCCATC 600
 QY 219 SerSerThrLysPheArgLysProSerValAlaThrLeuValIleCysLeuLeuTrpAla 238
 |||
 Db 601 TCTTCCAGAGAGTTCGGGAAGCCCTGTGGCCACCTG-GTAGATCGCTCGGTGGGC- 658
 QY 229 LeuSerPheIleSerIleThrProValTrpLeuTrpValArgLeuIleProPheProGly 258
 |||
 Db 659 CTCCTCTTCATCAGAGATCACCCCTGTGTGCTGTATGCCAGACTCATCCCTTCCAGGA 718
 QY 259 GlnAlaValGlyCysGlyIleArgLeuProAsnProAspThrAspLeuTrpPheThr 278
 |||
 Db 719 GGTGAGAGGGGCTCGGCAATCGCTGACAAACAACTGAAGCTCTACTAGTTGTCACC 778
 QY 279 -LeuTrpTrpIlePhePheLeuAlaPheAlaLeuProPheValIleThrAlaAlaTrpVal 298
 |||
 Db 779 ACTGTACAGATATTCCTGGGCTTTGACCCGCTTTTGCCATTCACGCGCAATCC 838
 QY 298 1--ArgIleLeuGlnArgMetThrSerSerValAlaProAlaSerGlnArgSerIleArg 317
 |||
 Db 839 GTGAGATCCTCTGAGGAGCATAGCGTCCCAAGATGGCCGCTTCCACACGAGATCAG 898
 QY 317 GLeuArg 319
 |||
 Db 899 CCGGAGA 905

Alignment Scores:

RESULT 6	834 bp	MRNA	linear	EST 22-NOV-2000
BF342364				
LOCUS	602013155F1	NCI_CGAP_Brn64	Homo sapiens	cDNA clone IMAGE:4148940
DEFINITION	5', mRNA sequence.			
ACCESSION	BF342364			
VERSION	BF342364.1	GI:11289365		
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo.			
AUTHORS	1 (bases 1 to 834)			
TITLE	NIH-MGC http://mgs.nci.nih.gov/ .			
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)			
COMMENT	unpublished (1999)			
	Contact: Robert Strausberg, Ph.D.			
	Email: cgapbs-remail.nih.gov			
	Tissue Procurement: David N. Louis, M.D.			
	cDNA Library Preparation: Life Technologies, Inc.			
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)			
	DNA sequencing by: Incyte Genomics, Inc.			
	Clone distribution: MGC clone distribution information can be			
	found through the I.M.A.G.E. Consortium/LLNL at:			
	http://image.llnl.gov			
	Plate: L14M9409 row: n column: 13			
	High quality sequence start: 20			
	High quality sequence stop: 730.			
FEATURES	Location/Qualifiers			
SOURCE	1..834			
	/organism="Homo sapiens"			
	/db_xref="taxon:9606"			
	/clone_image="4148940"			
	/clone_lib="NCI_CGAP_Brn64"			
	/tissue_type="glioblastoma with EGFR amplification"			
	/lab_host="DH10B (T1 phage-resistant)"			
	/note="Organ: Brain; Vector: pCMV-Sport6; Site:1: NotI;			
	Site:2: SalI; Cloned unidirectionally. Primer: Oligo dt.			
	Average insert size 1.57 kb. Constructed by Life			
	Technologies. Note: this is a NCI_CGAP Library."			
BASE COUNT	142 a	271 c	232 g	188 t
ORIGIN	I others			
Alignment Scores:				
Pred. No.:	1..27e-102	Length:	834	
Score:	1097.50	Matches:	235	
Percent Similarity:	88.24%	Conservative:	5	
Best local Similarity:	46.40%	Mismatches:	28	
Query Match:	49.62%	Indels:	10	
DB:	12	Gaps:	2	
US-09-885-478-2 (1-422) x BF342364 (1-834)				
QY	20	SerGlyCysGlnAlaThrGluGlnAspProLeuProAspCysGlyAlaCysAlaProGly		
DB	21	AGCGCGTCGACG-CCATCGGAGAGATGACCCCTTCCTCCGACTCGGGGCTTCCTCCGGGA		
QY	40	GlnGlyGlyArgArgArgArgLeuProGlnProAlaArgPValGlnGlySerSerAlaArg		
DB	80	CAAGGTGCGAGCGCGCTGGAGCTCGGCGAGCCTGCGTGGGAGGGAGACTGACTCGG		
QY	60	LeuTrpGlnGlnAlaThrGlyThrGlyTrpMetAspLeuGlnAlaSerLeuLeuProThr		
DB	140	TTTGGGAGGAGCGAGC-GGCACTGGCTGGATGGACCTGGAGAGCCTGCGTGGCCACT		
QY	80	GlyProAsnAlaSer-AsnThrSerAspGlyProAspAsnLeuThrSerAlaGlySerP		
DB	199	GATCCCAAGCGCAGCAAGACCTCGATGGCCCGATTAACCTGACTTGGCAGAGTACC		
QY	99	oProlArgThyGlySerIleSerTyrIleAsnIleIleMetProSerValAlaGlyThrIle		
DB	259	TCTTCGACGCGGGAGGATCTCTACATCAACATCAATCAATGCTTCGGTGGTGGACCAAT		

FEATURES	SOURCE
119 ecysleuengly1leileglyasnsertthvallephelavalayalysyserry	139
319 ctgcctccttgccgatcatggsaactccacggtatctctccggctctgaagaagtcaca	378
139 sleuHsttrpcyasnasnvalproaspllephelilelansleuservalyalsple	159
379 gcttcacatgctgacacacgctcccgacatcttcatcatcaccctctcggtagtagatct	438
159 ulenpheluleuenglymetprophemerlehisglleuemetglyasnlyvaltrph	179
439 cctcttctccttgccgatcgcttattatgaccacagctctatgggcataigggstgggca	498
179 sphegllylurthmetcysrthleuilethralametasplalaansersinphethrse	199
499 ctttgsggaagacacatgtgcacccctatcacggcactgatgaccAAATGATGATGATGATG	558
199 rthtthylleuethralametalaleasparglyleualathralhisprollese	219
559 caccatcatcttcttmacgc-atggccattgacgc-taccctggccactgtccaccccatctc	616
219 rsetrthlysphearglysproservalalathrleuvalleecysleuenutrpalaie	239
617 ttccacacaaattccgsaagaccctctgtggc-acccctgatatcttgcctctgaggccct	675
239 userphelieserlethrprovaltrpleuhytrpaleuileprophroglycl	259
676 ctccctcatcagatcatcaccctctgtggt-gtttgacagatcatccttccacagagag	733
259 yalavalglycysglyleargleuproasnbroasphrthraspleuhytrpethrle	279
734 ttgcagtgagggttgagg--catagccctggcaccacacagatgactcttggttcccttg	790
279 utyrglnphepheleualalphealaleuprope	290
791 tccaggtttcttgacctt-----tgccctgccttgagg	818
RESULT 7	
BF966511	845 bp mRNA linear EST 23-JAN-2001
LOCUS	60226863bf1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:4375863 5',
DEFINITION	mRNA sequence.
ACCESSION	BF966511
VERSION	BF966511.1 GI:12333726
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE	1 (bases 1 to 845)
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/-
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgabbs-remail.nih.gov Tissue Procurement: Miklos Palkovits, M.D., Ph.D. cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shitaki Toshiyuki and Piero Carninci (RIKEN) cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM10041 row: m column: 16 High quality sequence stop: 661. Location/Qualifiers 1..845

Db 455 CCCATGCCAGACACCTCTGATGGCCCCGATACCTCTACTTGGCAGATCACCCT 514

OY 101 ATgThGlySerlleSerYrilleasnllelmetProserValPheglYThrIleCys 120
|||||
Db 515 CGCAGGGGGGAGCTCTCCATCAATCAATCAATCGCTTGGGTTCGACCATCTGC 574
|||||

OY 121 leuLeuGlyllelleglYasnSerThValIlePheAlaValIlylYsSerlyleu 140
|||||

Db 575 CTCCTGGGATCATCGGGAATCCACGGGTCACTTCGGGGTCGGAGAAAGTCCAACTG 634

OY 141 -HsTrpCysAsnAsnValProAspIlePheIleIleasnLeuSerValValAspLeu 160
:::|||||
Db 635 CAACCTGTGCACACACGCTCCGACATCTTCATCACTCAACCTCGGTAGATCTCTCT 694

OY 160 upheleuLeuGlyMetProPheMetIleHisGlnleuMetGlyasnGlyValTrpHisph 180
|||||

Db 695 CTTTCCTCTGGGATCGCTTCATGATCCACAGCTCATGGGCAATGGGGTGGACATA 734

OY 180 eglYgluThrMetCysThrleuIleThrAlaMetAspAlaasnSerGlnPheThr 200
:::|||||

Db 755 TGGGAGACCATGTGCACCCCTCATCATCAGCGGATGGATTGCATGATTCACACAGAC 814

OY 200 rTyrlleuThrAla 205
|||||

Db 815 CTACATCTCTACCGCA 830

RESULT 9
BI818110 685 bp mRNA linear EST 04-OCT-2001
LOCUS 603032324F1 NIH_MGC_115 Homo sapiens cdna clone IMAGE:5173852 5',
DEFINITION mRNA sequence.
ACCESSION BI818110
VERSION BI818110.1 GI:15928318
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 685)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM11432 row: 0 column: 05
High quality sequence stop: 679.
Location/Qualifiers
1. 685
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5173852"
/clone_lib="NIH_MGC_115"
/lab_host="DH10B"
/note="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."

BASE COUNT 132 a 205 c 212 g 136 t

ORIGIN

Alignment Scores:
Pred. NO.: 3 94e-94 Length: 685
Score: 1014.00 Matches: 188
Percent Similarity: 99.47% Conservative: 0
Best Local Similarity: 99.47% Mismatches: 1
Query Match: 45.84% Indels: 0
DB: 13 Gaps: 0

US-09-885-478-2 (1-422) x BI818110 (1-685)

OY 1 MetSerValAlaValAlaMetlylYsGlyValGlyArgAlaValGlyleuGlyleuSer 20
|||||

Db 115 ATGTCACTGGAGACCATGAAAGAGAGTGGAGGAGGAGAGTGGGCTTGGAGGGAGC 174

OY 21 GLYCSGlnAlaThrGluGluAspProleuProAspCysGlyAlaCysAlaProGlyGln 40
|||||

Db 175 GGCCTGCAGGCTACGGAGAGAACCCCTTCCGACTCGGGGCTTGGCTCCGGACAA 234

OY 41 GlyGlyArgArgTrpArgleuProGlnProAlaTrpValGlyGlySerSerAlaArgleu 60
|||||

Db 235 GGTGGCAGGCGCTGGAGGCTGCCGACGCTGGTGGTGGAGGAGGAGTCTCGGCTTG 294

OY 61 TrpGluGlnAlaThrGlyThrGlyTrpMetAspLeuGluAlaSerleuProThrGly 80
|||||

Db 295 TGGGAGCAGGCGCAGCGCATGCTGCTGATGACCTGGAAGCTCGCTGCTGCCACTGGT 354

OY 81 ProAsnAlaSerAsnThrSerAspGlyProAspAsnleuThrSerAlaGlySerProPro 100
|||||

Db 355 CCCAATGCGACAAACACCTCTGTGAGCCCGATTAACCTCACTTCGGGAGATCACTCTCT 414

OY 101 ArgThrGlySerlleSerYrilleasnllelmetProserValPheglYThrIleCys 120
|||||

Db 415 CGCAGCGGAGGATCTCTCATCAATCAATCAATGCTCGGTGTGGCACCATCTGC 474

OY 121 leuLeuGlyllelleglYasnSerThValIlePheAlaValIlylYsSerlyleu 140
|||||

Db 475 CTCTGGGCAATCGGGAATCTCACGGTCACTTCGGGTGGTGAAGAACTCCAACTG 534

OY 141 HsTrpCysAsnAsnValProAspIlePheIleIleasnLeuSerValValAspLeu 160
|||||

Db 535 CACTGTGTGCACAAACGTCGCCGACATCTTCATCAATCAATCAATCTCGGTAGATCTCTCT 594

OY 161 PheleuLeuGlyMetProPheMetIleHisGlnleuMetGlyasnGlyValTrpHisPhe 180
|||||

Db 595 TTTCTCTGGGCAATCGCTTCATGATCCACGACTCATAGGCAATGGGCTGTGGCACTTA 654

OY 181 GlyGluThrMetCysThrleuIleThr 189
|||||

Db 655 GGGAGACCATGTGCACCTCATCAGC 681

RESULT 10
BE312747 859 bp mRNA linear EST 26-OCT-2000
LOCUS 601150756F1 NIH_MGC_19 Homo sapiens cdna clone IMAGE:3503484 5',
DEFINITION mRNA sequence.
ACCESSION BE312747
VERSION BE312747.1 GI:9131846
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 859)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
 plate: LLCM176 row: p column: 13
 High quality sequence start: 3
 High quality sequence stop: 733.

FEATURES

source

Location/Qualifiers

1..859
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3503484"
 /clone_lib="NIH_MGC_19"
 /tissue_type="neuroblastoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: brain; Vector: pOMB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

BASE COUNT 151 a 267 c 254 g 186 t 1 others
 ORIGIN

Alignment Scores:

Pred. No.: 3.24e-80 Length: 859
 Score: 880.50 Matches: 183
 Percent Similarity: 91.58% Conservative: 2
 Best Local Similarity: 90.59% Mismatches: 10
 Query Match: 39.81% Indels: 7
 DB: 10 Gaps: 1

US-09-885-478-2 (1-422) x BE312747 (1-859)

QY 1 MetcervAlaGlyAlaMetLysGlyGlyValGlyArgAlaValGlyLeuGlyGlySer 20
 DB 194 ATGTCAGTGGAGCAGCATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGC 253
 QY 21 GLYCysGlnAlaThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 40
 DB 254 GCGTGCAGGCGTACGAGGAGAGACCCCTTCCGACTCGGGGCTGGCGTCCGGGACAA 313
 QY 41 GLYGlyArgArgTrpArgLeuProGlnProAlaTrpValGlyLysSerSerAlaArgLeu 60
 DB 314 GGTGGCAGGCGCTGGAGGCTGCCGACCTGCGTGGGTGGAGGAGGAGGAGGAGGAGG 373
 QY 61 TrpGlnGlnAlaThrGlyThrGlyTrpMetAspLeuGlnAlaSerLeuLeuProThr-61 80
 DB 374 TGGAGCAGGCGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 433
 QY 80 Y-ProAsnAlaSerAsnThrSerAspGlyProAspAsnLeuThrSerAlaGlySerProp 100
 DB 434 TTCCCATGCCAGCACACCTCTGATGGCCCGGATACCTCATTCCGGCAGAGATCACCTC 493
 QY 100 roArgThrGlySerLleSerTyrLleAsnLleLleMetProSerValPheGlyThrLleC 120
 DB 494 CTCGACGCGGAGATCTCTACATCAACATCATCTCCCTTGCTGCGCACCACTCT 553
 QY 120 ySLeuLeuGlyLleLleGlyAsnSerThrValLlePheAlaValAlaLysLysSerLysL 140
 DB 554 GCGTTCGGGCGATCATCGGAACTCCACGCTCATCTTCGGGTGTAAGAAAGTCCAAAGC 613
 QY 140 euHISTrpCysAsnAsnValProAspLle-PheLleLleAsnLeuSerVal-ValAspLe 159
 DB 614 TGCACGTGGTCACACAGTCCCGACATCTTTCATCATCAACCTTCGGTAGTACCT 673
 QY 159 u--LeuPheLeuLeuGly-MetProPheMetLleHisGlnLeuMetGlyAsnGlyValT 178
 DB 674 CCCTTCCTTCTCCTGTGGCTATCCNCTCATATGATCCACAGCTCATGGGCGGTGT 733
 QY 178 rPHIS-PheGlyGlnThrMetCysThrLeuLleThrAlaMetAspAlaAsnSer 195
 DB 734 GGCACATTGGGAGACCTGTGTGCCCTCATACACGAGCATGGGTGGCCCTGTGC 787

RESULT 11

BE312542

LOCUS

BE312542

600 bp

mRNA

linear EST 26-OCT-2000

DEFINITION

mRNA sequence.

60115002331 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503020 5',

ACCESSION

BE312542

GI:9131383

VERSION

BE312542

EST.

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS

1 (bases 1 to 600)

TITLE

NIH-MGC http://mgc.nci.nih.gov/

JOURNAL

National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT

Unpublished (1999)

CONTACT

Contact: Robert Strausberg, Ph.D.

Tissue Procurement: ATCC

Email: c9apbs-remail.nih.gov

CDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: LLCM175 row: m column: 05

High quality sequence start: 7

High quality sequence stop: 574.

Location/Qualifiers

1..600

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:3503020"

/clone_lib="NIH_MGC_19"

/tissue_type="neuroblastoma"

/lab_host="DH10B (phage-resistant)"

/note="Organ: brain; Vector: pOMB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

BASE COUNT 113 a 174 c 197 g 116 t
 ORIGIN

Alignment Scores:

Pred. No.: 6.92e-61 Length: 600
 Score: 691.00 Matches: 132
 Percent Similarity: 99.25% Conservative: 0
 Best Local Similarity: 99.25% Mismatches: 1
 Query Match: 31.24% Indels: 1
 DB: 10 Gaps: 0

US-09-885-478-2 (1-422) x BE312542 (1-600)

QY 1 MetcervAlaGlyAlaMetLysGlyGlyValGlyArgAlaValGlyLeuGlyGlySer 20
 DB 195 ATGTCAGTGGAGCAGCATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGC 254
 QY 21 GLYCysGlnAlaThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 40
 DB 255 GCGTGCAGGCGTACGAGGAGAGACCCCTTCCGACTCGGGGCTGGCGTCCGGGACAA 314
 QY 41 GLYGlyArgArgTrpArgLeuProGlnProAlaTrpValGlyLysSerSerAlaArgLeu 60
 DB 315 GGTGGCAGGCGCTGGAGGCTGCCGACCTCGGGTGGAGGAGGAGGAGGAGGAGGAGG 374
 QY 61 TrpGlnGlnAlaThrGlyThrGlyTrpMetAspLeuGlnAlaSerLeuLeuProThrGly 80
 DB 375 TGGAGCAGGCGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 434
 QY 81 ProAsnAlaSerAsnThrSerAspGlyProAspAsnLeuThrSerAlaGlySerProp 100

Db 435 CCCAATGCCAGACACCTGATGCCCGATCACTTGCAGAGATCACTCT 494
 Qy 101 ArgThcylserIleSerThrIleasnIleIleMetProSerValPheGlyThrIleCys 120
 Db 495 CGCAGGGAGAGATCTCCACATCAACATCATGCTTCGGTGGTGGCACCACATCTGC 554
 Qy 121 LeuLeuGlyIleIleGlyAsnSerThrValIlePheAla 133
 Db 555 CTCCTGGCATCATCGGAACTCCCG-GTCATCTTCCCG 592
 RESULT 12
 LOCUS F07228 345 bp mRNA linear EST 20-FEB-1995
 DEFINITION HSC12P101 normalized infant brain cDNA Homo sapiens cDNA clone
 c-1zf10, mRNA sequence.
 ACCESSION F07228
 VERSION F07228.1 GI:672877
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 345)
 AUTHORS Aufray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C., Devignes
 /M.D., Duprat,S., Houllatte,R., Juneau,M.N., Lamy,B., Lorenzo,F.,
 SebstianI,Kabackchis,C. and Tessier,A.
 TITLE IMAGE: molecular integration of the analysis of the human genome
 and its expression
 JOURNAL C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
 MEDLINE 95277534
 COMMENT Contact: Genethon
 Genexpress-Genethon
 Genethon Centre de recherche sur le Genome Humain
 1,rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
 Tel: 33169472800
 Fax: 33160778698
 Email: genexpress@genethon.fr
 Single read.
 Genexpress library Idt: C; Genexpress_sequence_idt: y1c-1zf10
 Seq primer: (-21)M13 universal.
 FEATURES
 source Location/Qualifiers
 1..345
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 /db_xref="taxon:9606"
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 /clone_lib="normalized infant brain cDNA"
 /sex="Female"
 /tissue_type="total brain"
 /dev_stage="3 months old"
 /note="Organ: brain; Vector: lafmid BA; Site_1: HindIII;
 Site_2: NotI; sex:Female; dev_stage=3 months old;
 Isolate=muscular atrophy patient; tissue_type=total brain
 ; total mRNA was oligo-(dT) primed and directionally
 cloned 5' -> 3' into the HindIII -> NotI sites of the
 lafmid BA vector. Clone library from B.Souares, Psychiatry
 Dept. Columbia University, USA
 Bento Soares, P.N.A.S. in press" Normalization_method:
 BASE COUNT 67 a 118 c 80 t 1 others
 ORIGIN
 Alignment Scores:
 Pred. No.: 6,51e-51 Length: 345
 Score: 591.00 Matches: 114
 Percent Similarity: 99.13% Conservative: 0
 Best Local Similarity: 99.13% Mismatches: 1
 Query Match: 26.72% Indels: 0
 DB: 14 Gaps: 0
 US-09-885-478-2 (1-422) x F07228 (1-345)
 Qy 122 LeuGlyIleIleGlyAsnSerThrValIlePheAlaValIleGlySerIleuHis 141

Db 1 CTGGGATCATGGGAACTCCAGGTCATCTTCCGGTGTGAAGAATCCAACTGCAC 60
 Qy 142 TrpCysAsnAsnValProAspIlePheIleIleAsnLeuSerValValAspLeuIleuHe 161
 Db 61 TGGTGCAACAAGTCCCGCATGCTTCATCATCAACCTCTGGTACTAATCTCTCTTT 120
 Qy 162 LeuLeuGlyMetProPheMetIleHisGlnLeuMetCysAsnGlyValIleTrpHisPheGly 181
 Db 121 CTCCTGGGATGCCCTTCATCATGCACAGCTCATGGGCAATGGGCTGTGGCATTTGGG 180
 Qy 182 GluThrMetCysThrLeuIleThrAlaMetAspAlaAsnSerGlnPheThrSerThrTyr 201
 Db 181 GGACCATGTGCACCTTCATCATCGCCATGATGCCAATAATGATGATTCACACGACCTTAC 240
 Qy 202 IleLeuThrAlaMetAlaIleAspArgTyrLeuAlaThrValHisProIleSerThr 221
 Db 241 ATCTGTACCCGCGCATTCGATTCACGCTACTGGCAGCTGTCCACCCCATCTTTTCACG 300
 Qy 222 LysPheArgLysProSerValAlaThrLeuValIleCysLeuLeu 236
 Db 301 AAGTTCGGAAACCTCTGTGGCCACCTGTGATCTGCTCTCTG 345
 RESULT 13
 LOCUS BE647763 387 bp mRNA linear EST 06-SEP-2000
 DEFINITION UI-M-BH1-ant-c-04-0-UI-r1 NIH_BMAP_M.S2 Mus musculus cDNA clone
 UI-M-BH1-ant-c-04-0-UI 5', mRNA sequence.
 ACCESSION BE647763
 VERSION BE647763.1 GI:9973583
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 387)
 AUTHORS Bonaldi,M.F., Lennon,G. and Soares,M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene
 discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477
 COMMENT Contact: Chin, H
 National Institute of Mental Health
 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
 20892-9643, USA
 Tel: 301 443 1706
 Fax: 301 443 9890
 Email: mestr@mail.nih.gov
 CDNA library Preparation: M.B. Soares lab Clone distribution:
 Researchers may obtain BMAP CDNA clones from RESEARCH GENETICS. It
 should be noted that Bento Soares is generating a small number of
 additional specialized non-redundant arrays of BMAP cDNAs whose
 availability will be considered under appropriate and limited
 collaborative arrangements
 Seq primer: M13 Reverse.
 FEATURES
 source Location/Qualifiers
 1..387
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UI-M-BH1-ant-c-04-0-UI"
 /clone_lib="NIH_BMAP_M.S2"
 /dev_stage="27-32 days"
 /lab_host="DH10B (Life Technologies)"
 /note="Vector: pTZ19D-Pac (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; The
 NIH_BMAP_M.S2 library is a subtracted library derived from
 NIH_BMAP_M.S1, which in turn is a subtracted library
 derived from a mixture of normalized libraries from ten
 regions of the mouse brain (cerebellum, brain stems,
 olfactory bulbs, hypothalamus, cortex, amygdala, basal
 ganglia, pineal gland, striatum, hippocampus). The driver
 used for subtraction consisted of a pool of 5,000 clones

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 19, 2003, 11:05:52 ; Search time 283 Seconds

(without alignments)
3358.103 Million cell updates/sec

Title: us-09-885-478-2

Perfect score: 2212

Sequence: 1 MSYGAMKKGVGRAVGLGGG.....LRAVSNAGTADERTESKGN 422

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=x1h
-O=/cgn2_1/USPTO.spool/US09885478/rnat.13022003.105050.12757/app_query.fasta_1.583
-DB=N.Geneseq.101002 -OPMT=fastlap -SUFRTX=ring -MINMATCH=0.1 -LOOPEXT=0
-LOOPEXT=0 -UNITS=bits -STRAT=1 -END=1 -MATRIX=blonsum62 -TRANS=human40.cd1
-LIFT=45 -DOCALLIGN=200 -THR_SCORE=pcpt -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USBR=US09885478 -CGCN_1.1.187 -trunat.13022003.105050.12757 -ICPU=3
-NO_XLPHY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: N.Geneseq.101002.*

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23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2212	100.0	1269	21	AAA63240	Human MCH1 recepto
2	2212	100.0	1269	22	ABK14548	Human cDNA encodin
3	2207	99.8	1269	22	AAD13654	Human melanin conc
4	2207	99.8	1269	22	AAA91189	Human MCH-R3 codin
5	2207	99.8	1269	22	AAH47297	Human long form MC
6	2207	99.8	1275	21	AAAF2918	Human SLC-1 cDNA s
7	2207	99.8	1275	22	AAAF6232	Human melanin conc
8	2207	99.8	1275	22	AAAF6875	Human SLC-1 coding
9	2207	99.8	1275	24	ABK10854	DNA encoding human
10	2207	99.8	1275	24	ABA92411	Human SLC-1 encod1
11	2207	99.8	1275	24	AAI69442	Human SLC-1 cDNA.
12	2207	99.8	1283	21	AAAF2924	Human SLC-1 (L) cd
13	2207	99.8	1283	22	AAAF6235	Human melanin conc
14	2207	99.8	1283	22	AAAF6981	Human SLC-1 coding
15	2207	99.8	1283	24	ABAF92417	Human SLC-1 (L) nu
16	2207	99.8	1283	24	AAI69448	Human SLC-1 (L) nu
17	2197	99.3	1269	22	AAH47302	Human long form/am
18	2197	99.3	1269	22	AAH47311	Human long form/am
19	2184	98.7	1254	22	AAD13653	Human melanin conc
20	2184	98.7	1254	22	AAA91188	Human MCH-R2 codin
21	2164	97.8	1385	19	AAV28115	Human IICB splice
22	2164	97.8	1385	20	AAAF60230	Human IICB splice
23	2164	97.8	1385	22	AAD09345	Nucleotide sequenc
24	2085	94.3	2152	21	AAZ90522	Human IICBY cDNA.
25	2000	90.4	3488	21	AAA30875	Human GPCR protein
26	1971	89.1	2483	22	AAA91191	Human 11cby gene.
27	1968	89.0	2148	21	AAAF5886	Human MCH-R3 full
28	1880	85.0	2080	22	AAH47299	Murine 11cby recep
29	1824	82.5	1062	22	AAD13652	Human melanin conc
30	1824	82.5	1062	22	AAA91187	Human MCH-R1 codin
31	1824	82.5	1062	22	AAAF4298	Human short form M
32	1824	82.5	1062	22	ABK10702	Human melanin conc
33	1824	82.5	1074	21	AAAF72923	Human SLC-1 (S) cd
34	1824	82.5	1074	22	AAAF6234	Human melanin conc
35	1824	82.5	1074	22	AAAF6980	Human melanin conc
36	1824	82.5	1074	24	ABA92416	Human SLC-1 (S) nu
37	1824	82.5	1074	24	AAI69447	Human SLC-1 (S) nu
38	1824	82.5	2133	23	AB198036	TSNR-GS-alpha fusi
39	1819	82.2	1062	23	AB197927	Non-endogenous hum
40	1818	82.2	1062	23	AB197897	Non-endogenous hum
41	1818	82.2	1062	23	AB197921	Non-endogenous hum
42	1817	82.1	1062	22	AB197924	Non-endogenous hum
43	1814	82.0	1062	22	AAH47301	Human short form/m
44	1814	82.0	1062	23	AB197909	Non-endogenous hum
45	1814	82.0	1062	23	AB197915	Non-endogenous hum

ALIGNMENTS

RESULT 1
ID AAA63240 standard; DNA; 1269 BP.

AAA63240;

17-NOV-2000 (first entry)

Human MCH1 receptor coding sequence.

Human; MCH1 receptor; melanin concentrating hormone; neuroregulator;
G-protein coupled; PKX.HR-TL231; feeding; water balance;
energy metabolism; arousal; attention; memory; cognitive function;
psychiatric disorder; stress; sexual activity; hormone disorder;
hypertension; diabetes; cardiovascular; gastrointestinal;
electrolyte balance; respiratory; asthma; reproductive function;
immune; endocrine; musculoskeletal; Alzheimer's disease;
sensory modulation; transmission; motor coordination;

KW	Parkinson's disease; olfaction; urinary; depression; seizure; pain;
KW	schizophrenia; morphine tolerance; opiate addiction; migraine; ss.
XX	
OS	Homo sapiens.
XX	
PH	Key
FT	1..1269
FT	CDS
FT	Location/Qualifiers
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PN	WO200039279-A2.
XX	
PD	06-JUL-2000.
XX	
PF	30-DEC-1999; 99WO-US31169.
XX	
PR	31-DEC-1998; 98US-0224426.
XX	
PA	(SYNA-) SYNAPTIC PHARM CORP.
XX	
PI	Salon JA, Laz TM, Nagorny R, Wilson AE;
XX	
DR	WPI; 2000-548644/50.
XX	P-PSDB; AAB13436.
PT	Novel nucleic acid encoding human melanin concentrating hormone
PT	receptor useful for treating cardiovascular disorders, hypertension and
PT	diabetes, whose mutant form is activated by melanin concentrating
PT	hormone -
XX	
PS	Claim 26; Fig 1; 173pp; English.

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aa      Sequence 1269 BP; 234 A; 419 C; 347 G; 269 T; 0 other;
SQ
Alignment Scores:
Pred. No.:       7,19e-185          length:         1269
Score:           2212.00            matches:        422
Percent Similarity: 100.00%          Conservative:    0
Best Local Similarity: 100.00%        Mismatches:     0
Query Match:     100.00%             Indels:         0
DB:              21                  gaps:          0
US-09-885-478-2 (1-422) x AAA65240 (1-1269)
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Qy	1	Me	Se	Val	G	I	A	L	a	k	e	t	y	S	I	S	G	I	Y	a	L	G	I	a	L	a	V	a	L	G	I	L	e	u	G	I	G	I	S	e	r	20								
Db	1	A	T	G	C	A	G	T	G	G	A	G	C	A	T	G	A	A	G	A	G	A	G	C	A	G	C	A	G	C	A	G	C	A	G	C	A	G	C	A	60									
Qy	21	G	L	y	C	S	G	I	a	L	a	r	h	r	g	I	u	a	s	p	r	e	u	P	r	o	a	s	p	C	y	S	G	I	a	L	a	C	y	S	a	L	a	P	r	o	G	I	y	400

Db	61	GGCGCCAGGCGTACGGAGAGACCCCCCTTCCCGACTCGGGGGCTTGCGCTCCGGAGCA	120
Qy	41	GLYGLVARGATGTPAAGLEUPROGINPROIALATPVALGIUGLYSERSEALATVLEU	60
Db	121	GGTGAGAGGGCGCTGGAGGGCTGCCGACGCTGGTGGGTGGAGGGAGACTGACGTGGGTTG	180
Qy	61	TRPGUGINALATHRGTYTHRGTYTPMETASPLEUGLUALASERLEULEUPROTHGLY	80
Db	181	TGGGAGACGGCGACCGGCACCTGGCTGGATGACCTGGAAAGCCTGGCTGCTCCACTGGT	240
Qy	81	PROASNALASERANTHRSEALASPGLYPROASPAANLEUTHRSERIALGLYSERPROPRO	100
Db	241	CCCATGCGCAGCAACACCTCTGTATGGCCCCCGATACTCATCTCAGCAGATCACTCTCT	300
Qy	101	ARGTHRGYSERLIESERTYRILEANLIELLEMETPROSERVALPHEGLYTHRIECSY	120
Db	301	CGCACGGGGAGACATCTCTCATCAACAATCATCATGCGCTGGGTGGTGGACCATCTGC	360
Qy	121	LEULEUGLITLIEGLIYASNSERTVALIIPHEALAVAILYLSYSESYLEU	140
Db	361	CTTCGGGCATCATCGGGAACTCCAGGTCATCTTCGGCGTGTAANAAGTCCAACTG	420
Qy	141	HISTRPCYSASNAANVALPROASPIIPEHLEIELLEASNLEUSERVALIASPLEULEU	160
Db	421	CACGTGTCACAACACGTCGCCGACATCTCATCAATCAACCTCTCGGTGATGATCTCTC	480
Qy	161	PHEULEULEUGLYMETPROPIEMETLIEHISGLINLEMETGLYASGLYVALTPRHISPE	180
Db	481	TTTTCTCCGGGACATGCCCTTATGATGATCAACACCTCATGSGCATGGGGTGTGGCACTTT	540
Qy	181	GLYGLNTHRMETCYSTRHLEULIETHRIALAMETASPALAASNSEGLINPHETHRSETRH	200
Db	541	GGGGAGACCATGTGCACCTCATCAACGCGCATGATGACCAATAGCACTTCACCAAGACCC	600
Qy	201	TYRITLLEUTHRALAMETALIALIASPATGYTLEULATHVALHISPROIISERSE	220
Db	601	TYCATCTCGACCGGCATGGCATGTGACCGCTACCTG6GCACITGTCACCCCATCTCTCC	660
Qy	221	THRILVSPHEATGLVSPROSERVALIATHRIEVALIIECSYLEULEUTRPALEUSER	240
Db	661	ACGAAAGTTCCGGAAGCCCTGTGTGGCCACCTGGATGTGCTCTGTGG6GCGCTCTCC	720
Qy	241	PHETIESERTIETHPROVALTTPRLEUTYRALATRGLEULIIPROPHPROGLIYALA	260
Db	721	TTTCATCACACATCACCCCTGTGTGGCTGTATGCAAGCACTATCCCTCCACAGAGTCA	780
Qy	261	VALGIYCSGLIYLEATRGLEUPROASNPROASPTHRASPLEUTYTRPHETHRLEUTHYR	280
Db	781	GTGGGCTGGGGATAGAGCTGTGCCAACCCAGACACTGACTCTACGTGHTCACCTGTAC	840
Qy	281	GLINPHEPHELEUALIAPHEALALEUPROPHVEVALIIEETHRIALALATHVALARGILE	300
Db	841	CAGTTTTCCTGGGCTTGGCCCTTGGCTCTGTGTGTGATACAGCGCATAGCTGGATC	900
Qy	301	LEUGINATGMETHRSESERSEVALIAPROALASERGLIARGSERILEATRGLEUATGRTH	320
Db	901	CTGACAGCATGACGCTCTCTCAGTGTGGCCCCGCGCTCCAGAGGACGATCGGGTGGGACA	960
Qy	321	LYSARGVALTHRARGTHRALIIEALALIECSYLEUVALPHEPHEVALCYSTRPALAPRO	340
Db	961	AAGAGGATGACCCGACAGCATGCGCATGTGCTGTCTTTGTGTGGTGGGACCC	1020
Qy	341	TYRTYVALIENGLINLEUTHRGLEUSERLIESERARGPROTHRIEUTHPHEVALTYR	360
Db	1021	TACTATGTGCTACACTACCAAGTTGTCCATACGCGCCGACACCTTCACCTTTGTCTAC	1080
Qy	361	LEUTYASNALALALIESETRLEUCLITYRALAASNSERCYSLEUASNPROPHVEVALTYR	380
Db	1081	TTTATACAAATGGGGCATCAGCTGGGCTATGCCAACAGCTGACCTCAACCCCTTTGTGTAC	1140
Qy	381	ILIEVALLEUCYSGLINTHRPHEARGLYARGLEUVALLEUSERVALIYSPROALALAGIN	400
Db	1141	ATGCTGCTCTGTGAACGCTTCCGAAGCGTGTGTCTCTGTGTGGTGAAGCCTCAGCCAG	1200

Qy	401	GlycineLeuArgAlaValSerAsnAlaGlnThrAlaAspIleuLys	420
Db	1201	GGGAGCTTCGGCGCTGTCAGCAAGCTCAGAGGCTGACGAGAGAGAGACAGAAACGAAA	1260
Qy	421	GlyThr	422
Db	1261	GGCACC	1266
RESULT 2			
ABK14548			
ID	ABK14548	standard; cDNA; 1269 BP.	
AC	ABK14548;		
XX			
DT	08-MAY-2002	(first entry)	
XX			
DE	Human cDNA encoding melanin concentrating hormone receptor, MCH1.		
XX			
KW	Human; ss; gene; melanin concentrating hormone receptor; MCH1;		
KW	steroid hormone disorder; pituitary hormone disorder;		
KW	epinephrine release disorder; gastrointestinal disorder;		
KW	cardiovascular disorder; hypertension; diabetes; respiratory disorder;		
KW	asthma; reproductive function disorder; immune disorder;		
KW	musculoskeletal disorder; neuroendocrine disorder; cognitive disorder;		
KW	memory disorder; motor coordination disorder; obesity; eating disorder;		
KW	dopaminergic function disorder; pain; psychosis; opiate addiction;		
KW	affective disorder; migraine; transgenic.		
XX			
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	CDS	1..1269	
FT		/*tag= a	
FT		/product= "MCH1"	
XX			
PN	MO200202744-A2.		
XX			
PD	10-JAN-2002.		
XX			
PF	05-JUL-2001; 2001WO-0521350.		
XX			
PR	05-JUL-2000; 2000US-0610635.		
XX			
PA	(SYNA-) SYNAPTIC PHARM CORP.		
XX			
P1	Salon JA, Laz TM, Nagorny R, Wilson AE;		
XX			
DR	WPI: 2002-164532/21.		
XX	P-PSDB; AAU75853.		
XX			
PT	Purified human melanin concentrating hormone receptor protein and polynucleotides for screening modulator useful for treating memory		
PT	disorder, sensory modulation and transmission disorder, motor		
PT	coordination disorder -		
XX			
PS	Claim 2; Fig 1; 524pp; English.		
CC	The invention relates to a purified human melanin concentrating hormone		
CC	(MCH1) receptor protein and its encoding nucleic acid (or mutant		
CC	activated by MCH or its analogue or homologue). Also included are		
CC	expression vectors, probes, transformed insect cells, antisense		
CC	oligonucleotides, anti-MCH1 antibodies, an agent capable of inhibiting		
CC	the binding of the antibody to MCH1, a transgenic animal expressing the		
CC	protein, or a homologous knockout or antisense complementary to the MCH1		
CC	nucleic acid, ant/agonists of MCH1, and methods of isolating chemical		
CC	compounds which activate MCH1. The protein, nucleic acid, antibody,		
CC	ant/agonists and compound are useful for diagnosing and treating a		
CC	steroid or pituitary hormone disorder, an epinephrine release disorder, a		
CC	gastrointestinal disorder, cardiovascular disorder, electrolyte balance		
CC	disorder, hypertension, diabetes, respiratory disorder, asthma,		
CC	reproductive function disorder, immune disorder, endocrine disorder,		
CC	musculoskeletal disorder, neuroendocrine disorder, cognitive disorder,		

CC	memory disorder, sensory modulation and transmission disorder, motor
CC	coordination disorder, sensory integration disorder, motor integration
CC	disorder, dopaminergic function disorder, sensory transmission disorder
CC	olfaction disorder, sympathetic innervation disorder, pain, psychotic
CC	behaviour, morphine tolerance, opiate addiction, affective disorder,
CC	stress-related disorder, fluid-balance disorder, seizure disorder or
CC	migraine, an eating disorder or obesity. The present sequence
CC	encodes human MCH1.
XX	
XX	Sequence 1269 BP; 234 A; 419 C; 347 G; 269 T; 0 other;
US-09-885-478-2 (1-422) x ABK14548 (1-1269)	
Alignment Scores:	
Pred. No.:	7.19e-185
Score:	2212.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	24
	gaps: 0
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DB	1 ANGTAGTGGGAGCCATAGAGAGGAATGGGGAGGCGAGTGGGCTTGGAGGGCGAGC
QY	21 G1yCysG1nAlaTrpGluG1uAspProLeuProAspCysG1yAlaCysAlaProG1yGln
DB	61 GGCTGCCAGGCTACGAGAGAGACCCCTTCCGACGTGGGGGCTTGCGTCCGGAGCA
QY	41 G1yG1yAArgArGTrpArgLeuProGlnProAlaTrpAlaG1uG1ySerSerAlaArgLeu
DB	121 GGTGGCAGGCGCTGGAGGCTGCCACGCTCGGTGGGTGGAGGGAGGACTACGTCGGTTG
QY	61 TrpG1nG1nAlaTrpG1yTrpMetAspLeuG1uAlaSerLeuLeuProTrpG1y
DB	181 TGGGAGCAGGGGACCGGACGTGGTGATGAGTGCCTGGAACTCGTGCCTGCCACTGGT
QY	81 ProAsnAlaSerAsnTrpSerAspG1yProAspAsnLeuTrpSerAlaG1ySerProPro
DB	241 CCCAATGCCACCAACACCTCTGATGGCCCGATMACTCACTTCACAGAGATCACCTCC
QY	101 ArgTrpArgSerTrpSerTrpL1aSn11eLeuMetProSerAlaPheG1yTrpTr1eCys
DB	301 CGCAGGGGAGACATCTCTACATACAATCAATCAATGCTTGCGTGGTGGGACCATCTGC
QY	121 LeuLeuG1yLe11eG1yAsnSerTrpVal11ePheAlaVal1AlaLysLysSerLysLeu
DB	361 CTCCTGGGCATCATCGGGAACCTCCAGCGTCATCTTGGCGTCTGGAAAGATCCAAGCTG
QY	141 HisTrpCysAsnAsnValProAsp11ePhe11eLeu11eAsnLeuSerVal1AlaAspLeuLeu
DB	421 CACGTGTGCAACAACGTCGCCGACATCTTATCATCAACCTCTCGGTAGATGATCTCTC
QY	161 PheLeuLeuG1yMetProPheMet11eHisG1nLeuMetG1yAsnG1yVal1TrpP11eS1p1e
DB	481 TTTCTCTCGGGCATGCCCTTCATGATGCACACAGCTCACTGGGCAATGGGGTGGCACTTT
QY	181 G1yG1uTrpMetCysTrpLeu11eTrpAlaMetAspAlaAsnSerG1nPheTrpSerTrp
DB	541 GGGGAGACCATGTCCACCTTCATCACGGCATGGATGCCAATAGTCAGTTCACACAGCAC
QY	201 Tyr11eLeuTrpAlaMetAla11eAspArgTyrLeuAlaTrpVal1HisPro11eSerSer
DB	601 TACATCTGACCGGCATGGCATTTGACCGGTACTGGCCACTGTCCACACCCCATCTTCTCC
QY	221 ThrLysPheArG1ySProSerVal1AlaTrpLeuVal11eCysLeuLeuTrpAlaLeuSer
DB	661 ACGAAGTTCGGGAAGCCCTCTGTGGGCAACCCGTGTATCTGCTCTGTGGGCGCTCTCC
QY	241 Phe11eSer11eTrpProVal1TrpLeuTrpAlaArgLeu11eProPheProG1yAla
DB	721 TTTATCGACATACCCCTGTGTGGCTGTATGCCAGACTATCCCTTCCAGAGGTGCA

```
QY 261 ValGlyCysGlyIleAroIeuProAsnProAspThrAspLeuThrTrpPheThrIeuTyr 280
PT |||||||
DB 781 GTGGGCTGGGCTACGCTGGCCCAACCCAGACACTGACTCTACTGGGTCACTGTTAC 840
QY 281 GluPhePheLeuAlaPheAlaLeuProPheValIleThrAlaAlaTyrValArgIle 300
PT |||||||
DB 841 CACTTTTCTGCGCTTTGGCCCTGGCTTTGGTGCATCAGACGCCCATACGTGAGGATC 900
QY 301 LeuGluArgMetThrSerSerValAlaProAlaSerGlnArgSerIleArgLeuArgThr 320
PT |||||||
DB 901 CTCAGAGGCTAGACGTCTCTAGTGGCCCCCGCTCCACAGCAATCCGGCTGGGACA 960
QY 321 LysArgValThrArgThrAlaIleAlaIleCysLeuValPhePheValCysTrpAlaPro 340
PT |||||||
DB 961 AAGAGGGTGACCCGACAGCCATGCCATCTGCTGCTCTTTTGTGCTGGGACCC 1020
QY 341 TyrTyrValLeuGluIleuThrGlnLeuSerIleSerArgProThrLeuThrPheValTyr 360
PT |||||||
DB 1021 TACTATGTGCTACAGCGACCCAGTTGTCCATCAGCGCGCCGACCTCAGCTTGTCTAC 1080
QY 361 LeuTyrAsnAlaAlaIleSerLeuGlyTyrAlaAsnSerCysLeuAsnProPheValTyr 380
PT |||||||
DB 1081 TTTATCATGCGCGCATACACTTGGCTATGCCAACAGCTGCCTCAACCCCTTGTGTAC 1140
QY 381 IleValLeuCysGluThrPheArgLysArgLeuValLeuSerValLysProAlaAlaGln 400
PT |||||||
DB 1141 ATGCTGCTCTGTAGACGTTCCGAAACGCTTGCTCTGCGGTGAAGCTGCAGCCGAC 1200
QY 401 GlyGluLeuArgAlaValSerAsnAlaGlnThrAlaAspGluIuArgThrGluSerLys 420
PT |||||||
DB 1201 GGGCAGCTTGCCTGTCAACAGCTCAGACGCGTGCAGAGGAGAGACAGAAACAA 1260
QY 421 GlyThr 422
PT |||||||
DB 1261 GGCACC 1266

RESULT 3
AAD13654
ID AAD13654 standard; cDNA; 1269 BP.
AC AAD13654;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human melanin-concentrating hormone receptor variant #3 cDNA.
XX
KW Human; melanin-concentrating hormone; MCH analogue; signal transduction;
KW appetite; therapy; anorexia; acquired immune deficiency syndrome; AIDS;
KW wasting; cachexia; frail elderly; weight maintenance; cancer; anorectic;
KW pain reduction; stress reduction; sexual dysfunction; variant; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 1..1269
FT /tag= a
FT /product= "Human MCH receptor protein variant #3"
XX
XX WO200157070-A1.
XX
XX 09-AUG-2001.
XX
XX 01-FEB-2001; 2001WO-US03293.
XX
XX 03-FEB-2000; 2000US-0179967.
XX
XX (MERI ) MERCK & CO INC.
XX
XX Bednarek M;
XX
XX WPI; 2001-483416/52.
XX
XX P-PSDB; AAE07330.
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XX
PT Novel peptide encoding a melanin-concentrating hormone analog useful
PT for increasing weight or appetite
XX
XX PS Disclosure; Page 33; 66pp; English.
XX
CC The present invention relates to truncated melanin-concentrating hormone
CC (MCH) analogues active at the MCH receptor. The truncated MCH analogues
CC are optionally modified peptide derivatives of mammalian MCH. The MCH
CC analogues can bind to the MCH receptor and bring about signal
CC transduction. The MCH agonists can be used to facilitate a weight gain,
CC maintenance of weight and/or an appetite increase. The MCH agonists can
CC also be used to treat disorders such as anorexia, acquired immune
CC deficiency syndrome (AIDS), wasting, cachexia and frail elderly. The MCH
CC antagonists can be used to facilitate weight loss, appetite decrease,
CC weight maintenance, cancer treatment, pain reduction, stress reduction
CC and/or treatment of sexual dysfunction. The present sequence is a human
CC MCH receptor variant cDNA.
XX
SQ Sequence 1269 BP; 234 A; 420 C; 347 G; 268 T; 0 other;

Alignment Scores:
Pred. No.: 1,98e-184 Length: 1269
Score: 2207.00 Matches: 421
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.76% Mismatches: 0
Query Match: 99.77% Indels: 0
DB: Gaps: 0

US-09-885-478-2 (1-422) x AAD13654 (1-1269)
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QY 21 GlyGlnAlaThrGluGluAspProLeuProAspCysGlyAlaCysAlaProGlyGln 40
DB 61 GCGTCCAGGCTACGAGAGAAAGACCCCTCCCACTCGGGGCTTGCGTCCGGGACAA 120
QY 41 GlyIleArgArgTrpArgLeuProGlnProAlaTrpValGlyIleSerSerAlaArgLeu 60
DB 121 GGTGGCAGGCGCTGGAGGCTGCCGACGCTGCTGGTGGAGGGAGTCAAGCTCGGTG 180
QY 61 TrpGluGlnAlaThrGlyThrGlyTrpMetAspLeuGluAlaSerLeuProThrGly 80
DB 181 TGGGAGCAGGAGCGGACCTGCTGATGGACCTGGAACCTGCTGCTGCCCATCTGT 240
QY 81 ProAsnAlaSerAsnThrSerAspGlyProAspAsnLeuThrSerAlaGlySerProPro 100
DB 241 CCCAACGCCAGCAACACCTGTGATGGCCCCGATAACTCTACTCGGACAGATCACTCT 300
QY 101 ArgThrGlySerIleSerTyrIleAsnIleIleMetProSerValPheGlyThrIleCys 120
DB 301 CGCAGCGGAGCATCTCTCATCAATCAATCATCATGCTTGCGTGTGGCACCATCTGC 360
QY 121 LeuLeuGlyIleIleGlyAsnSerThrValIlePheAlaValAlaLysSerLysLeu 140
DB 361 CTCCTGGGATCATCGGGAATCCACGGTCACTTCGGGCTGTGMAAAGATCCAAAGCTG 420
QY 141 HisTrpCysAsnAsnValProAspIlePheIleIleAsnLeuSerValValAspLeuLeu 160
DB 421 CACTGGTGCAACACGTCGCCGACATCTTCATCATCAACCTCTCGGTGATGATCTCTTC 480
QY 161 PheLeuLeuGlyMetProPheMetIleHisGlnLeuMetGlyAsnGlyValTrpHisPhe 180
DB 481 TTTCTCTGGGATGCGCTTCTCATGATCCACCGCATAGGGGAATGGGCTGGGACATTT 540
QY 181 GlyGluThrMetCysThrLeuIleThrAlaMetAspAlaAsnSerGlnPheThrSerThr 200
DB 541 GGGGAGACCATGTGACCCCTCATCAAGGCGCATGATGCCAATAGTCAGTTGACCGACCC 600
QY 201 TyrIleLeuThrAlaMetAlaIleAspArgGlyIleAsnIleThrValHisProIleSerSer 220
PT |||||||
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Dp	601	TACATCTCAGCCG	CCATGG	CCATTACG	CCGCTAC	CTGGCC	ACCTGTCC	ACACCC	ACTCTTCC	660
Qy	221	ThrlsPheArGLysProSerValAlaThrLeuValIleCysLeuLeuTPAlaLeuSer	240							
Dp	661	ACGAAAGTCCGG	AAAGCCCTCTGTGG	CCACCCCTGG	AGATCTGCTCTCTGTGG	CCCTTCC	720			
Qy	241	PheIleSerIleThrProValTrpLeuTYrAlaArgLeuIleProPheProGLyValA	260							
Dp	721	TTTCATGAGCATCACC	CTGTGTGG	CTGTATGG	CACATCATCCCTTCC	AGAGGTGCA	780			
Qy	261	ValGLYCysGLYIleArgLeuProAsnProAspThrAspLeuTYrTTPheThrLeuTYr	280							
Dp	781	GTTGGGTGGGG	CTACGCTGG	CCCAACCAAG	CACTGACCTTACTGTGTTAC	CCCTGAC	840			
Qy	281	GLIIPhePheLeuAlaPheAlaLeuProPheValIleIleThrAlaAlaTYrValArgIle	300							
Dp	841	CAGTTTTTCTCTGG	CTTTGCCCTTGTGGT	CTATCAG	CCGCCATACGGCATACGTGAGATC	900				
Qy	301	LeuGlnArgMetThrSerSerValAlaProAlaSerGlnArgSerIleArgLeuArgThr	320							
Dp	901	CTCCAGCGCATG	ACGCTCTCAGTGG	CCCCCGCTCC	CAAGCAGCATCCGGCTCCGGACA	960				
Qy	321	LysArgValThrArgThrAlaIleAlaIleCysLeuValIlePhePheValCysTrpAlaPro	340							
Dp	961	AAGAGGGTGAC	CCGCACAGCATCG	CCATCTGCTGTCTTCTTGTGTGG	GGGCAACC	1020				
Qy	341	TYrTYrValLeuGlnLeuThrGlnLeuSerIleSerArgProThrLeuThrPheValTYr	360							
Dp	1021	TACTATGTGTACAG	CTGACCCAGTGTCTATC	TACAGCCG	CCACCTCACTTGTGTAC	1080				
Qy	361	LeuTYrAsnAlaAlaIleSerLeuGLYTYrAlaAsnSerCysLeuAsnProPheValTYr	380							
Dp	1081	TTATACAAATCG	GGCCATCAGCTTGG	CTATGCAACAG	CTGCTCAACCCCTTGTGTAC	1140				
Qy	381	IleValLeuCysGlnThrPheArgLysArgLeuValLeuSerValLysProAlaAlaGln	400							
Dp	1141	ATCTGTCTCTGTAG	ACGTTCCGCAACCTTGTCTGTCTGTGTAG	ACCTGTGAC	CCAG	1200				
Qy	401	GLYGLnLeuArgAlaValSerAsnAlaGlnThrAlaAspGLuGLuArgThrGluSerLys	420							
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Qy	421	GLYThr 422								
Dp	1261	GGCAC	1266							
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AC	AAA91189;									
DT	08-MAY-2001	(first entry)								
IX		Human MCH-R3 coding sequence.								
XX										
KW		Human; melanin-concentrating hormone receptor; MCH-R1; MCH-R2; MCH-R3;								
KM		weight loss; weight gain; cancer; pain; diabetes; stress; therapy;								
KW		sexual dysfunction; ds.								
XX										
OS		Homo sapiens.								
XX										
FH	Key	Location/Qualifiers								
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FT		/tag= a								
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PN	W0200105947-A1.									
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ED	25-JAN-2001.									
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XX	10-JUL-2000;	2000WO-US18733.								

Accession	Sequence	Score	Length	Matches	Conservative	Mismatches	Indels	Gaps
XX	14-JUL-1999: 99US-0143706.							
XX	(MERI) MERCK & CO INC.							
XX								
XX	Howard AD:							
XX	WPI: 2001-159528/16.							
XX	P-PSDB: AAY97670.							
XX								
PT	Melanin-concentrating hormone receptor polypeptides for increasing or							
PT	decreasing appetite, reducing stress and to screen for compounds that							
PT	bind to the receptor -							
XX								
PS	Claim 7; Page 22; 43pp: English.							
XX								
CC	This sequence encodes a melanin-concentrating hormone (MCH) receptor							
CC	protein of the invention, designated MCH-R3. MCH receptor fragments and							
CC	polypeptides are useful in assays to screen for compounds that bind to							
CC	the MCH receptor and modulate the activity of the receptor. MCH Receptor							
CC	activity is modulated to achieve weight loss, weight gain, to treat							
CC	cancer (e.g. colon or breast), reduce pain, treat diabetes, reduce stress							
CC	or treat sexual dysfunction. Nucleic acid coding for the MCH receptor can							
CC	be used to cause an increase in appetite and to create a test system							
CC	(e.g. a transgenic animal) for screening for compounds affecting MCH							
CC	receptor expression. Inhibition of MCH receptor nucleic acid activity is							
CC	useful to inhibit appetite or stress.							
XX								
XX	Sequence 1269 BP; 234 A; 420 C; 347 G; 268 T; 0 other;							
SO								
Alignment Scores:								
Pred. No.:	1,98e-184	Length:	1269					
Score:	2207.00	Matches:	421					
Percent Similarity:	100.00%	Conservative:	1					
Best Local Similarity:	99.76%	Mismatches:	0					
Query Match:	99.77%	Indels:	0					
DB:	22	Gaps:	0					
US-09-885-478-2 (1-422) x AAA91189 (1-1269)								
QY	1 MetserValGIyAlaMetLysGIyValGIyArGAlaValGIyLeuGIyGIySer	20						
Db	1 ATGTCAGTGGGAGCCATGAAGAAGGAGTGGGAGGAGGAGTGGCTTGGAGCGGACAC	60						
QY	21 GlycysGlnAlaThrGluGluAspProLeuProAspCysGIyAlaCysAlaProGlyGln	40						
Db	61 GGGTGGCCAGGGTACGAGGAAGACCCCTTCCTCCAACTCGGCGCTTCCGGAGCA	120						
QY	41 GlyIyArGArGTTPArGLeuProGlnProAlaTrpValGIyGIySerSerAlaArgLeu	60						
Db	121 GGTGGACAGGCGCTGGAGCGTGCCCACTCGCGGTGGAGGAGGAGCTCAGCTCGTGTG	180						
QY	61 TrpGIuGlnAlaThrGluGluThrTrpMetAspLeuGlnAlaSerLeuLeuProThrGly	80						
Db	181 TGGGAGCAGGGGACCGGACACTGGGTGATGGACCTGGAGCCTCGTGGCCCACTG	240						
QY	81 ProAsnAlaSerAsnThrSerAspGlyProAspAsnLeuThrSerAlaGIySerProp	100						
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QY	101 ArgThrGlySerIleSerTrpIleAsnIleIleMetProSerValAlaThrGlyThrIleCys	120						
Db	301 CGCAGGGGAGACATCTCTCAATATACATATCATGTGCTTGGTGTGGCAGCACATCTGC	360						
QY	121 LeuLeuGIyIleIleGIyAsnSerThrValIlePheAlaValAlaIlyIysSerIyLeu	140						
Db	361 CTCCTGGGCAATCAATCCGGAATCTTCATCTTCGCGTCTGAAAGAGTCCAAAGCTG	420						
QY	141 HisTrpCysAsnAsnValProAspIlePheIleIleAsnLeuSerValAlaIleLeuLeu	160						
Db	421 CACTGGTGCACAAACGTCGCCGCAATCTTATCATCTCAACTCTTCGGTAGATCTCTTC	480						
QY	161 PheLeuLeuGIyMetProPheMetIleHisGIyLeuMetGIyAsnGIyValTrpHisPhe	180						

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QY      181 GtYgIuThrMetCysThrLeuIleThrAlaMetAspAlaAsnSerGlnPheThrSerThr 200
Db      541 GGGGAGACCATGTGACCTCTCATACAGGCGCATGATGCCAATAGTCACTGCACAGCACC 600
QY      201 TyrIleLeuThrAlaMetAlaIleAspArgTyrIleuAlaThrValHisProIleSerSer 220
Db      601 TACATCTCCACCGCATGGCCATTTAGCCCTTACCTGACCTGTCACCCCACTCTCTTCC 660
QY      221 ThrLysPheArgLysProSerValAlaThrLeuValIleCysLeuLeuThrAlaLeuSer 240
Db      661 ACAGAGTTCGGAGAGCCCTCTGTGGCCACCCGATGATGTGCTCTGTGGGGCCCTTCC 720
QY      241 PheIleSerIleThrProValIleThrLeuTyrAlaArgLeuIleProPheProGlyAla 260
Db      721 TTCATCAGATCACCCCTGTGGCTGTATGCGACACTCATCCCTCCACAGAGCTGCA 780
QY      261 ValGlyCysGlyIleArgLeuProAsnProAspThrAspLeuTyrThrPheThrLeuTyr 280
Db      781 GTGGGTGGGGCATACGCTGCTCCCAACCCAGACACTGACTCTTACTGGTTCACTCTAC 840
QY      281 GlnPhePheLeuAlaPheAlaLeuProPheValIleThrAlaAlaTyrValArgIle 300
Db      841 CAGTTTTCCTGGCCTTGGCCCTTGGCTTGTGGTCAACAGCGCATACGTGAGATC 900
QY      301 LeuGlnArgMetThrSerSerValAlaProAlaSerGlnArgSerIleArgLeuArgThr 320
Db      901 CTCACAGCATGACGTCCTCAGTGGGCCGCCCTCCACGCGAGCATCCGGCTGGGAGCA 960
QY      321 LysArgValThrArgThrAlaIleAlaIleCysLeuValPhePheValLysThrAlaPro 340
Db      961 AAGAGGTGACCCGCAACAGCATGCGCATGTGTGTCTTTTGTGTGCTGGGACCC 1020
QY      341 TyrTyrValLeuGlnLeuThrGlnLeuSerIleSerArgProThrLeuThrPheValTyr 360
Db      1021 TACTATGTGTACAGGTGACGCCAGTTGTCCATCAGCGGCCGACCTTGTGTCTAC 1080
QY      361 LeuTyrAsnAlaAlaIleSerLeuGlyTyrAlaAsnSerCysLeuAsnProPheValTyr 380
Db      1081 TTATACATCGCGCATACCTTGGCTATGCCAACAGCTGCTCAACCCCTTGTGTAC 1140
QY      381 IleValLeuGlyGlnThrPheArgLysArgLeuValLeuSerValLysProAlaAlaGln 400
Db      1141 ATCGTCTCTGTGAGAGCTTCCGMAACGCTGTGCTGTGCGTGAAGCCTGAGCCGAG 1200
QY      401 GlyGlnLeuArgAlaValSerAsnAlaGlnThrAlaAspGlnGluArgThrGlnSerLys 420
Db      1201 GGGGAGCTTGGCGCTGTACAGCAACGCTCAGAGCGGTGACGAGAGAGCAAGAACCAAA 1260
QY      421 GlyThr 422
Db      1261 GGCACC 1266

```

RESULT 5

AAH47297 standard; cDNA; 1269 bp.

AAH47297:

30-NOV-2001 (first entry)

Human long form MCHIR cDNA.

Melanin concentrating hormone receptor; MCHR; MCH; chimeric; fusion;

fluorescent polypeptide; orexigenic; anabolic; food intake; MCHIR; ss.

Homo sapiens.

Location/Qualifiers
 Key I..1269
 CDS /*tag- a

```

PN      WO200168706-A1.
XX      20-SEP-2001.
XX      14-MAR-2001; 2001WO-US08071.
XX      15-MAR-2000; 2000US-0189698.
XX      (MERI ) MERCK & CO INC.
XX      Marsh DJ;
XX      WPI: 2001-565791/63.
XX      P-PSDB; AAB85894.
XX      Fusion proteins comprising melanin concentrating hormone receptor
XX      peptides and fluorescent proteins, useful for identifying appetite
XX      stimulants -
XX      Example 1; Page 17-18; 71pp; English.
XX      The invention provides melanin concentrating hormone (MCH) receptor
XX      (MCHR) chimeric and fusion proteins. The MCHR chimeric proteins comprise
XX      MCHR polypeptide regions from different species. The MCHR fusion protein
XX      comprise MCHR polypeptide region and a fluorescent polypeptide region
XX      joined directly, or via a linker, to the carboxy side of the MCHR
XX      polypeptide region. The MCHR fusion proteins can be expressed by standard
XX      recombinant methodology. MCH action promotes feeding (orexigenic) and up
XX      regulation of MCH activity stimulates food intake. The present sequence
XX      represents a human long form MCHIR cDNA.
SQ      Sequence 1269 BP; 234 A; 420 C; 347 G; 268 T; 0 other;
Alignment Scores:
Pred. No.: 1.98e-184 Length: 1269
Score: 2207.00 Matches: 421
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.76% Mismatches: 0
Query Match: 99.77% Indels: 0
Gaps: 0
US-09-885-478-2 (1-422) x AAH47297 (1-1269)
QY      1 MetSerValGlyAlaMetLysGlyValGlyArgAlaValGlyLeuGlyGlySer 20
Db      1 ATGTGAGTGGGAGCCATGAGAAGAGGAGTGGGAGGCAATTGGGCTTGCAGCGCGCAGC 60
QY      21 GlyCysGlnAlaThrGluGluAspProLeuProAspCysGlyAlaCysAlaProGlyGln 40
Db      61 GGCCTCCAGGCTTACGAGAGAAAGACCCCTTCCCACTGCGGGCTTGGCTCCGGAGCAA 120
QY      41 GlyIleArgArgTyrPargLeuProGlnProAlaThrValGluGlySerSerAlaArgLeu 60
Db      121 GGTGGCAGGCGGTGAGAGCTGCGGACGCTGCTGGTGGAGGGAGTCAAGCTCGGTTG 180
QY      61 TrpGlnAlaAlaThrGlyTyrGlyTyrPheLaspLeuGluAlaSerLeuLeuProThrGly 80
Db      181 TGGGAGCAGAGCGACCGGACACTGTGATGACCTGGAAGCCTGCTGCTCCCACTGTGT 240
QY      81 ProAsnAlaSerAsnThrSerAspLysProAspAsnLeuThrSerAlaGlySerProPro 100
Db      241 CCCAAGCGCAGACACACCTGTATGGCCCCGATTAACCTCACTTGGCGAGATCACTCTCT 300
QY      101 ArgThrGlySerIleSerTyrIleAsnIleIleMetProSerValPheGlyThrIleCys 120
Db      301 CGCAGCGGAGAGATCTCTCAATCAACATCAATCAATCAATCGCTGCTGCGTGGCAGCATCTGC 360
QY      121 LeuLeuGlyIleIleGlyAsnSerThrValIlePheAlaValAlaValLysSerLysIleu 140
Db      361 CTCCTGGCATCATCGGGAATCCACAGGTCATCTTGGGCTGTGAAGAAGTCCAAAGCTG 420
QY      141 HistPrCysAsnAsnValProAspIlePheIleIleAsnLeuSerValValAspLeuLeu 160

```

[illegible]

KW	antcananemia; anabolic; orphan G protein-couple receptor protein; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200040725-A1.
XX	
PD	13-JUL-2000.
XX	
PF	27-DEC-1999; 99WO-JP07336.
XX	
PR	28-DEC-1998; 98JP-0374454.
PR	28-APR-1999; 99JP-0122688.
PR	02-SEP-1999; 99JP-0249300.
XX	
PA	(TAKE) TAKEDA CHEM IND LTD.
XX	
PI	Mori M, Shimomura Y, Takekawa S, Sugo T, Ishibashi Y, Kitada C;
PI	Suzuki N;
XX	
XX	
XX	WPI; 2000-475832/41.
DR	P-PSDB; AAB12779.

PT Screening methods for compounds as SLC-1 (antagonists useful in the
PT treatment of eating disorders and as preventives and remedies for e.g.
PI atomic bleeding and Prader-Willi syndrome -
XX
PS Example 8; Page 110-111; 123pp; Japanese.
XX

The present invention describes a method for screening components (I) or their salts that can alter the binding properties of melanin-concentrating hormone (MCH) or its derivative or salt to SLC-1 or its salt. Compounds identified by (I) are useful as SLC-1 (antagonists in eating disorders and as preventives and remedies for e.g. period pains, uterine recovery failure, caesarean section, artificial interruption of pregnancy, galactosistosis, tonic uterine contraction, foetal asphyxia, rupture of uterus, cervical rupture, premature birth and Prader-Willi syndrome. The present sequence represents the human SLC-1 cDNA sequence, which is used in an example from the present invention.

Sequence 1275 BP; 235 A; 420 C; 350 G; 270 T; 0 other;

Alignment Scores:	
Pred. No.:	1,99e-184
Score:	2207.00
Percent Similarity:	100.00%
Best Local Similarity:	99.76%
Query Match:	99.77%
DB:	21
Length:	1275
Matches:	421
Conservative:	1
Mismatches:	0
Indels:	0
Gaps:	0

US-09-885-478-2 (1-422) x AAA72918 (1-1275)

QY	1	MeSerValG1A1AlaMetLysIstysIyValG1LyrArgAlaValLylLeuL1ylG1ylSer	20
Db	7	ATGCTAGTGGGAGCCATGAAGAGGAATGGGAGGGCCAACTTGGCTTGAGCGCGGACG	66
QY	21	G1YCsG1Ala1AlaThrG1UG1UAspProLeuProAspG1YAlaCysAla1ProG1G1n	40
Db	67	GGCTGCCAGGCTACGAGAGAAACCCCTTCCCACTGCGGGGCTTGCCTCGGGAA	120
QY	41	G1YG1YArgArgTTrpArgLeuProG1nProAlaTTrpAlG1UG1YSerSerAlaArgLeu	60
Db	127	GGTGGCAGGCGCTGGAGAGCTGCCGAGGCTGCGGGTGGAGGGAGGAGCTGCAC	180
QY	61	TTrpUG1Ala1AlaThrG1YThrG1YTrpMetAspLeuG1UAlaSerLeuLeuProThrG1Y	80
Db	187	TGGGACACGAGCCAGCGGACAGTGGTGAATGACCTGGAAACCTCGCTGCCCACTG	248
QY	81	ProAsnAlaSerAsnThrSerAspG1YProAspAsnLeuThrSerAlaG1YSerProPro	100
Db	247	CCCAAGCCAGCAACAACCTTGATGAGCCCGGAGTAACTCACTTGGCAGAGTACACT	306
QY	101	ArgThrG1YSerL1SerTTrpL1asnL1e1LeuMetProSerValPheG1YThrL1eCys	120


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us-09-885-478-2 (1-422) x AAF86975 (1-1275)
OY 1 MetSerValGIAlaMetIleSylsGIAlaArgAlaValGIAlaLeuGIAlaSer 20
  |||||
Db 7 ATGTGAGTGGGAGCCATGAGAGAGAGAGTGGGAGGAGGAGTGGGCTTGGAGGCGGACG 66
OY 21 G1YcysG1aIaThrGluGluAspProIeuProAspCysG1aIaCysAlaIaProG1yGln 40
  |||||
Db 67 GCGTGCACAGCTACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 126
OY 41 G1YGIAlaArgIaIaThrArgIaIaProIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 60
  |||||
Db 127 GGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 186
OY 61 TrpGluGluAlaIaThrG1yThrG1yTrpMetAspLeuGluAlaIaSerIleuLeuProThrG1y 80
  |||||
Db 187 TGGGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 246
OY 81 ProAsnAlaSerAsnThrSerAspG1yProAspAsnLeuThrSerAlaG1ySerProPro 100
  |||||
Db 247 CCCAGAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 306
OY 101 ArgThrG1ySerIleSerTrpIleAsnIleIleMetProSerValPheG1yThrIleCys 120
  |||||
Db 307 CGCAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 366
OY 121 LeuLeuG1yIleIleG1yAsnSerThrValIlePheAlaValAlaIleSylsSerIleu 140
  |||||
Db 367 CTCCTGGGAGTCAACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 426
OY 141 HisTrpCysAsnAsnValProAspIlePheIleIleAsnLeuSerValAlaIleuLeu 160
  |||||
Db 427 CAGCTGGTCAACAAGCTCCCGGAGATCTCATATCACTCCGCTAGTACATCCCTCC 486
OY 161 PheLeuLeuG1yMetProPheMetIleHisGlnLeuMetG1yAsnG1yValIaIaIaIaIa 180
  |||||
Db 487 TTTCTCTCGGAGTGCCTTCATGATCCACAGCTCATGGGCAATGGGCTGGGACATCTT 546
OY 181 G1yG1uIaIaThrMetCysThrLeuIleIaIaMetAspAlaAsnSerIaIaIaIaIaIaIa 200
  |||||
Db 547 GGGGAGAGCCATGTGCACCCCTCATCAGGCGCATGATGATGATGATGATGATGATGATGATG 606
OY 201 TyrIleLeuThrAlaMetAlaIleAspArgTyrLeuAlaIaIaIaIaIaIaIaIaIaIa 220
  |||||
Db 607 TACATCTGTGACCGCATGAGCGCATGAGCGCTACCTGGCCACTGTCACCCCATCTCTTCC 666
OY 221 ThrIleSphearG1ySProSerValAlaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 240
  |||||
Db 667 ACGAAGTTCCGGAAGCCCTCTGTGGCCAGCCCTGTGATCTGCTCTGCTGCTGCTGCTGCT 726
OY 241 PheIleSerIleThrProValIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 260
  |||||
Db 727 TTTCAATCAGCATCACCTGTGTGTGTATGCAAGACTCATACCTCTCCAGAGAGTGC 786
OY 261 ValG1yCysG1yIleArgIleuProAsnProAspThrAspLeuTyrTrpPheThrLeuTyr 280
  |||||
Db 787 GTGGGCTGCGGAGATACCGCTGCCACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 846
OY 281 GlnPhePheLeuAlaPheAlaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 300
  |||||
Db 847 CAGTTTTCCTGGGCTTGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 906
OY 301 LeuGlnArgMetThrSerSerValAlaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 320
  |||||
Db 907 CTGAGAGCGCATGAGTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 966
OY 321 LysArgValIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 340
  |||||
Db 967 AAGAGGGTGAACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1026
OY 341 TyrTyrValIleuGlnLeuThrGlnLeuSerIleSerArgProThrLeuThrPheValTyr 360
  |||||

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Db 1027 TACTATGTCTACAGCTGACCCAGTTGTCCATCAGCCGCCGAGCCCTTGTCTAC 1086
OY 361 LeuTyrAsnIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 380
  |||||
Db 1087 TTTATACATGCGGAGATCAGCTTGGCTATGCAACAGCTGCTCAACCTTGTGTAC 1146
OY 381 IleValIeucysG1uIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 400
  |||||
Db 1147 ATCGTGTCTGTGAGAGCTTCCGCAACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1206
OY 401 G1yGlnLeuArgAlaValAsnAlaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 420
  |||||
Db 1207 GGGCAGCTTGGCGCTGTACCAACGCTCAGAGCGCTGACGAGAGAGAGAGAGAGAGAGAG 1266
OY 421 G1yThr 422
  |||||
Db 1267 GGCAGC 1272

RESULT 9
ABK10854
ID ABK10854 standard; DNA: 1275 BP.
XX
AC ABK10854;
XX
DT 05-JUN-2002 (first entry)
XX
DE DNA encoding human melanin concentrating hormone receptor, SLC-1.
XX
KW G protein-coupled orphan; receptor; SLC; melanin-concentrating hormone;
KW MCH; appetite stimulating agent; obesity; malignant mastocytosis;
KW exogenous obesity; hyperinsulinat obesity; sexual function disorder;
KW overpowering intermittent pain; still born; uterus rupture;
KW premature birth; Prader-Willi syndrome; SLC-1; human; gene; ds.
XX
OS Homo sapIens.
XX
FH Key Location/Qualifiers
FH CDS 7..1275
FH FT /*tag= a
FT FT /product= "SLC-1"
FT FT /note= "Melanin concentrating hormone receptor"
XX
PN WO200203070-A1.
XX
PD 10-JAN-2002.
XX
PF 04-JUL-2001; 2001WO-JP05809.
XX
PR 05-JUL-2000; 2000JP-0208254.
XX
PA (TAKE ) TAKEDA CHEM IND LTD.
XX
PI Mori M, Shimomura Y, Harada M, Sugo T, Shintani Y;
XX
DR WPI. 2002-164552/21.
XX
DR P-PSDB; AAU77541.
XX
PT Screening for compounds or salts which alter affinity of
PT melanin-concentrating hormone with its receptor to provide agonists as
PT appetite-stimulating agents and its antagonist for preventing or
PT treating obesity, uses a protein or hormone -
XX
PS Disclosure; Page 106-107; 112pp; Japanese.
XX
CC The invention describes a method of screening for compounds or their
CC salts that can change affinity of melanin-concentrating hormone (MCH)
CC with its G protein-coupled orphan receptor protein, SLC. The screened
CC MCH receptor agonists are useful as appetite-stimulating agents and its
CC antagonist for preventing or treating obesity e.g. malignant
CC mastocytosis, exogenous obesity and hyperinsulinat obesity, and also
CC for treating sexual function disorders, overpowering intermittent pains,
CC still borns, uterus rupture, premature birth and Prader-Willi syndrome.
CC This sequence encodes the human melanin concentrating hormone SLC-1,

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CC It may be combined with treatments for diabetes, hypertension or
CC arteriosclerosis. The present sequence encodes human SLC-1, which is
CC used the exemplification of the present invention.

XX Sequence 1275 BP; 235 A; 420 C; 350 G; 270 T; 0 other;

Alignment Scores:

Pred. No.:	1,99e-184	Length:	1275
Score:	2207.00	Matches:	421
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	99.76%	Mismatches:	0
Query Match:	99.77%	Indels:	0
DB:	24	Gaps:	0

US-09-885-478-2 (1-422) x ABA92411 (1-1275)

```

QY 1 MetSerValGlyAlaMetLysLysGlyValGlyArgAlaValGlyLeuGlyGlySer 20
   |||||
Db 7 ATGTCACTGGAGACCATGAAAGAGAGAGGAGGCGAGTTGGGCTTGAGAGCGGACGC 66
QY 21 GlyCysGlnAlaThrGluGluAspProLeuProAspCysGlyAlaCysAlaProGlyGln 40
   |||||
Db 67 GCGTCGACAGGCTACGAGAGAGACCCCTTCCCAACTCGCGGGGCTTGGCTCCGGAGCAA 126
QY 41 GlyGlyArgArgTrpArgLeuProGlnProAlaTrpValGlyGlySerSerAlaArgLeu 60
   |||||
Db 127 GGTGGAGAGGCGTGGAGGCTCGCGAGCCTGGTGGTGGAGGGAGGCTCAGCTCGTTG 186
QY 61 TrpGluGlnAlaThrGlyThrGlyTrpMetLysLeuGluAlaSerLeuLeuProThrGly 80
   |||||
Db 187 TGGGAGACGAGCGACCGGACCTGGCTGATGAGACTGGAGAGCCCTGCTGCCACTGCT 246
QY 81 ProAsnAlaSerAsnThrSerAspGlyProAspAsnLeuThrSerAlaGlySerProPro 100
   |||||
Db 247 CCCAAGCGCCAGCAACACTCTGATGGCCCCGATTAACCTCACTGGCAGAGATCACTCTCT 306
QY 101 ArgThrGlySerThrLeuSerTrpIleAsnIleIleMetProSerValPheGlyThrIleCys 120
   |||||
Db 307 CGCACGGGGAGCATCTCTCATCATCATCATCATCATCATCTCGGTTCGGCACCATCTGC 366
QY 121 LeuLeuGlyIleIleGlyAsnSerThrValIlePheAlaValValLysLysSerLysLeu 140
   |||||
Db 367 CTCTCGGCAATCAGGGAAGCTCCACGCTCATCTTCGGGCTCGTGAAGAAGTCCAAAGCTG 426
QY 141 HisTrpCysAsnAsnValProAspIlePheIleIleAsnLeuSerValValAspLeuLeu 160
   |||||
Db 427 CACTGGTGAACAACGTCGCCGACATCTTCATCATCAACTCTCGTAGTAGTCTCTCTC 486
QY 161 PheLeuLeuGlyMetProPheMetIleHisGlnLeuMetGlyAsnGlyValTrpHisPhe 180
   |||||
Db 487 TTTCCTCTGGGCAATGCCCTTCATGATCCACACGCTCATGGGCAATGGGAGTGGCACTTT 546
QY 181 GlyIleuThrMetCysThrLeuIleThrAlaMetAspAlaAsnSerGlnPheThrSerThr 200
   |||||
Db 547 GGGAGAGCAATGTCACCTCATACGCGCATGAGATGCCAATATGTCAGTTCCACAGAGACC 606
QY 201 TyrIleLeuThrAlaMetAlaIleAspArgTyrLeuAlaThrValHisProIleSerSer 220
   |||||
Db 607 TACATCTCTGACCGCCATGCGCATTTGACCGCTACTGGCCACTGTGCCACCCCATCTCTCC 666
QY 221 ThrLysPheArgLysProSerValAlaThrLeuValIleCysLeuLeuTrpAlaLeuSer 240
   |||||
Db 667 ACGAAGTTCCGGAAGCCCTGTGTGGCAACCCGTGTGATGTCCTGCTGGGCGCCCTCTCC 726
QY 241 PheIleSerIleThrProValTrpLeuTyrAlaArgLeuIleProPheProGlyGlyAla 260
   |||||
Db 727 TTCATCAGACATCACCCCTGTGTGCTGTATGCCAGACTCATCCCTTCCACGAGAGGTGCA 786
QY 261 ValGlyCysGlyIleArgLeuProAsnProAspThrAspLeuTyrTrpPheThrLeuTyr 280
   |||||
Db 787 GTGGGCTCGGCAATAGCGCTCTGCCACCCAGACACTGACCTCTGCTGTTCCACCTGTAC 846
QY 281 GlnPhePheLeuAlaPheAlaLeuProPheValValIleThrAlaIleTyrValArgIle 300

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Db 847 CAGTTTTCCTGGGCTTTGGCCCTGCTTTGTGTCATCAGACCCCATACGGAGATC 906
   |||||
QY 301 LeuGlnArgMetThrSerSerValAlaProAlaSerGlnArgSerIleArgLeuArgTrp 320
   |||||
Db 907 CTGACGGCATGACAGTCTCAGTGGCCCGCTCCAGGAGCATCCGGCTGGGAGACA 966
QY 321 LysArgValThrArgThrAlaIleAlaIleCysLeuValPhePheValCysTrpAlaPro 340
   |||||
Db 967 AAGAGGTGACCCGACAGCATTCGCCATCTGTCTGTTCTTGTGTGCTGGCACCC 1026
QY 341 TyrTrpValLeuGlnLeuThrGlnLeuSerIleSerArgProThrIleuThrPheValTyr 360
   |||||
Db 1027 TACTATGTGTACAGCTGACCCAGCTTGTCCATCAGCCGCCGACCTCATCTTTGTCTAC 1086
QY 361 LeuTrpAsnAlaAlaIleSerLeuGlyTyrAlaAsnSerCysLeuAsnProPheValTyr 380
   |||||
Db 1087 TTATATCAATGGGCGCATCAGCTTGGCTATGCCCACAGCTGCTCAACCCCTTGTGTAC 1146
QY 381 IleValLeuCysGlnThrPheArgLysArgLeuValLeuSerValLysProAlaAlaGln 400
   |||||
Db 1147 ATCTGTCTCTGTGAGAGCTTCCGAAAGCGTGGTCTCTGCGTGAAGCCTGCAGCCAG 1206
QY 401 GlyLeuLeuArgAlaValSerAsnAlaGlnThrAlaAspGluGluArgTrpGlySerLys 420
   |||||
Db 1207 GGCAGGCTTCGCGCTGTACAGCAACGCTCAGAGCGGCTGACGAGGAGAGACGAAAGCAA 1266
QY 421 GlyThr 422
   |||||
Db 1267 GGCACC 1272

RESULT 11
ID AAI69442
AAI69442 standard; DNA; 1275 BP.
XX AC
XX AAI69442:
XX 28-FEB-2002 (first entry)
XX DE
XX Human SLC-1 cDNA.
XX SLC-1; melanin-concentrating hormone antagonist; anorectic; depression;
XX antidiabetic; hypotensive; antiarteriosclerotic; antipneumatic; obesity;
XX antihistaminic; antidepressant; tranquilizer; malignant mastocytosis;
XX hypophysial adiposity; hypothyroid obesity; hyperphagia; diabetes;
XX hypertension; arteriosclerosis; hyperlipidemia; arthritis; anxiety;
XX human; ss.
XX OS
XX Homo sapiens.
XX FH
XX Key Location/Qualifiers
XX CDS 7..1275
XX FT /*tag= a
XX FT /product= "SLC-1"
XX PN WO200187834-A1.
XX PD 22-NOV-2001.
XX PF 15-MAY-2001; 2001WO-JP04015.
XX PR 16-MAY-2000; 2000JP-0148674.
XX PR 13-APR-2001; 2001JP-0116219.
XX PA (TAKE ) TAKEDA CHEM IND LTD.
XX PI Ishihara Y, Terauchi J, Suzuki N, Takekawa S, Aso K;
XX WPI: 2002-055668/07.
XX DR P-PSDB: AAG80611.
XX PT Use of new and known amine derivatives as melanin concentrating hormone
antagonists for treating e.g. obesity, diabetes, hypertension and

```


XX Mori M, Shimomura Y, Takekawa S, Sugo T, Ishibashi Y, Kitada C;
PI Suzuki N;
XX
XX WPI: 2000-475832/41.
DR
XX Screening methods for compounds as SLC-1 (ant)agonists useful in the
PT treatment of eating disorders and as preventives and remedies for e.g.
PT atonic bleeding and Prader-Willi syndrome
XX
XX Example 11: Page 115-116; 123pp: Japanese.
XX
XX The present invention describes a method for screening components (I) or
CC their salts that can alter the binding properties of melanin
CC concentrating hormone (MCH) or its derivative or salt to SLC-1 or its
CC salt. Compounds identified by (I) are useful as SLC-1 (ant)agonists in
CC eating disorders and as preventives and remedies for e.g. period pains,
CC uterine recovery failure, caesarean section, artificial interruption of
CC pregnancy, galactostosis, tonic uterine contraction, foetal asphyxia,
CC rupture of uterus, cervical rupture, premature birth and Prader-Willi
CC syndrome. The present sequence represents a human SLC-1 cDNA sequence,
CC which is used in an example from the present invention.
XX
XX Sequence 1283 BP; 238 A; 423 C; 350 G; 272 T; 0 other;
SO

Alignment Scores:
Pred. No.: 2.01e-184 Length: 1283
Score: 2207.00 Matches: 421
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.76% Mismatches: 0
Query Match: 99.77% Indels: 0
DB: 21 Gaps: 0

US-09-885-478-2 (1-422) x AAAT2924 (1-1283)

QY 1 MetSerValGlyAlaMetLysGlyValGlyArgAlaValGlyLeuGlyGlySer 20
DB 8 ATGTCAGTGGGAGCCATGAAGAAGGAGTGGGAGGCGACTGTGAGAGCGGACG 67
QY 21 GlyGlySerAlaThrGluGluAspProLeuProAspGlyAlaCysAlaProGlyGln 40
DB 68 GGGTGGCAGGCTACGGAGGAAGACCCCTTCCCAACTGCGGGGCTGCGTCCGGGACAA 127
QY 41 GlyGlyArgArgTTrpArgLeuProGlnProAlaTrpValGlyGlySerSerAlaArgLeu 60
DB 128 GGTGGCAGGCGCTGGAGGCTGCCAGCCTGCGTGGTGGAGGGAGACTACGCTGGTTG 187
QY 61 TrpGluGlnAlaThrGlyThrGlyTrpMetAspLeuGluAlaSerLeuLeuProThrGly 80
DB 188 TGGAGAGCAGCGGACCGGACACTGCTGGATGGACCTGCGACCTGCGCCACTGGT 247
QY 81 ProAsnAlaSerAsnThrSerAspGlyProAspAsnLeuThrSerAlaGlySerProPro 100
DB 248 CCCAAGCGCACCAACACCTGTGATGGCCCGATTAACCTTCTGGAGAGTCACTCTCT 307
QY 101 ArgThrGlySerIleSerTyrIleAsnIleIleMetProSerValPheGlyThrIleCys 120
DB 308 CGCAGCGGGAGCATCTCTTACATCAATCATCATGCTTGGTGGGAGCATCTGC 367
QY 121 LeuLeuGlyIleIleGlyAsnSerThrValIlePheAlaValIleLysLysSerLysLeu 140
DB 368 CTCTCGGCGCATCAACGGAACCTCCACGGTCACTTCCCGGCTGGAAGAAGTCCAAAGCTG 427
QY 141 HisTrpCysAsnAsnValProAspIlePheIleIleAsnLeuSerValIleAspLeuLeu 160
DB 428 CACTGTGTCAACACGTCCTCCGACATCTTCATCAACAACCTCTCGTAGTAGATCTCTTC 487
QY 161 PheLeuLeuGlyMetProPheMetIleHisGlnLeuMetGlyAsnGlyValITrPHisPhe 180
DB 488 TTTCCTCCCTGGGCGATGCCCTTTCATGATCACCAGCTCATGGGCAATGGGCTGTGGCACTTT 547
QY 181 GlyIuThrMetCysThrLeuIleThrAlaMetAspAlaAsnSerGlnPheThrSerThr 200
|||||

DB 548 GGGAGGACCATGTGACCCCTCATCAGCGCCATGATGCCAATAGTCACTTACCAGCACCC 607
QY 201 TyrIleLeuThrAlaMetAlaIleAspArgTyrLeuAlaThrValHisProIleSerSer 220
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QY 221 ThrLysPheArgLysProSerValAlaThrLeuValIleCysLeuLeuThrPalalaSer 240
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QY 241 PheIleSerIleThrProValITrPLeuTyrAlaArgLeuIleProPheProGlyGlyAla 260
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QY 421 GlyThr 422
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AC AAF86235;
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XX 05-JUL-2001 (first entry)
DE Human melanin concentrating hormone receptor (L) (SLC-1 L) related cDNA.
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XX Melanin concentrating hormone; MCH; antagonist; diamine compound;
KW anorectic; antididiabetic; ophthalmological; neuroprotective; nephrologic;
KW antiarteriosclerotic; antiarthritic; obesity; diabetes; arteriosclerosis;
KW arthritis; melanin concentrating hormone receptor; SLC-1; human; ss.
XX
OS Homo sapiens.
PN WO200121169-A1.
XX
XX 29-MAR-2001.
PD
XX
PF 19-SEP-2000; 2000WO-JP06376.
XX


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XX 29-MAR-2001.
PD 19-SEP-2000; 2000WO-JP06375.
XX
XX 20-SEP-1999; 99JP-0266298.
PR 16-DEC-1999; 99JP-0357889.
PR 20-APR-2000; 2000JP-0126272.
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XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX Kato K, Terauchi J, Mori M, Suzuki N, Shimomura Y, Takekawa S;
PI Ishihara Y;
XX WPI; 2001-354775/37.
XX
XX New aromatic compounds are melanin concentrating hormone antagonists,
XX PT useful as anorectic agents, for treating or preventing obesity, also
XX PT memory or hormonal disorders or diabetes
XX
XX Examples; Page 362-363; 363pp; English.
XX
XX The present invention describes aromatic compounds capable of acting as
XX CC melanin-concentrating hormone (MCH) antagonists. Melanin-concentrating
XX CC hormone is an appetite control factor and antagonists were expected to be
XX CC useful as anti-obesity agents. They can be used in the treatment of
XX CC obesity, including malignant mastocytosis, exogenous, hyperinsular
XX CC hypoplasmic, hypothyroid, hypothalamic, symptomatic, infantile, upper
XX CC body, alimentary, hypogonadal, simple and central obesity, systemic
XX CC mastocytosis and hypophyseal adiposity, hypertension, arteriosclerosis,
XX CC hyperphagia, emotional disorders, reproductive function disorders, memory
XX CC disorders, dementia, hormonal disorders, diabetes and gonitis. MCH binds
XX CC to the SLC-1 receptor. The present sequence is a version of the human
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XX 201 TyrIleLeuThrAlaMetAlaIleAspArgTyrLeuAlaThrValHisProIleSerSer 220
XX |||||||
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XX Human SLC-1 (u) nucleotide sequence SEQ ID NO:15.
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XX Human; SLC-1; melanin concentrating hormone antagonist; obesity;
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GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 19, 2003, 11:07:07 ; Search time 3647 Seconds
(without alignments)
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Title: US-09-885-478-2

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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22	1813	82.0	1062	6	AX280739 Sequence
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RESULT 1

ALIGNMENTS

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DEFINITION Sequence 1 from patent US 6291195.
ACCESSION ARI69785
VERSION ARI69785.1 GI:17907693
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1269)
AUTHORS Salton, J. A., Laz, T. M., Nagorny, R. and Wilson, A. E.
TITLE DNA encoding a human melanin concentrating hormone receptor (MCH1)
and uses thereof
JOURNAL Patent: US 6291195-A 1 18-SEP-2001;
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ACCESSION BC001736
VERSION BC001736.1 GI:12804624
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SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE 1 (bases 1 to 2042)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (16-JAN-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILMIL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca

Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susana Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Leticia Hsiao, Martin Krzywinski, Reta Kuschke, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Matheson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smalls, Michael Smith, Lorraine Spence, Jeff Scott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyerdun, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <http://image.lnl.gov>
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FEATURES

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Location/Qualifiers

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ORIGIN

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Pred. No.: 9,38e-149

Score: 2212.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 100.00%

DB: 9

Gaps: 0

US-09-885-478-2 (1-422) x BC001736 (1-2042)

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QY 21 GlyCysGlnAlaThrGluLysProLeuProAspCysGlyAlaCysAlaProGlyGln 40
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QY 41 GlyGlyArgArgTrpArgLeuProGlnProAlaTrpValGlyGlySerSerAlaArgLeu 60
DB 334 GTGGGAGGCGCTGGAGGCTGGCGAGCCTGGCTGGGAGGAGGAGCTCAGCTGGTGG 393
QY 61 TrpGluGlnAlaThrGlyThrGlyTrpMetAspLeuGluAlaSerLeuLeuProThrGly 80
DB 394 TGGGACGAGGCGACCGGACCTGGCTGATGGACCTGGAAAGCTCTCTCTCCCACTGGT 453
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DB 574 CTCCTGGGCATCATGGGAACTCCAGGCTCATCTTCGGGGTGTGAAGAAGTCCAACTG 633
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QY 161 PheLeuLeuGlyMetProPheMetIleIleGlnLeuMetGlyAsnGlyValIlePheSph 180
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QY 181 GlyGluThrMetCysThrLeuIleThrAlaMetAspAlaAsnSerGlnPheThrSerThr 200
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QY 381 IleValLeuCysGluThrPheArgLysArgLeuValLeuSerValLysProAlaAlaGln 400
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QY 401 GlyGlnLeuArgAlaValSerAsnAlaGlnThrAlaAspGluGluArgThrGlySerLys 420
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QY 421 GlyThr 422
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DEFINITION BC021146
ACCESSION BC021146
VERSION BC021146.1 GI:18088973
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SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 2042)
 AUTHORS Strausberg, R.
 TITLE Direct Submission
 JOURNAL Submitted (03-JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
 Contact: MGC help desk
 Email: cgabs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Rubin Laboratory
 DNA Sequencing by: Genome Sequence Centre,
 BC Cancer Agency, Vancouver, BC, Canada
 Info@cgsc.bc.ca

Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice Mcleavy, Steven Ness, Pavan Pandoh, Anna-Lisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smalins, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAL Plate: 40 Row: n Column: 6
 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.

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 Source Location/Qualifiers

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 SSTKRPKPSVATLVICLMLASFISTTPWLYARLPPFGGAVGGGILPMPDDILW
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BASE COUNT 454 a 600 c 565 g 423 t
 ORIGIN

Alignment Scores:
 Pred. No.: 9.38e-149 Length: 2042
 Score: 2212.00 Matches: 422
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Gaps: 0

US-09-885-478-2 (1-422) x BC021146 (1-2042)

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 Qy 21 GlyGlyGlnAlaThrGluGluAspProLeuProAspCysGlyAlaCysAlaProGlyGln 40
 Db 274 GGCTGCGAGGCTACGAGGAGGAGACCCCTTCGCCACTGCGGGGCTTCGCGGAGCA 333

Qy 41 GlyGlyArgArgTrpArgLeuProGlnProAlaTrpValGlyGlySerSerAlaArgLeu 60
 Db 334 GGTGGACAGCGCTGAGAGCGTCCGACACCTCGCTGGGTGGAGGAGGCTCACCTCGGTTG 393
 Qy 61 TrpGluGlnAlaThrGlyThrGlyTrpMetAspLeuGluAlaSerLeuLeuProThrGly 80
 Db 394 TGGAGAGGAGGAGCGGACCTGCTGATGAGACCTGGAAGCCCTGCTGCTCCACTGGT 453
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 Db 454 CCCAATGCGACACACACCTCTGATGGGCCCGATACCTCACTTCGCGACAGATCACTCT 513
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RESULT 4
BD013168
LOCUS BD013168 1275 bp DNA linear PART 02-AUG-2002
DEFINITION MCH receptor antagonist.
ACCESSION BD013168
VERSION BD013168.1 GI:22093357
KEYWORDS WO 0121169-A/7.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1275)
AUTHORS Kato,K., Mori,M., Suzuki,N., Shimomura,Y., Takekawa,S. and Cho,N.
TITLE MCH receptor antagonist.
JOURNAL Patent: WO 0121169-A 7 29-MAR-2001:
TAKEDA CHEMICAL INDUSTRIES LTD, KANEYOSHI KATO, MASAOKI MORI, NOBUHIRO
SUZUKI, YUKIO SHIMOMURA, SHIRO TAKEKAWA, NOBUO CHO
OS Homo sapiens (human)
PN WO 0121169-A/7
PD 29-MAR-2001
PF 19-SEP-2000 WO 2000JP006376
PR 20-SEP-1999 JP 99P 266278,17-JUL-2000 JP 00P 221055 PI
KANEYOSHI KATO, MASAOKI MORI, NOBUHIRO SUZUKI, YUKIO SHIMOMURA PI
SHIRO TAKEKAWA,
PI NOBUO CHO
PC A61K31/137, A61K31/27, A61K31/4035, A61K31/44, A61K31/445, PC
A61K31/4453,
PC A61K31/472, A61P43/00, A61P31/04, C07D211/14, C07D211/18 PC
C07D211/46, C07D211/58,
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FH Key Location/Qualifiers.

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source 1.1275 Location/Qualifiers
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BASE COUNT 235 a 420 c 350 g 270 t
ORIGIN

Alignment Scores:
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Score: 2207.00 Matches: 421
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.76% Mismatches: 0
Query Match: 99.77% Indels: 0
DB: 6 Gaps: 0

US-09-885-478-2 (1-422) x BD013168 (1-1275)

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RESULT 5
AB063174

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DEFINITION Homo sapiens SLC-1 mRNA for somatostatin receptor-like protein,
complete cds.
ACCESSION AB063174
VERSION AB063174.1 GI:14475646
KEYWORDS
SOURCE Homo sapiens
ORGANISM Homo sapiens cDNA to mRNA.
REFERENCE
AUTHORS Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE 1 (sites)
JOURNAL Shimomura,Y., Mori,M., Sugo,T., Ishibashi,Y., Abe,M., Kurokawa,T.,
Onda,H., Nishimura,O., Sumino,Y. and Fujino,M.
REFERENCE Isolation and identification of melanin-concentrating hormone as
the endogenous ligand of the SLC-1 receptor
AUTHORS Biochem Biophys. Res. Commun. 261 (3), 622-626 (1999)
JOURNAL 99373129
MEDLINE 2 (bases 1 to 1275)
REFERENCE Sugo,T. and Mori,M.
AUTHORS Direct Submission
JOURNAL Submitted (13-JUN-2001) Tsukasa Sugo, Takeda Chemical Industries,
Ltd., Discovery Research Laboratories I, Pharmaceutical Research
Division, Wadai 10, Tsukuba, Ibaraki 300-4247, Japan
(E-mail: Sugo_Tsukasa@takeda.co.jp, Tel: 81-298-64-5010(ex. 5010),
Fax: 81-298-64-5000)
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BASE COUNT 235 a 420 c 350 g 270 t
ORIGIN
Alignment Scores:
Pred. No.: 1,17e-148 Length: 1275
Score: 2207.00 Matches: 421
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.76% Mismatches: 0
Query Match: 99.77% Indels: 0
Gaps: 0
US-09-885-478-2 (1-422) x AB063174 (1-1275)

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QY 321 LysArgValThrArgThrAlaIleAlaIleCysLeuValPhePheValCysTrpAlaPro 340
DB 967 AAGAGGTTGACCCGACACACCAATCCGCACTGTGCTGCTTCTTGTGTGGTGGGACACC 1026
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DB 1087 TTATACAAATGCGGCATAGCTTGGGCTGTGCAACAGCTGCTCAACCCCTTGTGTAC 1146
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DB 1147 ATCGTCTCTGTAGAGCGTTGCGCAAAAGCTTGGCTGTGCTGTAAGCTTCACCCAG 1206
QY 401 GlyGluLeuArgAlaValSerAsnAlaGlnThrAlaAspGluGluArgThrGluSerLys 420
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RESULT 6
BD006649 standard; DNA; HUM; 1275 BP.

XX BD006649;

SV BD006649.1

DT 08-FEB-2002 (Rel. 70, Created)

DT 08-FEB-2002 (Rel. 70, Last updated, Version 1)

DE MCH receptor antagonist.

XX JP 03075319-T/7.

OS Homo sapiens (human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;

XX Eutheria; Primates; Catarrhini; Homidae; Homo.

XX [1]

RA Kato K., Mori M., Suzuki N., Shimomura Y., Takeka S., Cho N.;

RT "MCH receptor antagonist";

RL Patent JP03075319-T/7, 16-FEB-2001.

XX TAKEDA CHEMICAL INDUSTRIES LTD.

XX OS Homo sapiens (human)

CC PN JP 03075319-T/7

CC PD 16-FEB-2001

CC PF 19-SEP-2000 JP 2000006376

CC PR 20-SEP-1999 JP 99P 266278, 17-JUL-2000 JP 00P 221055

CC PI KANEOSHI KATO, MASAOKI MORI, NOBORITO SUZUKI, YUKIO SHIMOMURA,

CC PI SHIRO TAKEKAWA,

CC PI NOBUO CHO

CC PC A61K31/137, A61K31/27, A61K31/4035, A61K31/44, A61K31/445,

CC PC A61K31/4453,

CC PC A61K31/472, A61P43/00, A61P31/04, C07D211/14, C07D211/18,

CC PC C07D211/46, C07D211/58

CC PC C07D211/70, C07D401/12, C07D405/12, C07D409/12, C07D417/12

CC CC

CC CC

CC FH

CC FT

CC FT

XX

XX

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DEFINITION BD013174
ACCESSION BD013174.1 GI:22093363
VERSION WO 0121169-A/13.
KEYWORDS Homo sapiens.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1283)
AUTHORS Kato,K., Mori,M., Suzuki,N., Shimomura,Y., Takekawa,S. and Cho,N.
TITLE MCH receptor antagonist
JOURNAL Patent: WO 0121169-A 13 29-MAR-2001;
TAKEDA CHEMICAL INDUSTRIES LTD, KANEYOSHI KATO, MASAOKI MORI, NOBUHIRO
SUZUKI, YUKIO SHIMOMURA, SHIRO TAKEKAWA, NOBUO CHO
COMMENT OS Homo sapiens (human)
PN WO 0121169-A/13
PD 29-MAR-2001
PE 19-SEP-2000 WO 2000JP006376
PR 20-SEP-1999 JP 99P 266278, 17-JUL-2000 JP 00P 221055 PI
KANEYOSHI KATO, MASAOKI MORI, NOBUHIRO SUZUKI, YUKIO SHIMOMURA PI
, SHIRO TAKEKAWA,
PI NOBUO CHO
PC A61K31/137, A61K31/27, A61K31/4035, A61K31/44, A61K31/445, PC
A61K31/4433,
PC A61K31/472, A61P43/00, A61P31/04, C07D211/14, C07D211/18 PC
, C07D211/46, C07D211/58,
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source 1..1283 Location/Qualifiers
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Score: 2207.00 Matches: 421
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.76% Mismatches: 0
Query Match: 99.77% Indels: 0
Gaps: 0
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Oy 41 GlyValArgArgTrpArgLeuProGlnProAlaTrpValGlyGlySerSerAlaArgLeu 60
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Oy 61 TrpGluGlnAlaThrGlyThrGlyTrpMetAspLeuGlnAlaSerLeuLeuProThrGly 80
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Oy 141 HisTrpCysAsnAsnValProAspIlePheIleIleAsnLeuSerValAlaAspLeuLeu 160
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Oy 161 PheLeuLeuGlyMetProPheMetIleHisGlnLeuMetGlyAsnGlyValTrpHisPhe 180
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Oy 201 TyrIleLeuThrAlaMetAlaIleAspArgTrpLeuAlaThrValHisProIleSerSer 220
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RESULT 8
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ID BD006655 standard; DNA; HUM; 1283 BP.


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XX AC BD006655;
XX SV BD006655.1
XX DT 08-FEB-2002 (rel. 70, Created)
XX DT 08-FEB-2002 (rel. 70, Last updated, Version 1)
XX DE MCH receptor antagonist.
XX KM JP 03075319-T/13.
XX OS Homo sapiens (human)
XX OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX [1]
XX RP 1-1283
XX RA Kato K., Mori M., Suzuki N., Shimomura Y., Takeka S., Cho N.;
XX RT "MCH receptor antagonist";
XX RL Patent number JP03075319-T/13, 16-FEB-2001.
XX RL TAKEDA CHEMICAL INDUSTRIES LTD.
XX OS Homo sapiens (human)
XX PN JP 03075319-T/13
XX PD 16-FEB-2001
XX PE 19-SEP-2000 JP 2000006376
XX PR 20-SEP-1999 JP 99P 266278, 17-JUL-2000 JP 00P 221055
XX PI KANEYOSHI KATO, MASAOKI MORI, NOBUHIRO SUZUKI, YUKIO SHIMOMURA,
XX PI SHIRO TAKEKAWA,
XX PC A61K31/137, A61K31/27, A61K31/4035, A61K31/44, A61K31/445,
XX PC A61K31/472, A61P43/00, A61P31/04, C07D211/14, C07D211/18,
XX PC A61K31/4453,
XX PC C07D211/46, C07D211/58,
XX PC C07D211/70, C07D401/12, C07D405/12, C07D409/12, C07D417/12
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Alignment Scores:
Pred. No.: 1,18e-148 Length: 1283
Score: 2207.00 Matches: 421
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.76% Mismatches: 0
Query Match: 99.77% Indels: 0
DB: 23 Gaps: 0

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QY 21 GlyCysGlnAlaThrGluGluAspProLeuProAspCysGlyAlaCysAlaProGlyGln 40
DB 68 GGTCTGACAGCTTACGAGGAGAGACCCCTTCCCAACTGCGGGCTTGGCTCCGGGACAA 127
QY 41 GlyGlyArgArgTrpArgLeuProGlnProAlaTrpValGluGlySerSerAlaArgLeu 60
DB 128 GGTGGAGGCGGCTGAGAGGCTGCGGACCTGCGTGGGTGGAGGAGGAGCTGAGCTCGGTG 187
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DB 188 TGGAGAGCGGAGCAACCGGCACTGGCTGGATGAGACCTGGAGACCTGCTGCCACTGTG 247
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DB 248 CCCAAGCCGAGCAACACCTTGATGGCCCGATACCTCACTTGGGAGATCACCTCTCT 307
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DEFINITION	Macaca mulatta melanin-concentrating hormone receptor subtype 1 (MCH1R) mRNA, complete cds.				
ACCESSION	AF513988				
VERSION	AF513988.1				
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SOURCE					
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 LOCUS
 DEFINITION Sequence 1 from patent US 6362326.
 ACCESSION AR202509
 VERSION AR202509.1 GI:20257048
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 3488)
 AUTHORS Sathe, G., Ellis, C.E., Halsey, W. and Bergsma, D.
 TITLE 11 cby genomic sequence
 JOURNAL Patent: US 6362326-A 1 26-MAR-2002;
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HS229A8
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DEFINITION Human DNA sequence from clone 229A8 on chromosome 22q13. Contains
3-phosphate dehydrogenase (EC 1.2.1.12) pseudogene, the gene for
SLC1 (G Protein-Coupled Receptor GPR24, 7 transmembrane receptor
D2S279, a ca repeat polymorphism and a putative CpG island,
complete sequence.
286090
VERSION 286090.10 GI:4972260
KEYWORDS HTG; ca repeat polymorphism; CPG Island; D2S279; GAMP; GPR24;
ribosomal protein L4; RPL4; SLC1.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 122557)
Lloyd, D.
DIRECT SUBMISSION
COMMENT Submitted (19-AUG-1999) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humqueny@sanger.ac.uk
Request: clone requests@sanger.ac.uk
On Jun 2, 1999 this sequence version replaced gi:4938278.
This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated human repeat sequence elements (e.g. Alu). Where the
sequence is ambiguous, there is an annotation using the 'unsure'
feature key.
This sequence was generated from part of bacterial clone contigs of
human chromosome 22, constructed by the Sanger Centre Chromosome 22
Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr22
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em: EMBL; SW: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence is
the entire insert of clone 229A8. The true right end of clone
591N18 (AL031594) is at 28405 in this sequence. The start of this
sequence overlaps with the end of sequence 298048.
229A8 is from the human BAC library described in U-J. Kim et al.
(1996) Genomics 34, 213-218. VECTOR: pBAC108L.
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US-09-885-478-2 (-1-422) x HS229A8 (1-122557)		
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 ACCESSION BD013173.1 GI:22093362
 VERSION WO 0121169-A/12.
 KEYWORDS Homo sapiens.
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 1 (bases 1 to 1074)
 Kato, K., Mori, M., Suzuki, N., Shimomura, Y., Takekawa, S. and Cho, N.
 MCH receptor antagonist.
 Patent: WO 0121169-A 12 29-MAR-2001.
 TAKEKAWA CHEMICAL INDUSTRIES LTD, KANEYOSHI KATO, MASAOKI MORI, NOBUHIRO
 SUZUKI, YUKIO SHIMOMURA, SHIRO TAKEKAWA, NOBUO CHO
 OS Homo sapiens (human)
 PN WO 0121169-A/12
 PD 29-MAR-2001
 PF 19-SEP-2000 WO 2000J006376
 PR 20-SEP-1999 JP 99P 266278, 17-JUL-2000 JP 00P 221055 PI
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 , SHIRO TAKEKAWA,
 PI NOBUO CHO
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Alignment Scores:

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SV BD006654.1
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DT 08-FEB-2002 (Rel. 70, Last updated, Version 1)
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XX JP 03075319-T/12.
XX KW Homo sapiens (human)
XX OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
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XX RN Kato K., Mori M., Suzuki N., Shimomura Y., Takeka S., Cho N.;
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XX CC PR 20-SEP-1999 JP 99P 266278, 17-JUL-2000 JP 00P 221055
XX CC PI KANEOSHI KATO, MASAOKI MORI, NOBUHIRO SUZUKI, YUKIO SHIMOMURA,
CC PI SHIRO TAKEKAWA,
CC PI NOBUO CHO
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VERSION AX280965.1 GI:16608240
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SOURCE human.
ORGANISM Homo sapiens
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AUTHORS Lehmann-Bruinsma, K., Liaw, C.W. and Lin, I.T.
TITLE Non-endogenous, constitutively activated known g protein-coupled receptors
JOURNAL Patent: WO 0177172-A 588 18-OCT-2001.
ARENA Pharmaceuticals, Inc. (US)
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XX      Novel nucleic acid encoding human melanin concentrating hormone
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XX      diabetes, whose mutant form is activated by melanin concentrating
XX      hormone -
XX      Claim 7; Fig 2; 173pp; English.
XX      Neuroregulators modulate communication in the nervous system. Melanin
XX      concentrating hormone 1 (MCH1) is one such neuroregulator. MCH may serve
XX      as an integrative neuropeptide, involved in stress response, feeding
XX      regulation and sexual activity. Also, MCH is thought to participate in
XX      water balance regulation, energy metabolism, general arousal/attention
XX      state, memory and cognitive functions and psychiatric disorders. The
XX      present sequence is the human MCH1 receptor. The present sequence is a
XX      G-protein coupled receptor and has 7 transmembrane regions. MCH1 receptor
XX      may be used in the therapy for a variety of disorders: steroid or
XX      pituitary hormone disorder, epinephrine release disorder,
XX      gastrointestinal disorder, cardiovascular release disorder, electrolyte balance
XX      disorder, hypertension, diabetes, respiratory disorder, asthma,
XX      reproductive function disorder, immune disorder, endocrine disorder,
XX      musculoskeletal disorder, neuroendocrine disorder, cognitive disorder,
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XX      transmission disorder, motor coordination disorder, sensory integration
XX      disorder, dopaminergic function disorder e.g. Parkinson's disease,
XX      olfaction disorder, sympathetic innervation disorder, depression, stress,
XX      fluid imbalance disorder, urinary disorder e.g. urinary incontinence,
XX      seizure, pain, psychotic behaviour e.g. schizophrenia, morphine
XX      tolerance, opiate addiction or migraine. The coding sequence for the
XX      present protein is also contained in plasmid pEX1.HR-TL231 (ATCC 203197).
XX      Sequence 422 AA;
XX      Query Match 100.0%; Score 2212; DB 21; Length 422;
XX      Best Local Similarity 100.0%; Pred. No. 1.2e-223;
XX      Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      241 FISTPVWILARLIPFGVAGGIRLPNDPTDLYWFTLQFELAPLFPVITAAVRI 300
DQ      241 FISTPVWILARLIPFGVAGGIRLPNDPTDLYWFTLQFELAPLFPVITAAVRI 300
QY      301 LQRTSSVAPASORSIRLRTKRVTRTAIAICLVFVCGWADPYVYLQTLQSLSPRTLFPY 360
DQ      301 LQRTSSVAPASORSIRLRTKRVTRTAIAICLVFVCGWADPYVYLQTLQSLSPRTLFPY 360
QY      361 LYNAISLGYANSCINFPYVIVLCETFRKRLVLSVRAAGGOLRAVNAQTADERTESK 420
DQ      361 LYNAISLGYANSCINFPYVIVLCETFRKRLVLSVRAAGGOLRAVNAQTADERTESK 420
QY      421 GT 422
DQ      421 GT 422

```

```

RESULT 2
ID      AAU75853
AAU75853 standard; Protein; 422 AA.
ID      AAU75853;
AAU75853;
08-MAY-2002 (first entry)
Human melanin concentrating hormone receptor, MCH1.
Human; melanin concentrating hormone receptor; MCH1;
steroid hormone disorder; pituitary hormone disorder;
epinephrine release disorder; gastrointestinal disorder;
cardiovascular disorder; hypertension; diabetes; respiratory disorder;
asthma; reproductive function disorder; immune disorder;
musculoskeletal disorder; neuroendocrine disorder; cognitive disorder;
memory disorder; motor coordination disorder; obesity; eating disorder;
dopaminergic function disorder; pain; psychosis; opiate addiction;
affective disorder; migraine; transgenic.
Homo sapiens.
WO200202744-A2.
10-JAN-2002.
05-JUL-2001; 2001WO-US21350.
05-JUL-2000; 2000US-0610635.
(SYNA-) SYNAPTIC PHARM CORP.
Salon JA, Laz TM, Nagorny R, Wilson AE;
WPI; 2002-164532/21.
N-PSDB; ABR14548.
Purified human melanin concentrating hormone receptor protein and
polynucleotides for screening modulator useful for treating memory
disorder, sensory modulation and transmission disorder, motor
coordination disorder -
Example; Fig 2; 524pp; English.
The invention relates to a purified human melanin concentrating hormone
(MCH1) receptor protein and its encoding nucleic acid (or mutant
activated by MCH or its analogue or homologue). Also included are
expression vectors, probes, transformed insect cells, antisense
oligonucleotides, anti-MCH1 antibodies, an agent capable of inhibiting
the binding of the antibody to MCH1, a transgenic animal expressing the
protein, or a homologous knockout or antisense complementary to the MCH1
nucleic acid, ant/agonists of MCH1, and methods of isolating chemical
compounds which activate MCH1. The protein, nucleic acid, antibody,
ant/agonists and compound are useful for diagnosing and treating a
steroid or pituitary hormone disorder, an epinephrine release disorder, a
gastrointestinal disorder, cardiovascular disorder, electrolyte balance

```

CC disorder, hypertension, diabetes, respiratory disorder, asthma,
CC reproductive function disorder, immune disorder, endocrine disorder,
CC musculoskeletal disorder, neuroendocrine disorder, cognitive disorder,
CC memory disorder, sensory modulation and transmission disorder, motor
CC coordination disorder, sensory integration disorder, motor integration
CC disorder, dopaminergic function disorder, sensory transmission disorder,
CC olfaction disorder, sympathetic innervation disorder, pain, psychotic
CC behaviour, morphine tolerance, opiate addiction, affective disorder,
CC stress-related disorder, fluid-balance disorder, seizure disorder or
CC migraine, an eating disorder or obesity. The present sequence
CC represents human MCH1.

XX Sequence 422 AA;

Query Match 100.0%; Score 2212; DB 23; Length 422;

Best Local Similarity 100.0%; Pred. No. 1.2e-223; Mismatches 0; Indels 0; Gaps 0;

Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSVGAMKGVRAVGLGGSGCQATEEDPLPCGACAPGGGGRMRLLPPAWVEGSSARL 60

DB 1 MSVGAMKGVRAVGLGGSGCQATEEDPLPCGACAPGGGGRMRLLPPAWVEGSSARL 60

QY 61 WEQATGTGMDLEASLLPTGPNASNTSDGPDNLTSAGSPPTGSISYINIMPSVFGTIC 120

DB 61 WEQATGTGMDLEASLLPTGPNASNTSDGPDNLTSAGSPPTGSISYINIMPSVFGTIC 120

QY 121 LLGIIIGNSTVFAYVKKSKLHMCNNVPDITINLSVVDLLFLGMPFMIHQLMGNCVWHF 180

DB 121 LLGIIIGNSTVFAYVKKSKLHMCNNVPDITINLSVVDLLFLGMPFMIHQLMGNCVWHF 180

QY 181 GETMCTLTAMDANSQFTSYIILFAMAIDRYLATVHPISSTKFRKPSVATLVICLMAALS 240

DB 181 GETMCTLTAMDANSQFTSYIILFAMAIDRYLATVHPISSTKFRKPSVATLVICLMAALS 240

QY 241 FISTPFWLVARLLPPFGAGVCGIRLPNPDTLWFTLYQFLAALPFWVITAAVYRI 300

DB 241 FISTPFWLVARLLPPFGAGVCGIRLPNPDTLWFTLYQFLAALPFWVITAAVYRI 300

QY 301 LQRTSSVAPASQSRIRLTKRVRTAIAICLVFVCMARYVYLQTLQSLSPRTLTFYV 360

DB 301 LQRTSSVAPASQSRIRLTKRVRTAIAICLVFVCMARYVYLQTLQSLSPRTLTFYV 360

QY 361 LYNAAISLGVANSCINLPFVYIVLCETFRKRLVLSVKPAAGQLRAVSNQTADEERTESK 420

DB 361 LYNAAISLGVANSCINLPFVYIVLCETFRKRLVLSVKPAAGQLRAVSNQTADEERTESK 420

QY 421 GT 422

DB 421 GT 422

RESULT 3
AAB12779 standard; Protein; 422 AA.

XX AAB12779;

DT 22-NOV-2000 (first entry)

DE Human SLC-1 protein sequence SEQ ID NO:11.

XX SLC-1; MHC; melanin concentrating hormone; screening; eating;

KW appetite stimulator; appetite regulator; period pain; atonic bleeding;

KW caesarean section; milk congestion; antibiotic agent; drug;

KW foetal asphyxia; cervical rupture; premature birth; uterine rupture;

KW Prader-Willi syndrome; anorectic; gynaecological; abortifacient;

XX antoanaemia; anabolic; orphan G protein-couple receptor protein.

OS Homo sapiens.
XX
XX WO200040725-A1.
XX
XX 13-JUL-2000.
PD

XX 27-DEC-1999; 99WO-JP07336.
XX 28-DEC-1998; 98JP-0374454.
PR 28-APR-1999; 99JP-0122688.
PR 02-SEP-1999; 99JP-0249300.
XX (TAKE) TAKEDA CHEM IND LTD.
XX Mori M, Shlomura Y, Takekawa S, Sugo T, Ishibashi Y, Kitada C;
PI Suzuki N;
XX WPI: 2000-475832/41.
DR N-PSDB: AAA72918.

PT Screening methods for compounds as SLC-1 (ant)agonists useful in the
PT treatment of eating disorders and as preventives and remedies for e.g.
PT atonic bleeding and Prader-Willi syndrome -
XX Claim 6; Page 111-113; 123pp; Japanese.

CC The present invention describes a method for screening components (I) or
CC their salts that can alter the binding properties of melanin-
CC concentrating hormone (MCH) or its derivative or salt to SLC-1 or its
CC salt. Compounds identified by (I) are useful as SLC-1 (ant)agonists in
CC eating disorders and as preventives and remedies for e.g. period pain,
CC uterine recovery failure, caesarean section, artificial interruption of
CC pregnancy, galactostasis, tonic uterine contraction, foetal asphyxia,
CC syndrome of uterus, cervical rupture, premature birth and Prader-Willi
CC syndrome. The present sequence represents the human SLC-1 protein
CC sequence, which is used in an example from the present invention.

XX Sequence 422 AA;

Query Match 99.8%; Score 2207; DB 21; Length 422;

Best Local Similarity 99.8%; Pred. No. 3.9e-223; Mismatches 421; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSVGAMKGVRAVGLGGSGCQATEEDPLPCGACAPGGGGRMRLLPPAWVEGSSARL 60

DB 1 MSVGAMKGVRAVGLGGSGCQATEEDPLPCGACAPGGGGRMRLLPPAWVEGSSARL 60

QY 61 WEQATGTGMDLEASLLPTGPNASNTSDGPDNLTSAGSPPTGSISYINIMPSVFGTIC 120

DB 61 WEQATGTGMDLEASLLPTGPNASNTSDGPDNLTSAGSPPTGSISYINIMPSVFGTIC 120

QY 121 LLGIIIGNSTVFAYVKKSKLHMCNNVPDITINLSVVDLLFLGMPFMIHQLMGNCVWHF 180

DB 121 LLGIIIGNSTVFAYVKKSKLHMCNNVPDITINLSVVDLLFLGMPFMIHQLMGNCVWHF 180

QY 181 GETMCTLTAMDANSQFTSYIILFAMAIDRYLATVHPISSTKFRKPSVATLVICLMAALS 240

DB 181 GETMCTLTAMDANSQFTSYIILFAMAIDRYLATVHPISSTKFRKPSVATLVICLMAALS 240

QY 241 FISTPFWLVARLLPPFGAGVCGIRLPNPDTLWFTLYQFLAALPFWVITAAVYRI 300

DB 241 FISTPFWLVARLLPPFGAGVCGIRLPNPDTLWFTLYQFLAALPFWVITAAVYRI 300

QY 301 LQRTSSVAPASQSRIRLTKRVRTAIAICLVFVCMARYVYLQTLQSLSPRTLTFYV 360

DB 301 LQRTSSVAPASQSRIRLTKRVRTAIAICLVFVCMARYVYLQTLQSLSPRTLTFYV 360

QY 361 LYNAAISLGVANSCINLPFVYIVLCETFRKRLVLSVKPAAGQLRAVSNQTADEERTESK 420

DB 361 LYNAAISLGVANSCINLPFVYIVLCETFRKRLVLSVKPAAGQLRAVSNQTADEERTESK 420

QY 421 GT 422

DB 421 GT 422

RESULT 4
AAE07330

[illegible]

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Db      241 FISTIPWVLVRLRIPPEGAGVCSIRLPNDPTDLIWTTLQFPLAFRLPVPVITAAVR 300
Oy      301 LQRTSSVAPASQSRISIRLTKRVTRTAIALCLVEFVQVAPYYVLQTLQSLSRPTLTFVY 360
Db      301 LQRTSSVAPASQSRISIRLTKRVTRTAIALCLVEFVQVAPYYVLQTLQSLSRPTLTFVY 360
Oy      361 LYNAAISIGVANSCLINPFVYIVLCETPRKRLVLSVKRAAGQLRAVSNNAQTADERESK 420
Db      361 LYNAAISIGVANSCLINPFVYIVLCETPRKRLVLSVKRAAGQLRAVSNNAQTADERESK 420
Oy      421 GT 422
Db      421 GT 422

RESULT 5
AAB81123
ID      AAB81123 standard; Protein; 422 AA.
XX
XX      AAB81123;
XX
XX      05-JUL-2001 (first entry)
XX
XX      Human melanin concentrating hormone receptor (SLC-1).
XX
XX      Melanin concentrating hormone; MCH; antagonist; diamine compound;
XX      anorectic; antidiabetic; ophthalmological; neuroprotective; nephrotropic;
XX      antiarteriosclerotic; antiarthritic; obesity; diabetes; arteriosclerosis;
XX      arthritis; melanin concentrating hormone receptor; SLC-1; human.
XX
XX      Homo sapiens.
XX
XX      WO200121169-A1.
XX
XX      29-MAR-2001.
XX
XX      19-SEP-2000; 2000MO-JP06376.
XX
XX      20-SEP-1999; 99JP-0266278.
XX      17-JUL-2000; 2000JP-0221055.
XX
XX      (TAKE ) TAKEDA CHEM IND LTD.
XX
XX      Kato K, Mori M, Suzuki N, Shimomura Y, Takekawa S, Choh N;
XX      WPI; 2001-328055/34.
XX      DR      N-PSDB; AAF86229.
XX
XX      Melanin concentrating hormone antagonists comprise new and known
XX      diamine compounds for treating obesity -
XX
XX      Examples; Page 271-273; 284pp; Japanese.
XX
XX      This invention relates to melanin concentrating hormone (MCH)
XX      antagonists, comprising a diamine compound or its prodrug and/or salt.
XX      Use of the MCH antagonists can result in anorectic, antidiabetic,
XX      ophthalmological, neuroprotective, nephrotropic, antiarteriosclerotic,
XX      and antiarthritic activity. Melanin concentrating hormone (MCH)
XX      antagonists can be used for treating obesity (e.g. exogenous obesity,
XX      hypophyseal adiposity, hypothalamic obesity and hyperphagia) and
XX      associated disorders such as diabetes, diabetic complications (such as
XX      diabetic retinopathy, diabetic neuropathy and diabetic nephropathy),
XX      arteriosclerosis and arthritis in the knees. The present sequence
XX      represents the human melanin concentrating hormone receptor (SLC-1). The
XX      SLC-1 cDNA is used in examples to demonstrate the use of the antagonists
XX      of the invention.
XX
XX      Sequence      422 AA;
XX
Query Match      99.8%; Score 2207; DB 22; Length 422;
Best Local Similarity 99.8%; Pred. No. 3,9e-23;
Matches 421; Conservative 1; Mismatches 0; Indels 0; Gaps 0.

```

```

QY 1 MSVGMKKGVGRAVGLGGSGCQATEEDPLPDGACAPGCGGRRWRLPQPAWEGSSARL 60
DB 1 MSVGMKKGVGRAVGLGGSGCQATEEDPLPDGACAPGCGGRRWRLPQPAWEGSSARL 60
QY 61 WEQATGTGMDLEASLPTGPNASNTSDGPDNLTSAGSPRTGISYINIMPSVETGIC 120
DB 61 WEQATGTGMDLEASLPTGPNASNTSDGPDNLTSAGSPRTGISYINIMPSVETGIC 120
QY 121 LLGIIGNSTVIFAVVKKSKLHMCNNVPDIFILNSVVDLFLLGMPFMIHQMGNGVMHF 180
DB 121 LLGIIGNSTVIFAVVKKSKLHMCNNVPDIFILNSVVDLFLLGMPFMIHQMGNGVMHF 180
QY 181 GETMCTLTITAMDANSQFTSYIILTAMADRYLATVHPDISSTKFRKPSVATVLCILMALS 240
DB 181 GETMCTLTITAMDANSQFTSYIILTAMADRYLATVHPDISSTKFRKPSVATVLCILMALS 240
QY 241 FISITPWLVARLIPFPGAGVCGIRLPNPDOLDYMTLQFOFLAPALPFWVITAAYVR 300
DB 241 FISITPWLVARLIPFPGAGVCGIRLPNPDOLDYMTLQFOFLAPALPFWVITAAYVR 300
QY 301 LQRMSSVAPASQSRISRLTKRVRTRTAIAICLVFVCMAPYVYLQTLQSLISRPITLFEY 360
DB 301 LQRMSSVAPASQSRISRLTKRVRTRTAIAICLVFVCMAPYVYLQTLQSLISRPITLFEY 360
QY 361 LYNAISIGVANSCLNPVYIVLCETFRKRLVLSVKPAAGOLRAVNAQTADERTESK 420
DB 361 LYNAISIGVANSCLNPVYIVLCETFRKRLVLSVKPAAGOLRAVNAQTADERTESK 420
QY 421 GT 422
DB 421 GT 422

RESULT 6
AAB96871
ID AAB96871 standard; Protein: 422 AA.
AC AAB96871;
XX
DT 06-JUL-2001 (first entry)
DE Human SLC-1.
XX
KW Rat; human; SLC-1; MCH receptor; melanin-concentrating hormone;
KW obesity; diabetes; hypertension; arteriosclerosis; hyperphagia;
KW emotional disorder; reproductive disorder; memory disorder;
KW dementia; hormonal disorder; gonitis.
XX
OS Homo sapiens.
XX
PN WO200121577-A2.
PD
XX
XX 29-MAR-2001.
PE 19-SEP-2000; 2000WO-JP06375.
XX
XX 20-SEP-1999; 99JP-0266298.
PR 16-DEC-1999; 99JP-0357889.
XX
XX 20-APR-2000; 2000JP-0126272.
PA (TAKE ) TAKEDA CHEM IND LTD.
XX
XX Kato K, Terauchi J, Mori M, Suzuki N, Shimomura Y, Takekawa S;
PI Ishihara Y;
XX
XX WPI: 2001-354775/37.
DR N-PSDB; AAF86975.
XX
XX New aromatic compounds are melanin concentrating hormone antagonists,
XX useful as anorectic agents, for treating or preventing obesity, also
XX memory or hormonal disorders or diabetes
XX
XX Examples; Page 358-360; 363pp; English.

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XX
XX The present invention describes aromatic compounds capable of acting as
CC melanin-concentrating hormone (MCH) antagonists. Melanin-concentrating
CC hormone is an appetite control factor and antagonists were expected to be
CC useful as anti-obesity agents. They can be used in the treatment of
CC obesity, including malignant mastocytosis, exogenous, hyperinsular,
CC hypoplasmic, hypothyroid, hypothalamic, symptomatic, infantile, upper
CC body, alimentary, hypogonadal, simple and central obesity, systemic
CC mastocytosis and hypophyseal adiposity, hypertension, arteriosclerosis,
CC hyperphagia, emotional disorders, reproductive function disorders, memory
CC disorders, dementia, hormonal disorders, diabetes and gonitis. MCH binds
CC to the SLC-1 receptor. The present sequence is the human SLC-1 protein
CC sequence.
SQ Sequence 422 AA;
XX
XX Query Match 99.8%; Score 2207; DB 22; Length 422;
XX Best Local Similarity 99.8%; Pred. No. 3.9e-223;
XX Matches 421; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSVGMKKGVGRAVGLGGSGCQATEEDPLPDGACAPGCGGRRWRLPQPAWEGSSARL 60
DB 1 MSVGMKKGVGRAVGLGGSGCQATEEDPLPDGACAPGCGGRRWRLPQPAWEGSSARL 60
QY 61 WEQATGTGMDLEASLPTGPNASNTSDGPDNLTSAGSPRTGISYINIMPSVETGIC 120
DB 61 WEQATGTGMDLEASLPTGPNASNTSDGPDNLTSAGSPRTGISYINIMPSVETGIC 120
QY 121 LLGIIGNSTVIFAVVKKSKLHMCNNVPDIFILNSVVDLFLLGMPFMIHQMGNGVMHF 180
DB 121 LLGIIGNSTVIFAVVKKSKLHMCNNVPDIFILNSVVDLFLLGMPFMIHQMGNGVMHF 180
QY 181 GETMCTLTITAMDANSQFTSYIILTAMADRYLATVHPDISSTKFRKPSVATVLCILMALS 240
DB 181 GETMCTLTITAMDANSQFTSYIILTAMADRYLATVHPDISSTKFRKPSVATVLCILMALS 240
QY 241 FISITPWLVARLIPFPGAGVCGIRLPNPDOLDYMTLQFOFLAPALPFWVITAAYVR 300
DB 241 FISITPWLVARLIPFPGAGVCGIRLPNPDOLDYMTLQFOFLAPALPFWVITAAYVR 300
QY 301 LQRMSSVAPASQSRISRLTKRVRTRTAIAICLVFVCMAPYVYLQTLQSLISRPITLFEY 360
DB 301 LQRMSSVAPASQSRISRLTKRVRTRTAIAICLVFVCMAPYVYLQTLQSLISRPITLFEY 360
QY 361 LYNAISIGVANSCLNPVYIVLCETFRKRLVLSVKPAAGOLRAVNAQTADERTESK 420
DB 361 LYNAISIGVANSCLNPVYIVLCETFRKRLVLSVKPAAGOLRAVNAQTADERTESK 420
QY 421 GT 422
DB 421 GT 422

RESULT 7
AAY97670
ID AAY97670 standard; Protein: 422 AA.
AC AAY97670;
XX
XX 08-MAY-2001 (first entry)
DE Human MCH-R3 protein sequence.
XX
XX Human MCH-R3 protein sequence.
XX
XX Human; melanin-concentrating hormone receptor; MCH-R1; MCH-R2; MCH-R3;
KW weight loss; weight gain; cancer; pain; diabetes; stress; therapy;
KW sexual dysfunction.
XX
XX Homo sapiens.
XX
XX WO200105947-A1.
XX
XX 25-JAN-2001.
XX

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PF 10-JUL-2000; 2000WO-US18733.
 XX
 XX 14-JUL-1999; 99US-0143706.
 XX
 XX (MERI) MERCK & CO INC.
 PA
 XX Howard AD;
 PI
 XX WPI; 2001-159528/16.
 DR N-PSDB; AAA91189, AAA91192.
 XX
 PT Melanin-concentrating hormone receptor polypeptides for increasing or
 PT decreasing appetite, reducing stress and to screen for compounds that
 PT bind to the receptor -
 XX
 XX
 XX Claim 21; Page 23; 43pp; English.
 XX
 CC This sequence is a melanin-concentrating hormone (MCH) receptor
 CC protein of the invention, designated MCH-R3. MCH receptor fragments and
 CC polypeptides are useful in assays to screen for compounds that bind to
 CC the MCH receptor and modulate the activity of the receptor. MCH Receptor
 CC activity is modulated to achieve weight loss, weight gain, to treat
 CC cancer (e.g. colon or breast), reduce pain, treat diabetes, reduce stress
 CC or treat sexual dysfunction. Nucleic acid coding for the MCH receptor can
 CC be used to cause an increase in appetite and to create a test system
 CC (e.g. a transgenic animal) for screening for compounds affecting MCH
 CC receptor expression. Inhibition of MCH receptor nucleic acid activity is
 CC useful to inhibit appetite or stress.
 CC
 XX
 XX Sequence 422 AA:
 SO
 Query Match 99.8%; Score 2207; DB 22; Length 422;
 Best Local Similarity 99.8%; Pred. No. 3.9e-223;
 Matches 421; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 MSVGAMKKYGRAVGLGGSGCQATEEDPLPDCGACAPGGGGRMRLLPQPAWEGSSARL 60
 1 MSVGAMKKYGRAVGLGGSGCQATEEDPLPNCGACAPGGGGRMRLLPQPAWEGSSARL 60
 61 WEQATGTGMMDLEASLLPTGPNASNTSDGPDNLTSAGSPRTGSISYINIMPSVFGTIC 120
 61 WEQATGTGMMDLEASLLPTGPNASNTSDGPDNLTSAGSPRTGSISYINIMPSVFGTIC 120
 61 WEQATGTGMMDLEASLLPTGPNASNTSDGPDNLTSAGSPRTGSISYINIMPSVFGTIC 120
 121 LGIGTGSTVFAYVKKSKLHWCNNVPDIFITNLSVVDLFLGMPFMIHQLMGNGVWHF 180
 121 LGIGTGSTVFAYVKKSKLHWCNNVPDIFITNLSVVDLFLGMPFMIHQLMGNGVWHF 180
 121 LGIGTGSTVFAYVKKSKLHWCNNVPDIFITNLSVVDLFLGMPFMIHQLMGNGVWHF 180
 181 GETMCTLTITAMDANSQFTSTYIITLTAIDRYLATVHPDISSTKFRKPSVATLVICLMAIS 240
 181 GETMCTLTITAMDANSQFTSTYIITLTAIDRYLATVHPDISSTKFRKPSVATLVICLMAIS 240
 181 GETMCTLTITAMDANSQFTSTYIITLTAIDRYLATVHPDISSTKFRKPSVATLVICLMAIS 240
 241 FISTTPVWLARLIPFGGAVGCGIRLPNPDLDLYWFTLYQFLALPFPVVTAAVRI 300
 241 FISTTPVWLARLIPFGGAVGCGIRLPNPDLDLYWFTLYQFLALPFPVVTAAVRI 300
 241 FISTTPVWLARLIPFGGAVGCGIRLPNPDLDLYWFTLYQFLALPFPVVTAAVRI 300
 301 LQRMSSVAPASORSIRLTKRVRTALAIQVFFVCMAPIYVQLTOLISIRPTLTFVY 360
 301 LQRMSSVAPASORSIRLTKRVRTALAIQVFFVCMAPIYVQLTOLISIRPTLTFVY 360
 301 LQRMSSVAPASORSIRLTKRVRTALAIQVFFVCMAPIYVQLTOLISIRPTLTFVY 360
 361 LYNAISIGYANSCINPFIYIVLCETFRKRLVSVKPAAGQLRAVNSAQTADERTESK 420
 361 LYNAISIGYANSCINPFIYIVLCETFRKRLVSVKPAAGQLRAVNSAQTADERTESK 420
 361 LYNAISIGYANSCINPFIYIVLCETFRKRLVSVKPAAGQLRAVNSAQTADERTESK 420
 421 GT 422
 421 GT 422
 421 GT 422

RESULT 8
 AAB85894
 ID AAB85894 standard; Protein: 422 AA.
 XX
 AC AAB85894;

XX
 DT 30-NOV-2001 (first entry)
 XX
 XX Human long form MCHIR sequence.
 DE
 XX Melanin concentrating hormone receptor; MCHR; MCH; chimeric; fusion;
 XX fluorescent polypeptide; orexigenic; anabolic; food intake; MCHIR.
 KW
 XX Homo sapiens.
 OS
 XX WO200168706-A1.
 PN
 XX 20-SEP-2001.
 PD
 XX 14-MAR-2001; 2001WO-US08071.
 PF
 XX 15-MAR-2000; 2000US-0189698.
 PR
 XX (MERI) MERCK & CO INC.
 PA
 XX Marsh DJ;
 XX
 XX WPI; 2001-565791/63.
 DR N-PSDB; AAA47297.
 XX
 XX Fusion proteins comprising melanin concentrating hormone receptor
 PT peptides and fluorescent proteins, useful for identifying appetite
 PT stimulants -
 PT
 XX
 XX Claim 1; Page 12-13; 71pp; English.
 XX
 XX The invention provides melanin concentrating hormone (MCH) receptor
 CC (MCHR) chimeric and fusion proteins. The MCHR chimeric proteins comprise
 CC MCHR polypeptide regions from different species. The MCHR fusion protein
 CC comprise MCHR polypeptide region and a fluorescent polypeptide region
 CC joined directly, or via a linker, to the carboxy side of the MCHR
 CC polypeptide region. The MCHR fusion proteins can be expressed by standard
 CC recombinant methodology. MCH action promotes feeding (orexigenic) and up
 CC regulation of MCH activity stimulates food intake. The present sequence
 CC represents a human long form MCHIR protein sequence.
 CC
 XX
 XX Sequence 422 AA:
 SO
 Query Match 99.8%; Score 2207; DB 22; Length 422;
 Best Local Similarity 99.8%; Pred. No. 3.9e-223;
 Matches 421; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 MSVGAMKKYGRAVGLGGSGCQATEEDPLPDCGACAPGGGGRMRLLPQPAWEGSSARL 60
 1 MSVGAMKKYGRAVGLGGSGCQATEEDPLPNCGACAPGGGGRMRLLPQPAWEGSSARL 60
 61 WEQATGTGMMDLEASLLPTGPNASNTSDGPDNLTSAGSPRTGSISYINIMPSVFGTIC 120
 61 WEQATGTGMMDLEASLLPTGPNASNTSDGPDNLTSAGSPRTGSISYINIMPSVFGTIC 120
 61 WEQATGTGMMDLEASLLPTGPNASNTSDGPDNLTSAGSPRTGSISYINIMPSVFGTIC 120
 121 LGIGTGSTVFAYVKKSKLHWCNNVPDIFITNLSVVDLFLGMPFMIHQLMGNGVWHF 180
 121 LGIGTGSTVFAYVKKSKLHWCNNVPDIFITNLSVVDLFLGMPFMIHQLMGNGVWHF 180
 121 LGIGTGSTVFAYVKKSKLHWCNNVPDIFITNLSVVDLFLGMPFMIHQLMGNGVWHF 180
 181 GETMCTLTITAMDANSQFTSTYIITLTAIDRYLATVHPDISSTKFRKPSVATLVICLMAIS 240
 181 GETMCTLTITAMDANSQFTSTYIITLTAIDRYLATVHPDISSTKFRKPSVATLVICLMAIS 240
 181 GETMCTLTITAMDANSQFTSTYIITLTAIDRYLATVHPDISSTKFRKPSVATLVICLMAIS 240
 241 FISTTPVWLARLIPFGGAVGCGIRLPNPDLDLYWFTLYQFLALPFPVVTAAVRI 300
 241 FISTTPVWLARLIPFGGAVGCGIRLPNPDLDLYWFTLYQFLALPFPVVTAAVRI 300
 241 FISTTPVWLARLIPFGGAVGCGIRLPNPDLDLYWFTLYQFLALPFPVVTAAVRI 300
 301 LQRMSSVAPASORSIRLTKRVRTALAIQVFFVCMAPIYVQLTOLISIRPTLTFVY 360
 301 LQRMSSVAPASORSIRLTKRVRTALAIQVFFVCMAPIYVQLTOLISIRPTLTFVY 360
 301 LQRMSSVAPASORSIRLTKRVRTALAIQVFFVCMAPIYVQLTOLISIRPTLTFVY 360
 361 LYNAISIGYANSCINPFIYIVLCETFRKRLVSVKPAAGQLRAVNSAQTADERTESK 420
 361 LYNAISIGYANSCINPFIYIVLCETFRKRLVSVKPAAGQLRAVNSAQTADERTESK 420
 361 LYNAISIGYANSCINPFIYIVLCETFRKRLVSVKPAAGQLRAVNSAQTADERTESK 420

Db 361 LYNAISLGYANSCNLPFYIVLCETFRKRLVSVKPAAGOLRAVSNQTADEERTSK 420
 QY 421 GT 422
 Db 421 GT 422

RESULT 9
 AAU77541
 ID AAU77541 standard; Protein; 422 AA.

AC AAU77541;
 XX
 DT 05-JUN-2002 (first entry)
 XX
 DE Human melanin concentrating hormone receptor, SLC-1.
 XX
 KW G protein-coupled orphan; receptor; SRT; melanin-concentrating hormone;
 KW MCH; appetite-stimulating agent; obesity; malignant mastocytosis;
 KW exogenous obesity; hyperinsulinar obesity; sexual function disorder;
 KW overpowering intermittent pain; still born; uterus rupture;
 KW premature birth; Prader-Willi syndrome; SLC-1; human.
 XX
 OS Homo sapiens.
 XX
 PN W0200203070-A1.
 XX
 PD 10-JAN-2002.
 XX
 PE 04-JUL-2001; 2001WO-JP05809.
 XX
 PR 05-JUL-2000; 2000JP-0208254.
 XX
 XX (TAKE) TAKEDA CHEM IND LTD.
 XX
 PA Mori M, Shimomura Y, Harada M, Sugo T, Shintani Y;
 PI WPI: 2002-164552/21.
 DR N-PSDB; ABK10854.
 XX
 PT Screening for compounds or salts which alter affinity of
 PT melanin-concentrating hormone with its receptor to provide agonists as
 PT appetite-stimulating agents and its antagonist for preventing or
 PT treating obesity, uses a protein or hormone -
 PS
 PS Disclosure; Page 103-105; 112pp; Japanese.
 XX
 CC The invention describes a method of screening for compounds or their
 CC salts that can change affinity of melanin-concentrating hormone (MCH)
 CC with its G protein-coupled orphan receptor protein, SRT. The screened
 CC MCH receptor agonists are useful as appetite-stimulating agents and its
 CC antagonist for preventing or treating obesity e.g. malignant
 CC mastocytosis, exogenous obesity and hyperinsulinar obesity, and also
 CC for treating sexual function disorders, overpowering intermittent pains,
 CC still borns, uterus rupture, premature birth and Prader-Willi syndrome.
 CC This is the amino acid sequence of the human melanin concentrating
 CC hormone SLC-1, described in the invention.
 XX
 XX Sequence 422 AA;
 SO

Query Match 99.8%; Score 2207; DB 23; Length 422;
 Best Local Similarity 99.8%; Pred. No. 3,9e-223;
 Matches 421; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSVGAMKKGVRAVGLGGSCCATTEBDPLPCGACAPGGGGRMRLLPQPAWEGSSARL 60
 Db 1 MSVGAMKKGVRAVGLGGSCCATTEBDPLPCGACAPGGGGRMRLLPQPAWEGSSARL 60
 QY 61 WEQATGTCMDLEASLLPTGPNASNTSDGPDNLTSAGSPRTSISYINIMPSVGTIC 120
 Db 61 WEQATGTCMDLEASLLPTGPNASNTSDGPDNLTSAGSPRTSISYINIMPSVGTIC 120
 QY 121 LIGIINSTVIFAVVKRSKLMCNNDPIFIINLSVVDLLFLGMPFMHQLMGNGVWHF 180

Db 121 LIGIINSTVIFAVVKRSKLMCNNDPIFIINLSVVDLLFLGMPFMHQLMGNGVWHF 180
 QY 181 GETMCTILITAMDANSQFTSYIITAMAIDRYLATVHPISSTFRKPSATLVICLMLALS 240
 Db 181 GETMCTILITAMDANSQFTSYIITAMAIDRYLATVHPISSTFRKPSATLVICLMLALS 240
 QY 241 FISTTPWMLYARLIPFGAGVGGCIRLPNDPDLVYFTLYQFLEAFALPEFVITAAVRI 300
 Db 241 FISTTPWMLYARLIPFGAGVGGCIRLPNDPDLVYFTLYQFLEAFALPEFVITAAVRI 300
 QY 301 LQRTSSVAPASQSRIRLRTKRVTRTAIAICLVFVCMAPIYVLOTQLSISRPPLTFVY 360
 Db 301 LQRTSSVAPASQSRIRLRTKRVTRTAIAICLVFVCMAPIYVLOTQLSISRPPLTFVY 360
 QY 361 LYNAISLGYANSCNLPFYIVLCETFRKRLVSVKPAAGOLRAVSNQTADEERTSK 420
 Db 361 LYNAISLGYANSCNLPFYIVLCETFRKRLVSVKPAAGOLRAVSNQTADEERTSK 420
 QY 421 GT 422
 Db 421 GT 422

RESULT 10
 ABB04941
 ID ABB04941 standard; Protein; 422 AA.
 XX
 AC ABB04941;
 XX
 DT 14-MAR-2002 (first entry)
 XX
 DE Human SLC-1 protein SEQ ID NO:9.
 XX
 KW Human; SLC-1; melanin concentrating hormone antagonist; obesity;
 KW anorectic; antidiabetic; hypotensive; antidiarteriosclerotic;
 KW diabetes; hypertension; arteriosclerosis.
 XX
 OS Homo sapiens.
 XX
 PN W0200182925-A1.
 XX
 PD 08-NOV-2001.
 XX
 PE 26-APR-2001; 2001WO-JP03614.
 XX
 PR 28-APR-2000; 2000JP-0134295.
 XX
 PR 13-DEC-2000; 2000JP-0384897.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Ishihara Y, Suzuki N, Takekawa S;
 DR WPI: 2002-075131/10.
 DR N-PSDB; ABA92411.
 XX
 PT Melanin aggregating hormone antagonist for treating obesity -
 PT
 PS
 PS Example; Page 210-212; 223pp; Japanese.
 XX
 CC The present invention describes a melanin aggregating hormone antagonist
 CC (1). (1) has anorectic, antidiabetic, antidiarteriosclerotic and
 CC hypotensive. (1) can be used in the treatment and prevention of obesity.
 CC It may be combined with treatments for diabetes, hypertension or
 CC arteriosclerosis. The present sequence represents human SLC-1, which is
 CC used the exemplification of the present invention.
 XX
 XX Sequence 422 AA;
 SO

Query Match 99.8%; Score 2207; DB 23; Length 422;
 Best Local Similarity 99.8%; Pred. No. 3,9e-223;
 Matches 421; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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OY 1 MSVGAMKKGVGRVGLGGSGCOATEEDPLPDCGACAPGGGGRWRRLPQPAWEGSSARL 60
DB 1 MSVGAMKKGVGRVGLGGSGCOATEEDPLPNCGACAPGGGGRWRRLPQPAWEGSSARL 60
OY 61 WEQATGTGMDLEASLLPTGPNASNTSDGPDNLTSSAGSPRTGSISYINIMPSVEGTIC 120
DB 61 WEQATGTGMDLEASLLPTGPNASNTSDGPDNLTSSAGSPRTGSISYINIMPSVEGTIC 120
OY 121 LLGTTGNSVTIFAAYVKKSKLHMCNNVPDIFITINSVDLFLGMPFIHOLMGNGVWHR 180
DB 121 LLGTTGNSVTIFAAYVKKSKLHMCNNVPDIFITINSVDLFLGMPFIHOLMGNGVWHR 180
OY 181 GETMCTLTAMDANSQFTSYITLTAMAIDRYLATVHPISSTKRRKPSVATLVICLMAALS 240
DB 181 GETMCTLTAMDANSQFTSYITLTAMAIDRYLATVHPISSTKRRKPSVATLVICLMAALS 240
OY 241 FISTTPWMLYARLIPFGGAVGCGIRLPNDPLXWFTLYOFFLAFALPFWITAAVRI 300
DB 241 FISTTPWMLYARLIPFGGAVGCGIRLPNDPLXWFTLYOFFLAFALPFWITAAVRI 300
OY 301 LQRMSSVAPASORSIRLTKRVRTAIAICLVFVCWAPYYVLTOLTSISRPTLTFVY 360
DB 301 LQRMSSVAPASORSIRLTKRVRTAIAICLVFVCWAPYYVLTOLTSISRPTLTFVY 360
OY 361 LYNAAISLGYANSCINPFIYIVLCETFRKRLVSVKPAQOGQLRAVNAQTADERTESK 420
DB 361 LYNAAISLGYANSCINPFIYIVLCETFRKRLVSVKPAQOGQLRAVNAQTADERTESK 420
OY 421 GT 422
DB 421 GT 422

RESULT 11
AAG80611
ID AAG80611 standard; Protein: 422 AA.
AC AAG80611;
XX
XX 28-FEB-2002 (first entry)
XX
XX Human SLC-1 protein.
DE
XX
XX SLC-1; melanin-concentrating hormone antagonist; anorectic; depression;
XX anti-diabetic; hypotensive; anti-arteriosclerotic; anti-lipemic; obesity;
XX anti-arthritic; antidepressant; tiranquilliser; malignant mastocytosis;
XX hypophyseal adiposity; hypothyroid obesity; hyperphagia; diabetes;
XX hypertension; arteriosclerosis; hyperlipidaemia; arthritis; anxiety;
XX human.
XX
XX Homo sapiens.
OS
XX
XX WO20018734-A1.
PN
XX
XX 22-NOV-2001.
PD
XX
XX 15-MAY-2001; 2001WO-JP04015.
PE
XX
XX 16-MAY-2000; 2000JP-0148674.
PR
XX 13-APR-2001; 2001JP-0116219.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
PA
XX
XX Ishihara Y, Terauchi J, Suzuki N, Takekawa S, Aso K;
XX
XX WPI; 2002-055668/07.
DR
XX
XX N-PSDB; AAI69442.
DR
XX
XX Use of new and known amine derivatives as melanin concentrating hormone
XX antagonists for treating e.g. obesity, diabetes, hypertension and
XX arteriosclerosis -
XX
XX Disclosure; Page 252-254; 283pp; Japanese.
PS

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XX
CC This invention describes a novel use of an amine derivative (I) as a
CC melanin concentrating hormone antagonist which has anorectic,
CC anti-diabetic, hypotensive, anti-arteriosclerotic, anti-lipemic,
CC anti-arthritic, antidepressant and tiranquilliser activity. The products of
CC the invention can be used as melanin concentrating hormone antagonists
CC for treating and preventing obesity (including malignant mastocytosis,
CC hypophyseal adiposity, hypothyroid obesity, infantile obesity and
CC hyperphagia), diabetes, hypertension and arteriosclerosis as well as
CC diabetic complications, hyperlipidaemia, arthritis, depression and
CC anxiety. This sequence represents the human melanin-concentrating hormone
CC SLC-1 gene described in the method of the invention.
CC
XX
SQ Sequence 422 AA:
Query Match 99.8%; Score 2207; DB 23; Length 422;
Best Local Similarity 99.8%; Pred. No. 3.9e-223;
Matches 421; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 MSVGAMKKGVGRVGLGGSGCOATEEDPLPDCGACAPGGGGRWRRLPQPAWEGSSARL 60
DB 1 MSVGAMKKGVGRVGLGGSGCOATEEDPLPNCGACAPGGGGRWRRLPQPAWEGSSARL 60
OY 61 WEQATGTGMDLEASLLPTGPNASNTSDGPDNLTSSAGSPRTGSISYINIMPSVEGTIC 120
DB 61 WEQATGTGMDLEASLLPTGPNASNTSDGPDNLTSSAGSPRTGSISYINIMPSVEGTIC 120
OY 121 LLGTTGNSVTIFAAYVKKSKLHMCNNVPDIFITINSVDLFLGMPFIHOLMGNGVWHR 180
DB 121 LLGTTGNSVTIFAAYVKKSKLHMCNNVPDIFITINSVDLFLGMPFIHOLMGNGVWHR 180
OY 181 GETMCTLTAMDANSQFTSYITLTAMAIDRYLATVHPISSTKRRKPSVATLVICLMAALS 240
DB 181 GETMCTLTAMDANSQFTSYITLTAMAIDRYLATVHPISSTKRRKPSVATLVICLMAALS 240
OY 241 FISTTPWMLYARLIPFGGAVGCGIRLPNDPLXWFTLYOFFLAFALPFWITAAVRI 300
DB 241 FISTTPWMLYARLIPFGGAVGCGIRLPNDPLXWFTLYOFFLAFALPFWITAAVRI 300
OY 301 LQRMSSVAPASORSIRLTKRVRTAIAICLVFVCWAPYYVLTOLTSISRPTLTFVY 360
DB 301 LQRMSSVAPASORSIRLTKRVRTAIAICLVFVCWAPYYVLTOLTSISRPTLTFVY 360
OY 361 LYNAAISLGYANSCINPFIYIVLCETFRKRLVSVKPAQOGQLRAVNAQTADERTESK 420
DB 361 LYNAAISLGYANSCINPFIYIVLCETFRKRLVSVKPAQOGQLRAVNAQTADERTESK 420
OY 421 GT 422
DB 421 GT 422

RESULT 12
AAB13440
ID AAB13440 standard; Protein: 422 AA.
AC AAB13440;
XX
XX 17-NOV-2000 (first entry)
XX
XX Mutant human MCH1 receptor encoded by plasmid R106.
DE
XX
XX Human; MCH1 receptor; melanin concentrating hormone; neuroregulator;
XX G-protein coupled; feeding; water balance; energy metabolism; arousal;
XX attention; memory; cognitive function; psychiatric disorder; stress;
XX sexual activity; hormone disorder; hypertension; diabetes;
XX cardiovascular; gastrointestinal; electrolyte balance; respiratory;
XX asthma; reproductive function; immune; endocrine; musculoskeletal;
XX Alzheimer's disease; sensory modulation; transmission;
XX motor coordination; Parkinson's disease; olfaction; urinary; depression;
XX seizure; pain; schizophrenia; morphine tolerance; opiate addiction;
XX migraine; mutant; mutein.
XX

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OS Homo sapiens.
 OS Synthetic.
 XX
 FT Key Location/Qualifiers
 FT Misc-difference 70
 FT /note= "Wild-type Met substituted by Ala"
 XX
 XX
 PN MO200039279-A2.
 XX
 FD 06-JUL-2000.
 XX
 PF 30-DEC-1999; 99WO-US31169.
 XX
 PR 31-DEC-1998; 98US-0224426.
 XX
 PA (SYNA-) SYNAPTIC PHARM CORP.
 XX
 PI Salon JA, Laz TM, Nagorny R, Wilson AE;
 XX
 DR WPI: 2000-548644/50.
 XX
 XX Novel nucleic acid encoding human melanin concentrating hormone
 PT receptor useful for treating cardiovascular disorders, hypertension and
 PT diabetes, whose mutant form is activated by melanin concentrating
 PT hormone -
 XX
 XX Claim 8; Fig 13; 173pp; English.
 PS
 XX
 CC Neuroregulators modulate communication in the nervous system. Melanin
 CC concentrating hormone 1 (MCH1) is one such neuroregulator. MCH may serve
 CC as an integrative neuropeptide, involved in stress response, feeding
 CC regulation and sexual activity. Also, MCH is thought to participate in
 CC water balance regulation, energy metabolism, general arousal/attention
 CC state, memory and cognitive functions and psychiatric disorders. The
 CC present sequence is the mutant human MCH1 receptor encoded by plasmid
 CC R106. The present sequence is a G-protein coupled receptor. MCH1 receptor
 CC pituitary hormone disorder, epinephrine release disorder,
 CC gastrointestinal disorder, cardiovascular release disorder,
 CC reproductive function disorder, diabetes, respiratory disorder, electrolyte balance
 CC disorder, hypertension, diabetes, respiratory disorder, asthma,
 CC musculoskeletal disorder, immune disorder, endocrine disorder,
 CC memory disorder e.g. Alzheimer's disease, sensory modulation and
 CC transmission disorder, motor coordination disorder, sensory integration
 CC disorder, dopaminergic function disorder e.g. Parkinson's disease,
 CC olfaction disorder, sympathetic innervation disorder, depression, stress,
 CC fluid-balance disorder, urinary disorder e.g. urinary incontinence,
 CC seizure, pain, psychotic behaviour e.g. schizophrenia, morphine
 CC tolerance, opiate addiction or migraine.
 XX
 XX Sequence 422 AA;
 SQ
 Query Match 99.7%; Score 2206; DB 21; Length 422;
 Best Local Similarity 99.8%; Pred. No. 5e-223;
 Matches 421; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 241 FISTPWLVARLIFPPGAGGCGIRLPNDPTDLKWFLLQFPLAFALPFFVITAAVYI 300
 QY 301 LQRMSSVAPASORSIRLTKRTVTAIAICLVEFCWAPYVYLQTLQISRPILTFEY 360
 DB 301 LQRMSSVAPASQSRIRLTKRTVTAIAICLVEFCWAPYVYLQTLQISRPILTFEY 360
 QY 361 LYNAISISGYANSCINLPFYIVLCETFRKRLVSVKPAAGOLRAVSNQTADEETESK 420
 DB 361 LYNAISISGYANSCINLPFYIVLCETFRKRLVSVKPAAGOLRAVSNQTADEETESK 420
 QY 421 GT 422
 DB 421 GT 422
 DB 421 GT 422
 RESULT 13
 AAU75857
 ID AAU75857 standard; Protein: 422 AA.
 XX
 AC AAU75857;
 XX
 DT 08-MAY-2002 (first entry)
 XX
 DE Human melanin concentrating hormone receptor. MCH1, R106 mutant.
 XX
 KW Human; melanin concentrating hormone receptor; MCH1; R106;
 KW steroid hormone disorder; pituitary hormone disorder;
 KW epinephrine release disorder; gastrointestinal disorder; mutein;
 KW cardiovascular disorder; hypertension; diabetes; respiratory disorder;
 KW asthma; reproductive function disorder; immune disorder; mutant;
 KW musculoskeletal disorder; neuroendocrine disorder; cognitive disorder;
 KW memory disorder; motor coordination disorder; obesity; eating disorder;
 KW dopaminergic function disorder; pain; psychosis; opiate addiction;
 KW affective disorder; migraine; transgenic.
 KW
 OS Homo sapiens.
 OS Synthetic.
 FT Key Location/Qualifiers
 FT Misc-difference 70
 FT /note= "Wild-type Met substituted by Ala"
 XX
 XX WO200202744-A2.
 XX
 XX 10-JAN-2002.
 XX
 XX 05-JUL-2001; 2001WO-US21350.
 XX
 XX 05-JUL-2001; 2001WO-US21350.
 XX
 XX 05-JUL-2000; 2000US-0610635.
 XX
 XX (SYNA-) SYNAPTIC PHARM CORP.
 XX
 XX Salon JA, Laz TM, Nagorny R, Wilson AE;
 XX
 XX WPI: 2002-164532/21.
 DR
 PT Purified human melanin concentrating hormone receptor protein and
 PT polynucleotides for screening modulator useful for treating memory
 PT disorder, sensory modulation and transmission disorder, motor
 PT coordination disorder -
 XX
 XX
 PS Claim 8; Fig 13; 524pp; English.
 XX
 CC The invention relates to a purified human melanin concentrating hormone
 CC (MCH1) receptor protein and its encoding nucleic acid (or mutant
 CC activated by MCH or its analogue or homologue). Also included are
 CC expression vectors, probes, transformed insect cells, antisense
 CC oligonucleotides, anti-MCH1 antibodies, an agent capable of inhibiting
 CC the binding of the antibody to MCH1, a transgenic animal expressing the
 CC protein, or a homologous knockout or antisense complementary to the MCH1
 CC nucleic acid, ant/agonists of MCH1, and methods of isolating chemical
 CC compounds which activate MCH1. The protein, nucleic acid, antibody,

CC ant/agonists and compound are useful for diagnosing and treating a
CC steroid or pituitary hormone disorder, an epinephrine release disorder, a
CC gastrointestinal disorder, cardiovascular disorder, electrolyte balance
CC disorder, hypertension, diabetes, respiratory disorder, asthma, XX
CC reproductive function disorder, immune disorder, endocrine disorder,
CC musculoskeletal disorder, neuroendocrine disorder, cognitive disorder,
CC memory disorder, sensory modulation and transmission disorder, motor
CC coordination disorder, sensory integration disorder, motor integration
CC disorder, dopaminergic function disorder, sensory transmission disorder,
CC olfaction disorder, sympathetic innervation disorder, pain, psychotic
CC behaviour, morphine tolerance, opiate addiction, affective disorder or
CC stress-related disorder, fluid-balance disorder, seizure disorder or
CC migraine, an eating disorder or obesity. The present sequence
CC represents human MCH1 mutant encoded by plasmid R106, which has a
CC methionine residue mutated to alanine in order to investigate the true
CC start codon of MCH1.

XX Sequence 422 AA;

Query Match 99.7%; Score 2206; DB 23; Length 422;
Best Local Similarity 99.8%; Pred. No. 5e-223;
Matches 421; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSVGMKKGVRANGLOGSGSCQATEEDPLPDGACAPGQGRMRRLPQPAWVESSARL 60
DB 1 MSVGMKKGVRANGLOGSGSCQATEEDPLPDGACAPGQGRMRRLPQPAWVESSARL 60
QY 61 WEQATGTGMDLEASLPTGPNASNTSDGPDNLTSGSPRRGTSISYINIIMPVFGTIC 120
DB 61 WEQATGTGMDLEASLPTGPNASNTSDGPDNLTSGSPRRGTSISYINIIMPVFGTIC 120
QY 121 LLGIIIGNSTVFAVYKSKLHMCNNVPDIFITINLSVVDLLFLGMPFMHOLMGNGVWHF 180
DB 121 LLGIIIGNSTVFAVYKSKLHMCNNVPDIFITINLSVVDLLFLGMPFMHOLMGNGVWHF 180
QY 181 GEIMCTLTAMDANSQFTSYILLTAMADRYLATVHPISSTFKRPSVATVTCILMAIS 240
DB 181 GEIMCTLTAMDANSQFTSYILLTAMADRYLATVHPISSTFKRPSVATVTCILMAIS 240
QY 241 FISTPFWLVYRLPFPGAVGCGIRLPNDPDLVYFTTYQFFLFAFPVYTAAYRI 300
DB 241 FISTPFWLVYRLPFPGAVGCGIRLPNDPDLVYFTTYQFFLFAFPVYTAAYRI 300
QY 301 LQRMSSVAPASQSRIRLTKRYTRALAIQVFCWAPYVLOLTOLISRPPLTVY 360
DB 301 LQRMSSVAPASQSRIRLTKRYTRALAIQVFCWAPYVLOLTOLISRPPLTVY 360
QY 361 LYNAAISLGYANSCLNPFVIVICETFRKRLVSVKPAQOGLRAVNSAQTADERTESK 420
DB 361 LYNAAISLGYANSCLNPFVIVICETFRKRLVSVKPAQOGLRAVNSAQTADERTESK 420
QY 421 GT 422
DB 421 GT 422

RESULT 14

AB13441
ID AB13441 standard; Protein; 422 AA.

AC AB13441;

XX 17-NOV-2000 (first entry)

DE Mutant human MCH1 receptor encoded by plasmid R114.

XX Human; MCH1 receptor; melanin concentrating hormone; neuroregulator;
KW G-protein coupled; feeding; water balance; energy metabolism; arousal;
KW attention; memory; cognitive function; psychiatric disorder; stress;
KW sexual activity; hormone disorder; hypertension; diabetes;
KW cardiovascular; gastrointestinal; electrolyte balance; respiratory;
KW asthma; reproductive function; immune; endocrine; musculoskeletal;
KW Alzheimer's disease; sensory modulation; transmission.

KW motor coordination; Parkinson's disease; olfaction; urinary; depression;
KW seizure; pain; schizophrenia; morphine tolerance; opiate addiction;
KW migraine; mutant; mutin.

OS Homo sapiens.

XX Synthetic.

FT Key Location/Qualifiers

FT Misc-difference 6 /note= "Wild-type Met substituted by Ala"

FT Misc-difference 70 /note= "Wild-type Met substituted by Ala"

PN WO200039279-A2.

PD 06-JUL-2000.

XX 30-DEC-1999; 99WO-US31169.

XX 31-DEC-1998; 98US-0224426.

PA (SYNA-) SYNAPTIC PHARM CORP.

PI Salton JA, Laz TM, Nagorny R, Wilson AE;

DR WPI; 2000-548644/50.

PT Novel nucleic acid encoding human melanin concentrating hormone
PT receptor useful for treating cardiovascular disorders, hypertension and
PT diabetes, whose mutant form is activated by melanin concentrating
PT hormone -

PS Claim 9; Fig 14; 173pp; English.

CC Neuroregulators modulate communication in the nervous system. Melanin
CC concentrating hormone 1 (MCH1) is one such neuroregulator. MCH may serve
CC as an integrative neuropeptide, involved in stress response, feeding
CC regulation and sexual activity. Also, MCH is thought to participate in
CC water balance regulation, energy metabolism, general arousal/attention
CC state, memory and cognitive functions and psychiatric disorders. The
CC present sequence is the mutant human MCH1 receptor encoded by plasmid
CC R114. The present sequence is a G-protein coupled receptor. MCH1 receptor
CC may be used in the therapy for a variety of disorders: steroid or
CC pituitary hormone disorder, epinephrine release disorder,
CC gastrointestinal disorder, cardiovascular disorder, electrolyte balance
CC disorder, hypertension, diabetes, respiratory disorder, asthma,
CC reproductive function disorder, immune disorder, endocrine disorder,
CC musculoskeletal disorder, neuroendocrine disorder, cognitive disorder,
CC memory disorder e.g. Alzheimer's disease, sensory modulation and
CC transmission disorder, motor coordination disorder, sensory integration
CC disorder, dopaminergic function disorder e.g. Parkinson's disease,
CC olfaction disorder, sympathetic innervation disorder, depression, stress,
CC fluid-imbalance disorder, urinary disorder e.g. urinary incontinence,
CC seizure, pain, psychotic behaviour e.g. schizophrenia, morphine
CC tolerance, opiate addiction or migraine.

XX Sequence 422 AA;

Query Match 99.5%; Score 2200; DB 21; Length 422;
Best Local Similarity 99.5%; Pred. No. 2.1e-222;
Matches 420; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSVGMKKGVRANGLOGSGSCQATEEDPLPDGACAPGQGRMRRLPQPAWVESSARL 60

DB 1 MSVGMKKGVRANGLOGSGSCQATEEDPLPDGACAPGQGRMRRLPQPAWVESSARL 60

QY 61 WEQATGTGMDLEASLPTGPNASNTSDGPDNLTSGSPRRGTSISYINIIMPVFGTIC 120

DB 61 WEQATGTGMDLEASLPTGPNASNTSDGPDNLTSGSPRRGTSISYINIIMPVFGTIC 120

QY 121 LLGIIIGNSTVFAVYKSKLHMCNNVPDIFITINLSVVDLLFLGMPFMHOLMGNGVWHF 180

DB 121 LLGIIIGNSTVFAVYKSKLHMCNNVPDIFITINLSVVDLLFLGMPFMHOLMGNGVWHF 180

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QY 181 GETMCTLTITAMDANSQFTSYIILTAAMADRYLATVHPISSTKRRKPSVATVLCILMAL5 240
DB 181 GETMCTLTITAMDANSQFTSYIILTAAMADRYLATVHPISSTKRRKPSVATVLCILMAL5 240
QY 241 FISTPWLVARLIPFEGAVGCGIRLPNDPDLVMTLYQFLALALPFPVITAYVRI 300
DB 241 FISTPWLVARLIPFEGAVGCGIRLPNDPDLVMTLYQFLALALPFPVITAYVRI 300
QY 301 LQRMSSVAPASQSRIRLRTKRVTRTAIAICLVFVCMAPRYVYLQTLQISRPDLTFEY 360
DB 301 LQRMSSVAPASQSRIRLRTKRVTRTAIAICLVFVCMAPRYVYLQTLQISRPDLTFEY 360
QY 361 LYNAISLGYANSCNLPFPYIVLCETFRKRLVLSVKPAAGOLRAVSNQOTADEERTESK 420
DB 361 LYNAISLGYANSCNLPFPYIVLCETFRKRLVLSVKPAAGOLRAVSNQOTADEERTESK 420
QY 421 GT 422
DB 421 GT 422

RESULT 15
AAU75858
ID AAU75858 standard; Protein; 422 AA.
AC AAU75858;
DT 08-MAY-2002 (first entry)
DE Human melanin concentrating hormone receptor, MCH1, R114 mutant.
XX Human melanin concentrating hormone receptor; MCH1, R114 mutant.
KW Human: melanin concentrating hormone receptor; MCH1; R114;
KW steroid hormone disorder; pituitary hormone disorder;
KW epinephrine release disorder; gastrointestinal disorder; mutein;
KW cardiovascular disorder; hypertension; diabetes; respiratory disorder;
KW asthma; reproductive function disorder; immune disorder; mutant;
KW musculoskeletal disorder; neuroendocrine disorder; cognitive disorder;
KW memory disorder; motor coordination disorder; obesity; eating disorder;
KW dopaminergic function disorder; pain; psychosis; opiate addiction;
KW affective disorder; migraine; transgenic.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 6 /note= "Wild-type Met substituted by Ala"
FT FT Misc-difference 70 /note= "Wild-type Met substituted by Ala"
FT
XX
PN WO200202744-A2.
PD 10-JAN-2002.
PE 05-JUL-2001; 2001WO-US61350.
PR 05-JUL-2000; 2000US-0610635.
PA (SYNA-) SYNAPTIC PHARM CORP.
PI Salon JA, Laz TM, Nagorny R, Wilson AE;
XX WPI; 2002-164532/21.
DR
XX Purified human melanin concentrating hormone receptor protein and
XX polynucleotides for screening modulator useful for treating memory
XX disorder, sensory modulation and transmission disorder, motor
XX coordination disorder -
XX Claim 9; Fig 14; 52App; English.
XX
CC The invention relates to a purified human melanin concentrating hormone
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CC (MCH1) receptor protein and its encoding nucleic acid (or mutant
CC activated by MCH or its analogue or homologue). Also included are
CC expression vectors, probes, transformed insect cells, antisense
CC oligonucleotides, anti-MCH1 antibodies, an agent capable of inhibiting
CC the binding of the antibody to MCH1, a transgenic animal expressing the
CC protein, or a homologous knockout or antisense complementary to the MCH1
CC nucleic acid, ant/agonists of MCH1, and methods of isolating chemical
CC compounds which activate MCH1. The protein, nucleic acid, antibody,
CC ant/agonists and compound are useful for diagnosing and treating a
CC steroid or pituitary hormone disorder, an epinephrine release disorder, a
CC gastrointestinal disorder, cardiovascular disorder, electrolyte balance
CC disorder, hypertension, diabetes, respiratory disorder, asthma,
CC reproductive function disorder, immune disorder, endocrine disorder,
CC musculoskeletal disorder, neuroendocrine disorder, cognitive disorder,
CC memory disorder, sensory modulation and transmission disorder, motor
CC coordination disorder, sensory integration disorder, motor integration
CC disorder, dopaminergic function disorder, sensory transmission disorder,
CC olfaction disorder, sympathetic innervation disorder, pain, psychotic
CC behaviour, morphine tolerance, opiate addiction, affective disorder,
CC stress-related disorder, fluid-balance disorder, seizure disorder or
CC migraine, an eating disorder or obesity. The present sequence
CC represents human MCH1 mutant encoded by plasmid R114, which has a
CC methionine residue mutated to alanine in order to investigate the true
CC start codon of MCH1.
XX
SQ Sequence 422 AA;
Query Match 99.5%; Score 2200; DB 23; Length 422;
Best Local Similarity 99.5%; Pred. No. 2, 1e-22;
Matches 420; Conserved 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MSVGAKMKGVRAVGLGGSGCQATEEDPLPDGACAPGGGGRMRLLPPAWEGSSARL 60
DB 1 MSVGAKMKGVRAVGLGGSGCQATEEDPLPDGACAPGGGGRMRLLPPAWEGSSARL 60
QY 61 WEQATGTGMDLEASLLPTGPNASNTSDGPDNLTAGSPPRGTSISYINIMPSVFGTIC 120
DB 61 WEQATGTGMDLEASLLPTGPNASNTSDGPDNLTAGSPPRGTSISYINIMPSVFGTIC 120
QY 121 LGGITGNTVEFAVYKRSKLLHMCNNVPDIFILNSVDLFLGMPFTHOLMGNGVMHF 180
DB 121 LGGITGNTVEFAVYKRSKLLHMCNNVPDIFILNSVDLFLGMPFTHOLMGNGVMHF 180
QY 181 GETMCTLTITAMDANSQFTSYIILTAAMADRYLATVHPISSTKRRKPSVATVLCILMAL5 240
DB 181 GETMCTLTITAMDANSQFTSYIILTAAMADRYLATVHPISSTKRRKPSVATVLCILMAL5 240
QY 241 FISTPWLVARLIPFEGAVGCGIRLPNDPDLVMTLYQFLALALPFPVITAYVRI 300
DB 241 FISTPWLVARLIPFEGAVGCGIRLPNDPDLVMTLYQFLALALPFPVITAYVRI 300
QY 301 LQRMSSVAPASQSRIRLRTKRVTRTAIAICLVFVCMAPRYVYLQTLQISRPDLTFEY 360
DB 301 LQRMSSVAPASQSRIRLRTKRVTRTAIAICLVFVCMAPRYVYLQTLQISRPDLTFEY 360
QY 361 LYNAISLGYANSCNLPFPYIVLCETFRKRLVLSVKPAAGOLRAVSNQOTADEERTESK 420
DB 361 LYNAISLGYANSCNLPFPYIVLCETFRKRLVLSVKPAAGOLRAVSNQOTADEERTESK 420
QY 421 GT 422
DB 421 GT 422
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Search completed: February 13, 2003, 13:58:00
Job time : 35.4921 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 13, 2003, 13:55:16 ; Search time 24.477 Seconds

(without alignments)
2971.347 Million cell updates/sec

Title: US-09-885-478-28

Perfect score: 1824
Sequence: 1 MDLEASLPTGPNASNTSDG.....LRVSNAGTADERTESKGT 353

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1824	100.0	422	4	O96S47
2	1824	100.0	422	4	O96V08
3	601	32.9	121	6	O96Z01
4	565.5	31.0	340	4	O969V1
5	559.5	30.7	340	4	O96X8
6	559.5	30.7	340	4	O8S054
7	522	28.6	370	13	O8UW15
8	521.5	28.6	346	4	O96GT0
9	515.5	28.3	356	4	O96T72
10	512.5	28.1	346	11	O91V73
11	502.5	27.5	367	13	O9PVG0
12	499.5	27.4	367	13	O9PVF9
13	494.5	27.1	346	6	O9SKS6
14	491	26.9	315	6	O9GKP7
15	486.5	26.7	380	7	O9DC06
16	469	25.7	390	13	O8G0C4

17	456	25.0	385	11	O9JK40	O9JK40 mus musculus
18	444	24.3	454	4	O9H573	O9H573 homo sapien
19	442.5	24.3	390	11	O8V171	O8V171 mus musculus
20	442.5	24.3	391	11	O8V170	O8V170 mus musculus
21	442.5	24.3	393	11	O9R1M0	O9R1M0 mus musculus
22	442.5	24.3	401	11	O9R1I9	O9R1I9 mus musculus
23	442.5	24.3	409	11	O8V169	O8V169 mus musculus
24	442.5	24.3	438	11	O9R0D1	O9R0D1 mus musculus
25	442.5	24.3	444	11	O9J1Y1	O9J1Y1 mus musculus
26	439	24.1	400	6	O95M54	O95M54 macaca fasc
27	435	23.8	383	13	O42324	O42324 catostomus
28	422	23.1	384	13	O98U11	O98U11 brachydanio
29	419.5	23.0	377	13	O98U14	O98U14 brachydanio
30	407	22.3	373	13	O57585	O57585 brachydanio
31	402.5	22.1	272	4	O9BWH1	O9BWH1 homo sapien
32	393.5	21.6	451	5	O9VW01	O9VW01 drosophila
33	388	21.3	362	11	O9J1N4	O9J1N4 rat
34	388	21.3	362	11	O8V174	O8V174 mus musculus
35	373	20.4	380	5	O9NEV2	O9NEV2 mus musculus
36	370.5	20.3	393	5	O9VW00	O9VW00 drosophila
37	367	20.1	291	11	O912Z4	O912Z4 mus musculus
38	367	20.1	325	11	O8VIN4	O8VIN4 mus musculus
39	367	20.1	330	11	O8V1P1	O8V1P1 mus musculus
40	367	20.1	370	11	O8V1P0	O8V1P0 mus musculus
41	366	20.1	380	5	O9NEV1	O9NEV1 lymnaea sta
42	364.5	20.0	380	5	O9NEV3	O9NEV3 lymnaea sta
43	363	19.9	380	5	O9NEV0	O9NEV0 lymnaea sta
44	361.5	19.8	359	13	O9PVY7	O9PVY7 anguilla an
45	361	19.8	423	5	O964D4	O964D4 periplaneta

ALIGNMENTS

RESULT 1

ID O96S47 PRELIMINARY; PRT; 422 AA.
AC O96S47;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Somatostatin receptor-like protein.
GN SIC-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Sugo T., Mori M.,
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=9373129; PubMed=10441476;
RA Shimomura Y., Mori M., Sugo T., Ishibashi Y., Abe M., Kurokawa T.,
RT "Isolation and Identification of the SIC-1 receptor."
RT endogenous ligand of the SIC-1 receptor."
RL Biochem. Biophys. Res. Commun. 261:622-626(1999).
DR EMBL: AB063174; BAB60890.1; -;
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1.1;
DR PRINTS: PR01559; DUFFYANTIGEN.
DR PROSITE: PS50262; G-PROTEIN-RECEP_FL_2; 1.
KW Receptor.
SQ
SEQUENCE 422 AA; 45962 MW; 3986919A18183818 CRC64;

Query Match 100.0%; Score 1824; DB 4; Length 422;
Best Local Similarity 100.0%; Pred. No. 1.2e-162;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MDLEASLPTGPNASNTSDGPNLTSGSPRTGISYINIMPVFGTCLGIGNST 60
|||||

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Db 70 MDLEASLPTGPNASNTSDGPNLTSAGSPRTGSIYINIIIMPVEFTICLLIGNST 129
QY 61 VIEAVVKKSKLHMCNNVPDIFIINLSVVDLLFLIGMPFMHQLMGVWHFEGTMCITLT 120
    |||||
Db 130 VIEAVVKKSKLHMCNNVPDIFIINLSVVDLLFLIGMPFMHQLMGVWHFEGTMCITLT 189
QY 121 AMDANSQFTSYITLTAADRYLATVHPISSTFRKRSVATLYICLLMALSFSITPVM 180
    |||||
Db 190 AMDANSQFTSYITLTAADRYLATVHPISSTFRKRSVATLYICLLMALSFSITPVM 249
QY 181 YARLIPPGAVGCGIRLPNPDLDLYWFTLYOFLAFALPFIYVITAAVYRILOQMTSSVA 240
    |||||
Db 250 YARLIPPGAVGCGIRLPNPDLDLYWFTLYOFLAFALPFIYVITAAVYRILOQMTSSVA 309
QY 241 PASQSRIRLRTKRYRTAIAICLVFVCWAPYYVQLQTQISRPITLFEYLYNAAISLG 300
    |||||
Db 310 PASQSRIRLRTKRYRTAIAICLVFVCWAPYYVQLQTQISRPITLFEYLYNAAISLG 369
QY 301 YANSCINPFYIVLCETFRKRLVSVKPAAGQLRAVSNAGTADERTESKGT 353
    |||||
Db 370 YANSCINPFYIVLCETFRKRLVSVKPAAGQLRAVSNAGTADERTESKGT 422

RESULT 2
Q9BV08 PRELIMINARY; PRT; 422 AA.
ID 09BV08
AC 09BV08;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Similar to G protein-coupled receptor 24 (Hypothetical 46.0 kDa
  protein).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiinae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=FROM N.A.
RC SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN [12]
RP TISSUE=FROM N.A.
RC SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN [12]
RP TISSUE=FROM N.A.
RC SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC001736; AAH01736.1; -.
DR EMBL; BC021146; AAH21146.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PRO1559; DUFFYANTIGEN.
DR PRINTS; PRO0237; GPCR_RHODPSN.
DR PROSITE; PS50262; G_PROTEIN_RECPT_FL_2; 1.
KW Receptor; Hypothetical protein.
SQ SEQUENCE 422 AA; 45963 MW; 86A9F398B5D5F397 CRC64;

Query Match 100.0%; Score 1824; DB 4; Length 422;
Best Local Similarity 100.0%; Pred. NO. 1.2e-162;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLEASLPTGPNASNTSDGPNLTSAGSPRTGSIYINIIIMPVEFTICLLIGNST 60
    |||||
Db 70 MDLEASLPTGPNASNTSDGPNLTSAGSPRTGSIYINIIIMPVEFTICLLIGNST 129
QY 61 VIEAVVKKSKLHMCNNVPDIFIINLSVVDLLFLIGMPFMHQLMGVWHFEGTMCITLT 120
    |||||
Db 130 VIEAVVKKSKLHMCNNVPDIFIINLSVVDLLFLIGMPFMHQLMGVWHFEGTMCITLT 189
QY 121 AMDANSQFTSYITLTAADRYLATVHPISSTFRKRSVATLYICLLMALSFSITPVM 180
    |||||
Db 190 AMDANSQFTSYITLTAADRYLATVHPISSTFRKRSVATLYICLLMALSFSITPVM 249
QY 181 YARLIPPGAVGCGIRLPNPDLDLYWFTLYOFLAFALPFIYVITAAVYRILOQMTSSVA 240

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Db 250 YARLIPPGAVGCGIRLPNPDLDLYWFTLYOFLAFALPFIYVITAAVYRILOQMTSSVA 309
QY 241 PASQSRIRLRTKRYRTAIAICLVFVCWAPYYVQLQTQISRPITLFEYLYNAAISLG 300
    |||||
Db 310 PASQSRIRLRTKRYRTAIAICLVFVCWAPYYVQLQTQISRPITLFEYLYNAAISLG 369
QY 301 YANSCINPFYIVLCETFRKRLVSVKPAAGQLRAVSNAGTADERTESKGT 353
    |||||
Db 370 YANSCINPFYIVLCETFRKRLVSVKPAAGQLRAVSNAGTADERTESKGT 422

RESULT 3
Q9MZ01 PRELIMINARY; PRT; 121 AA.
ID 09MZ01
AC 09MZ01;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Melanin-concentrating hormone receptor (Frogantl).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP TISSUE=FROM N.A.
RC SEQUENCE FROM N.A.
RA Matteri R.L.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF273611; AAF81827.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PRO0237; GPCR_RHODPSN.
DR PROSITE; PS50262; G_PROTEIN_RECPT_FL_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 121
SQ SEQUENCE 121 AA; 13583 MW; 884D8268B6F9F010 CRC64;

Query Match 32.9%; Score 601; DB 6; Length 121;
Best Local Similarity 99.2%; Pred. NO. 1.1e-48;
Matches 120; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 225 TAAVYRILOQMTSSVAPASQSRIRLRTKRYRTAIAICLVFVCWAPYYVQLQTQISLR 284
    |||||
Db 1 TAAVYRILOQMTSSVAPASQSRIRLRTKRYRTAIAICLVFVCWAPYYVQLQTQISLR 60
QY 285 PVLTFYLYNAAISLGIANSCINPFYIVLCETFRKRLVSVKPAAGQLRAVSNAGTAD 344
    |||||
Db 61 PVLTFYLYNAAISLGIANSCINPFYIVLCETFRKRLVSVKPAAGQLRAVSNAGTAD 120
QY 345 E 345
Db 121 E 121

RESULT 4
Q969Y1 PRELIMINARY; PRT; 340 AA.
ID 0969Y1
AC 0969Y1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE G protein-coupled receptor (Melanin-concentrating hormone 2 receptor)
  (Melanin-concentrating hormone receptor MCH-R2) (GPRV17).
OS Homo sapiens (Human).
GN SLT OR GPRV17.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiinae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

```


RX MEDLINE-11255282; PubMed-11355873; Sugo T., Watanabe T., Shimomura Y.,
 RA Mori M., Harada M., Terao Y.,
 RA Abe M., Shitani Y., Onda H., Nishimura O., Fujino M.;
 RT "Cloning of a novel g protein-coupled receptor, slt, a subtype of the
 RT melanin-concentrating hormone receptor.";
 RL Biochem. Biophys. Res. Commun. 283:1013-1018(2001).
 RN [2]
 RN RP
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE-21309932; PubMed-1104457;
 RA Seller A.W., Sano H., Zeng Z., McDonald T.P., Pan J., Pong S.-S.,
 RA Feighner S.D., Tan C.P., Fukami T., Iwaasa H., Hreniuk D.L.,
 RA Morin R.P., Sadowski S.J., Ito M., Ito M., Bansal A., Ky B.,
 RA Figueroa D.J., Jiang Q., Austin C.P., MacNeill D.J., Ishihara A.,
 RA Ihara M., Kanatani A., Van der Ploeg L.H.T., Howard A.D., Liu Q.;
 RT "Identification and characterization of a second melanin-concentrating
 RT hormone receptor, MCH-R2.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:7564-7569(2001).
 RN [3]
 RN RP
 RP SEQUENCE FROM N.A.
 RX MEDLINE-21433976; PubMed-11459838;
 RA Wang S., Behan J., O'Neill K., Weig B., Fried S., Laz T., Bayne M.,
 RA Gustafson E., Hawes B.E.;
 RT "Identification and pharmacological characterization of a novel human
 RT melanin-concentrating hormone receptor, MCH-R2.";
 RL J. Biol. Chem. 276:34664-34670(2001).
 RN [4]
 RN RP
 RP SEQUENCE FROM N.A.
 RA Kurama T., Matsumoto S., Takasaki J., Terai K., Matsumoto M.,
 RA Komura M., Saito T., Soga T., Saito Y., Oda T., Masuo Y.,
 RA Furuchi K.;
 RT "Molecular characterization of a novel melanin-concentrating hormone
 RT receptor: Evidence of its expression in lateral hypothalamus.";
 RL Submitted (MAR-2001) to the EMBL/Genbank/DBJ databases.
 RN EMBL: AB060151; BARS5677.1; -;
 DR EMBL: AI029596; AAK38157.1; -;
 DR EMBL: AF099337; AAL05528.1; -;
 DR EMBL: AB058849; BAB87842.1; -;
 DR Interpro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR POSSITE: PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
 DR POSSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
 DR RECEPT. 340 AA; 38849 MW; 754A302B951FAC6 CRC64;
 QO SEQUENCE

[illegible]

RESULT	5			
Q9BXA8		PRELIMINARY;	PRT;	340 AA.
ID	Q9BXA8			
AC	Q9BXA8;			
DT	01-JUN-2001 (TrEMBLrel, 17, Created)			
DT	01-JUN-2001 (TrEMBLrel, 17, Last sequence update)			
DT	01-DEC-2001 (TrEMBLrel, 19, Last annotation update)			
DE	G protein-coupled receptor MCH2.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidi; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21282939; PubMed=11274220;			
RA	Hill U., Duckworth M., Wurdock P., Rennie G., Sabido-David C.,			
RA	Ames R.S., Szekeres P., Wilson S., Bergsma D.J., Gloger I.S.,			
RA	Ley D.S., Chambers J.K., Muir A.I.;			
RT	"Molecular Cloning and Functional Characterization of MCH2, a Novel			
RT	Human MCH Receptor.";			
RL	J. Biol. Chem. 276:20125-20129(2001).			
DR	EMBL; AF347063; AAK32193.1; -			
DR	InterPro; IPR000276; GPCR_Rhodpsn.			
DR	Pfam; PFD0001; 7tm_1; 1.			
DR	PRINTS; PR00237; GPCRHOOPS.			
DR	PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.			
DR	PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.			
KW	Receptor.			
CO	SEQUENCE 340 AA; 38803 MW; 95A43ECB57511ACC CRC64;			

	Query Match	30.7%	Score 559.5	DB 4	Length 340
	Best Local Similarity	36.7%	Pred. No. 2,9e-44		
	Matches 112	Conservative	62	Mismatches 120	Indels 11
					Gaps 4
QY	41	TTMESVFETICLLGTTIGNSVIAFAYVKKSKLHCNVPDIFITINLSVDDLFLGLMPFMI	100		
DB	35	VILPSEMIIGLSTGVNMLIVETIIRSRK----KTVPDIYICNLAVADLHVIYGMPLI	90		
QY	101	HOLMGNGVHHGEMPCCTITAMDNSOFTSYIITLAMAIDBYIATVHPISSTKRRKPEVA	160		
DB	91	HOMARGGVWVGGLPCTIITISLDTCNQACSHIMTVMSVDIEFALVQFRLTRMTRYKT	150		
QY	161	TLVICLLALSFISTIPWLYARLIPFGAVGCGIRLPNDPTDLYWETLYOFELAFALP	220		
DB	151	IRINGELMAASFIALPVMVYSKVYIKFDGYESCAFDLTSPD-DVLYMTLYLITTFEFP	209		
QY	221	FVVTAAAVRL-----QRTSSVAPASQRI-RLRTRRYRTAICLVFVVCAPYYV	274		
DB	210	LPLIVCTILLCITYEMKYQONKIDRCNPNPVPKQXVYKMLTKMLVLVYVITLSNAPHV	269		
QY	275	LOLTQLSISRPPLTFVLYLYNNAISLGVANSCLNPFVYIVLCEPFRKRLYSVKPPAAGQL	334		
DB	270	IQLVNLQMEQPLTAFVYGVYIISLCISYASSINPFLYITLISGNQKRLPQIRRATEKEI	329		
QY	335	RAYSN 339			
DB	330	NNMGN 334			

RESULT 6

08S054 PRELIMINARY; PRT: 340 AA.

AC 08S054; DB 08S054; PRT: 340 AA.

DT 01-JUN-2002 (TREMBLrel. 21, Created)

DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE GPRV17.

GN GPRV17.

OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).

OC Eukaryota; Metazoa; Chordata; Cranata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

OC Cercopithecinae; Macaca.

OX NCBI_TaxID=9541;
RN [1]
SEQUENCE FROM N.A.
RA Kurama T., Matsumoto S., Takasaki J., Terai K., Matsumoto M.,
RA Kanohara M., Saito T., Soga T., Saito Y., Oda T., Masuhio Y.,
RA Furutachi K.;
RT "Molecular characterization of a novel melanin-concentrating hormone
receptor : Evidence of its expression in lateral hypothalamus.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB058850; BAB87843.1; -
SO SEQUENCE 340 AA; 38769 MW; BD22CF197232439 CRC64;

Query Match 30.7%; Score 559.5; DB 6; Length 340;
Best Local Similarity 36.7%; Pred. No. 2,9e-44;
Matches 112; Conservative 60; Mismatches 122; Indels 11; Gaps 4;

QY 41 IIMSVETICLLGIGSTYIFAVVKKSKLHMCNNPDIITNLAVDILLGMPMT 100
DB 35 VILPSMIGIICSTGLVGNILVFTIRSRK---KTPVDIYICMLAVADLVHIIIMPFLI 90
QY 101 HOLMGVWHEGEMCTLTITAMDANSOFTSTYILTAMADRYLATVHPISSTRKRPSSVA 160
DB 91 HQMARGSWVGEGLCTITTSIDICNOFACSAIMTVNSVDRYFLVOPFRILSTRKTKYT 150
QY 161 TLVITCLMALSFISTIPWYLARLIPPGAVGCGIRLPNPDLDLYWFTLYOFLAFALP 220
DB 151 IIRINGLMAASFILALPWIVISKYIKFKDGVESCAFDLTSPD-DLVMTYLLTITTFEFP 209
QY 221 FVVTITAAVRL-----QRMSSVAPASQSI-RLRTKRVTRIAICLVFVCMAPIYV 274
DB 210 LPLILVICYLLICYTWEMYQONKDAKRCNPSPKQVWKILKMLVAVAFIISAAPIYH 269
QY 275 IOLQLSIRPTLFEVLYNNAISLGYANSCLNPFVYIVLCETFRKRLVSVKRAAGQL 334
DB 270 IQVLNLMQEPFLAVYGYISICLSYASSINPFLYLLSGNFQKRLPQIQRYVDKEI 329
QY 335 RAVSN 339
DB 330 KNMGV 334

RESULT 7
Q8UWLS PRELIMINARY; PRT; 370 AA.
AC Q8UWLS;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Somatostatin receptor 2.
GN SSR2.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Acanthomorphi; Acanthopterygii; Percomorphi; Tetraodontiformes;
OC Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21564205; PubMed=11707075;
RA Bagheri-Fam S., Ferraz C., Demaille J., Scherer G., Pfeiffer D.;
RT "Comparative Genomics of the SOX9 Region in Human and Fugu rubripes:
RT Conservation of Short Regulatory Sequence Elements within Large
RT Intergenic Regions.";
RL Genomics 78:73-82(2001).
DR EMBL: AF329945; AAL32173.1; -
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PF00237; GPCR_Rhodopsn.
DR PROSITE: PS00237; G_PROTEIN_RECPT_F1_1; UNKNOWN_1.
DR PROSITE: PS50262; G_PROTEIN_RECPT_F1_2; 1.
KW Receptor.
SO SEQUENCE 370 AA; 41364 MW; 420B12F204946B6 CRC64;

Query Match 28.6%; Score 522; DB 13; Length 370;
Best Local Similarity 33.0%; Pred. No. 1e-40;
Matches 122; Conservative 75; Mismatches 131; Indels 42; Gaps 11;

QY 3 LEASLPTGPNASNSDGDNLTSAGSPRTSISYIN-----IMPSTGIC 51
DB 1 MDAMILP--PSPILNS--DHLIDYGEQANGSDHANTDHS�KSTSTVYTCMYFLVC 55
QY 52 LIGITNSYIVAVVKKSKLHMCNNPDIITNLAVDILLGMPMTHOLMGVWHE 111
DB 56 AVGLCGNALVIYIIRYAKM---KTYNTIYILNLAVADLVFMLGIPFLAIQL-ALVHPF 111
QY 112 GETMCTLTITAMDANSOFTSTYILTAMADRYLATVHPISSTRKRPVATVILMALIS 171
DB 112 GPVLCHVMTVDLNGFTSIFCLMVNSIDRYLAVHPKSTRKRPRAKTIIVAVMGAS 171
QY 172 FISITPWLILARLIPPGAVGCGIRLPNPDLDLYW-FILYOFILAFALPVIITAAVYR 230
DB 172 LVVNLPIVYSGITRKQDCF-CTIYWPEDBAAYTAEMIVTFILGFFLPLIVISLCYF 230
QY 231 ILQRMSSVAPASQSI-RLRTKRVTRIAICLVFVCMAPIYVLOLQLS-----IS 283
DB 231 IIVKVASSGIRGSSKRSKRSKRVTRMSIVAVFVLCMLPFYVNTSVGISATIVL 290
QY 284 RPTLFEVLYNNAISLGYANSCLNPFVYIVLCETFRKRL-VLSVKPAAQGLRAVSNQ 341
DB 291 RSIFAVV-----VVLGYANSCNPIIVAFLEENRKSPQNVLCIQ-----KVGLEDAE 339
QY 342 TADEERTESK 351
DB 340 RSDSRQDKSR 349

RESULT 8
Q96GEO PRELIMINARY; PRT; 346 AA.
AC Q96GEO;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Unknown (Protein for IMAGE:3354783) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RC TISSUE=EYE;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC009522; AAH09522.1; -
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PROSITE: PS00237; G_PROTEIN_RECPT_F1_1; UNKNOWN_1.
DR PROSITE: PS50262; G_PROTEIN_RECPT_F1_2; 1.
FT NON_TER 1
SO SEQUENCE 346 AA; 38790 MW; EA073A6CC05FEB72 CRC64;

Query Match 28.6%; Score 521.5; DB 4; Length 346;
Best Local Similarity 31.7%; Pred. No. 1.1e-40;
Matches 110; Conservative 73; Mismatches 125; Indels 39; Gaps 7;

QY 13 NASNTSDGPDNLTSAGSPRTSISYINIMPSVETICLLGIGSTYIFAVVKKSKLH 72
DB 6 NTSNQTPEPYDLS-----NAVLIFFIVVCIIGLGNITVYIIRYAKM- 51
QY 73 WCNVVDIFILNLAVDILLGMP-----MIHOLMGVWHEGEMCTLTITAMDANS 126
DB 52 --KTINIIYILNLADLDELFMGLPFLAMQVALVH-----WPGKAIQVWMTVDGIN 102
QY 127 QFTSTIILAMADRYLATVHPISSTRKRPVATVILCLMALSFISTIPWYLARLIP 186
DB 103 QFTSIFCLTVMSIDRYLAVVHPKSAKWRPRTAKITMAVGVSLVILPIMYAGLRS 162

ID	Q66TF2	PRELIMINARY;	PRT;	356 AA.
AC	Q66TF2;			
DT	01-DEC-2001 (TrEMBLrel. 19, Created)			
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)			
DT	01-MAR-2002 (TrEMBLrel. 20, Last annotation update)			
DE	Somatostatin receptor 2B.			
GN	SSR2.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidi; Homo.			
OX	NCBI_TaxId=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20084417; PubMed=10613939;			
RA	Petersen S., Rasch A.C., Presch S., Bell F.U., Schulte H.M.;			
RT	"Genomic structure and transcriptional regulation of the human			
RT	somatostatin receptor type 2."			
RL	Mol. Cell. Endocrinol. 157:75-85(1999).			
DR	EMBL; AF184174; AAF42810.1;			
DR	InterPro: IPR000276; GPCR_Rhodpsn.			
DR	Pfam: PFO0001; 7tm.1.1			
DR	PROSITE: PS00237; G-PROTEIN_RECP_F1.1; UNKNOWN.1.			
DR	PROSITE: PS00262; G-PROTEIN_RECP_F2.1;			
DR	SEQUENCE 356 AA; G40006 MW; DI0FA237FAED61F3 CRC64;			

AC 091Y73; 2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, last annotation update)
 DE Somatostatin receptor type 2.
 GN SMSMR2 OR SSR2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RE SEQUENCE FROM N.A.
 RC STRAIN=129; TISSUE=LIVER;
 RX MEDLINE=21201198; PubMed=11278805;
 RA Puente E., Saitt-Laurent N., Torrisani J., Furet C., Schally A.V.,
 RT Vayese N., Buscail L., Sushai C.;
 RL "Transcriptional Activation of Mouse ssr2 Somatostatin Receptor
 Promoter by Transforming Growth Factor-beta. Involvement of Smad4".
 RL J. Biol. Chem. 276:13461-13468(2001).
 DR EMBL; AF008914; AAD01420.1; -
 DR MGD; MGI:98328; Ssmr2.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm1.1; 1.
 DR PROSITE; PS00237; G_PROTEIN_RECP_FL1; UNKNOWN_1.
 DR PROSITE; PS50262; G_PROTEIN_RECP_FL2; 1.
 KW Receptor.
 SO SEQUENCE 346 AA; 38586 MW; D7A208EC1371C400 CRC64;

Query Match	28.18%	Score 512.5	DB 11	Length 346
Best Local Similarity	31.38%	Pred. No. 7.5e-40		
Matches 111	Conservative 75	Mismatches 126	Indels 43	Gaps
QY	2	DLEASLPTPNASNTSDPDNLITAGSPPRGISYSYINIMPEVETGLIGTGNSTV	61	
DB	20	DUNSGSPS--NSQNTPEYDMTS-----NAVLPTIYVVCVSGLCNTLV	64	
QY	62	IFAVYKSKSLHMCNNVPDIFITINLSVLDLLELGNP-----MIHOLMGVWHRGETM	11	
DB	65	IYVILRYAKK--KTTINIIYIINALADELEMLGPEFLAQVALVH-----WPGKAI	11	
QY	116	CTLTITANDANSOFTSYVILTNADIDRYATATHPISSTKFRKFRPSVATVYICLMALSFIS	17	
DB	115	CRVVMYVDGJNOSTSIFCLTYSIDRYATAVVHPISKAKMRPRPRAKINAVAWCSLVI	17	
QY	176	TPWLVYARLLPFGGAVGCGIRLPNDPDLX--WETLYQFLAFLPFFVYTTAAVYILIOR	23	
DB	175	LPNIIYAGLRSNQMGHSCSTINWPGESAWMTGFIYAFILGFLVPLTIIICLYEIIIK	23	
QY	235	MTSSVAPASQSRIRLTKRYVTATATLCLVFEVVCMAPIYVLOLTOLUIS--RPTLFFVY	29	
DB	235	VKSSGIRVGGSKRRKSEKVKTEWMSIYAVAFIPCMLEPFYIFNVSSVSAISPALKGMF	29	
QY	294	NAASISLIGVNSCINPEVYIVLCEFRKRL--VLSVRPAAGOLRAVSNOTADDEE	346	
DB	295	DFVYVILTYANSCANPLTVAFLFSLDNKKFSQVNDLVARA-----DNSQGAED	341	
RESULT 11				
Q9PVG0				
Q9PVG0	PRELIMINARY	PRT	367 AA.	
AC	Q9PVG0			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-MAR-2002 (TREMBLrel. 20, last annotation update)			
DE	Somatostatin receptor type 1 subtype A.			
GN	SET1A.			
OS	Carassius auratus (Goldfish).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;			
OC	Cyprinidae; Carassius.			
NCBI	Taxid=7957;			
XP	[1]			
RP	SEQUENCE FROM N.A.			

```

RC TISSUE=BRAIN;
RX MEDLINE=20005543; PubMed=10537151;
RA Lin X., Janovick J.A., Brothers S., Conn P.M., Peter R.E.;
RT "Molecular cloning and expression of two type one somatostatin
   receptors in goldfish brain.";
RL Endocrinology 140:5211-5219(1999).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
DR EMBL: AF097726; AAF08613.1; -
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCRHOPOPSN.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ SEQUENCE 367 AA; 41658 MW; BE85B6C26C103614 CRC64;

Query Match 27.5%; Score 502.5; DB 13; Length 367;
Best Local Similarity 30.1%; Pred. NO. 7e-39;
Matches 97; Conservative 80; Mismatches 120; Indels 25; Gaps 6;

QY 2 DLEASLPTGPNASNTSDGPDNLTSAGSPPTGTSISYINIMPSVEGTICLLGIGNSTV 61
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 9 NLEEGVILINSSNETHNGSHSSA-----IFISPIYSVCLVGLGNSMV 55

QY 62 IFPAVVKSKLHMCNNVPDIFITINLSVDLLFLGMPFMIHQLMGVNHGEMCTITTA 121
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 56 IYVIFRYAKMKATN---IYILNLAIDDLMLSVPLVTSLSLH--WFGSLCRVLVS 111

QY 122 MDANSOFTSTYILTFMAIDRYLATVHPISSTFKRPSVATVYICLLMALSFISTPVM 181
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 112 VDAINMFTSYICLVLSIDRISVYHPKARVRRPTIAKVNGLGVMFSLVILPITIF 171

QY 182 ARLIPPGAGVCGIRLPNDPTDLYW--FTLYQFLAFALPFVYITAAVRIIQRTSS 238
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 172 STTAPNSDGSVACNMQMEPERQ--WMAVFYIAFLMGFLFPVIAICMCIYLIVKRV 229

QY 239 VAPASQSRIRLTKRVTRTAICLVFPCVCAPIYVLOLTOLISRPITLFFVYLYNAIS 298
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 230 ALKAGMOQRKSKERKTLTMVMVTVFYICMPFHIMQLVSVFVOQHNT---LSQLAVI 286

QY 299 LGYANSCINPFYIYLCETFRK 320
   ||||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 287 LGYANSCANPILYGLSDNFR 308

RESULT 12
Q9PVF9 PRELIMINARY; PRT; 367 AA.
AC Q9PVF9;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Somatostatin receptor type 1 subtype B.
GN SST1B.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN 11
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=20005543; PubMed=10537151;
RA Lin X., Janovick J.A., Brothers S., Conn P.M., Peter R.E.;
RT "Molecular cloning and expression of two type one somatostatin
   receptors in goldfish brain.";
RL Endocrinology 140:5211-5219(1999).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC EMBL: AF097726; AAF08613.1; -
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1; 1.

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DR PRINTS: PR00237; GPCRHOPOPSN.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ SEQUENCE 367 AA; 41614 MW; A5BA0AE68D47CA55 CRC64;

Query Match 27.4%; Score 499.5; DB 13; Length 367;
Best Local Similarity 30.1%; Pred. No. 1.3e-38;
Matches 97; Conservative 80; Mismatches 120; Indels 25; Gaps 6;

QY 2 DLEASLPTGPNASNTSDGPDNLTSAGSPPTGTSISYINIMPSVEGTICLLGIGNSTV 61
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 9 NLEEDGYILNFSNETHNGSHSSA-----IFISPIYSVCLVGLGNSMV 55

QY 62 IFPAVVKSKLHMCNNVPDIFITINLSVDLLFLGMPFMIHQLMGVNHGEMCTITTA 121
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 56 IYVIFRYAKMKATN---IYILNLAIDDLMLSVPLVTSLSLH--WFGSLCRVLVS 111

QY 122 MDANSOFTSTYILTFMAIDRYLATVHPISSTFKRPSVATVYICLLMALSFISTPVM 181
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 112 VDAINMFTSYICLVLSIDRISVYHPKARVRRPTIAKVNGLGVMFSLVILPITIF 171

QY 182 ARLIPPGAGVCGIRLPNDPTDLYW--FTLYQFLAFALPFVYITAAVRIIQRTSS 238
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 172 STTAPNSDGSVACNMQMEPERQ--WMAVFYIAFLMGFLFPVIAICMCIYLIVKRV 229

QY 239 VAPASQSRIRLTKRVTRTAICLVFPCVCAPIYVLOLTOLISRPITLFFVYLYNAIS 298
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 230 ALKAGMOQRKSKERKTLTMVMVTVFYICMPFHIMQLVSVFVOQHNT---LSQLAVI 286

QY 299 LGYANSCINPFYIYLCETFRK 320
   ||||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 287 LGYANSCANPILYGLSDNFR 308

RESULT 13
Q9SKS6 PRELIMINARY; PRT; 346 AA.
AC Q9SKS6;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Somatostatin receptor subtype 1 (Fragment).
GN SST1.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN 11
RP SEQUENCE FROM N.A.
RC TISSUE=PUTITARY;
RA Debuss N., Dutour A., Vuaroqueaux V., Oliver C., Ouafik L.;
RT "The ovine somatostatin receptor subtype 1 (osst1): Partial cloning
   and tissue distribution.";
RL Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.
RN 12
RP SEQUENCE FROM N.A.
RC TISSUE=PUTITARY;
RA Debuss N.;
RL Thesis (1999).
RL Department of Inter-cellular communications in Endocrinology,
RL University of Aix-Marseilles II, Marseilles, France.
RL EMBL: AJ314853; CAC69545.1; -
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER
SQ SEQUENCE 346 AA; 38479 MW; 65547713CE2CA5C6 CRC64;

Query Match 27.1%; Score 494.5; DB 6; Length 346;

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Search completed: February 13, 2003, 14:00:17
Job time : 25.477 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 13, 2003, 13:50:36 ; Search time 11.5013 Seconds
(without alignments)
1273.004 Million cell updates/sec

Title: US-09-885-478-28

Perfect score: 1824
Sequence: 1 MDLEASLLPTGPNASNTSDG.....LRASNAQTADERTESKQT 353

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwisProt_40:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1763	96.7	353	1 GP24_RAT	P97639 ratius norv
2	1692	92.8	402	1 GP24_HUMAN	O99705 homo sapien
3	530.5	29.1	369	1 SSR2_HUMAN	P30874 homo sapien
4	529.5	29.0	369	1 SSR2_MOUSE	P30875 mus musculu
5	528	28.9	369	1 SSR2_BOVIN	P34993 bos taurus
6	524.5	28.8	369	1 SSR2_PIG	P34984 sus scrofa
7	524.5	28.8	369	1 SSR2_RAT	P30680 ratius norv
8	505.5	27.7	388	1 SSR4_HUMAN	P31391 homo sapien
9	504.5	27.7	418	1 SSR3_HUMAN	P32745 homo sapien
10	497.5	27.3	391	1 SSR1_RAT	P28646 ratius norv
11	496.5	27.2	391	1 SSR1_HUMAN	P30872 homo sapien
12	496.5	27.2	391	1 SSR1_MOUSE	P30873 mus musculu
13	494.5	27.1	384	1 SSR4_RAT	P30937 ratius norv
14	483	26.5	384	1 SSR4_MOUSE	P49660 mus musculu
15	480.5	26.3	428	1 SSR3_RAT	P30936 ratius norv
16	478.5	26.2	364	1 SSR5_HUMAN	P35346 homo sapien
17	472	25.9	428	1 SSR3_MOUSE	P30938 ratius norv
18	470.5	25.8	363	1 SSR5_RAT	P30938 ratius norv
19	456	25.0	362	1 SSR5_MOUSE	O08858 mus musculu
20	451	24.7	400	1 OPRD_HUMAN	P41143 homo sapien
21	450	24.7	400	1 OPRD_MOUSE	O99749 macaca mula
22	446.5	24.5	372	1 OPRD_RAT	P33533 ratius norv
23	444	24.3	400	1 OPRM_HUMAN	P35372 homo sapien
24	442.5	24.3	398	1 OPRM_MOUSE	P42866 mus musculu
25	442.5	24.3	401	1 OPRM_BOVIN	P79350 bos taurus
26	441	24.2	398	1 OPRM_RAT	P33535 ratius norv
27	441	24.2	372	1 OPRD_MOUSE	P32300 mus musculu
28	436.5	23.9	401	1 OPRM_PIG	O95247 sus scrofa
29	433.5	23.8	380	1 OPRK_HUMAN	P41145 homo sapien
30	426	23.4	380	1 OPRK_CAVPO	P41144 cavia porce
31	421	23.1	328	1 GPR7_HUMAN	P48145 homo sapien
32	419	23.0	380	1 OPRK_MOUSE	P33534 mus musculu
33	419	23.0	380	1 OPRK_RAT	P34975 ratius norv

34	418.5	22.9	370	1 OPRX_CAVPO	P47748 cavia porce
35	409.5	22.5	333	1 GPR8_HUMAN	P48146 homo sapien
36	408.5	22.4	370	1 OPRX_HUMAN	P41146 homo sapien
37	406.5	22.3	367	1 OPRX_MOUSE	P35377 mus musculu
38	406.5	22.3	367	1 OPRX_RAT	P35370 mus musculu
39	393.5	21.6	370	1 OPRX_PIG	P79292 sus scrofa
40	372.5	20.4	359	1 AG2R_CHICK	P79785 gallus gall
41	372.5	20.4	359	1 AG2R_MELGA	P33966 melagris g
42	370	20.3	363	1 AG2S_XENLA	P35373 xenopus lae
43	369	20.2	362	1 AG2R_XENLA	P32303 xenopus lae
44	359.5	19.7	352	1 P2Y7_HUMAN	O15722 homo sapien
45	350	19.2	353	1 CKR8_MOUSE	P56484 mus musculu

ALIGNMENTS

```
RESULT 1
GP24_RAT
ID GP24_RAT STANDARD; PRT; 353 AA.
AC P97639;
DT 01-NOV-1997 (Rel. 35, Created)
DI 15-JUL-1999 (Rel. 38, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Probable G protein-coupled receptor GPR24 (SLC-1).
GN GPR24 OR SLC1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain.
RX MEDLINE=96193144; PubMed=9531978;
RA Lakaye B., Minet A., Zorzi W., Grisar T.;
RA Cheng R., Heng H.H.Q., George S.R., O'Dowd B.F.;
RT "Cloning of the rat brain cDNA encoding for the SLC-1 G protein-
RL coupled receptor reveals the presence of an intron in the gene.";
RL Biochim. Biophys. Acta 1401:216-220(1998).
RN [2]
RP SEQUENCE OF 143-300 FROM N.A.
RX MEDLINE=97131607; PubMed=8977118;
RA Kolakowski L.F., Jr., Jung B.P., Nguyen T., Johnson M.P., Lynch K.R.,
RA Cheng R., Heng H.H.Q., George S.R., O'Dowd B.F.;
RT "Characterization of a human gene related to genes encoding
RL somatostatin receptors.";
RL FEBS Lett. 398:253-258(1996).
CC -!- FUNCTION: OPHAN RECEPTOR. DOES NOT SEEM TO BIND TO SOMATOSTATIN.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC SIMILAR TO SOMATOSTATIN RECEPTORS.
CC -----
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CC -----
CC EMBL: AF008650; AAC27977.1; -.
CC EMBL: U77953; AAC14588.1; -.
CC InterPro: IPR000276; GPCR_Rhodopsn.
CC InterPro: IPR004047; MCH1receptor.
CC Pfam: PF00001; 7tm1; 1.
CC PRINTS: PR00237; GPCR_RHODOPSIN.
CC PROSITE: PS00237; G-PROTEIN_RECPT_F1_1; FALSE_NEG.
CC PROSITE: PS00262; G-PROTEIN_RECPT_F1_2; 1.
CC G-protein coupled receptor: Transmembrane.
CC DOMAIN 1 45 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 46 66 1 (POTENTIAL).
CC DOMAIN 67 79 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 80 100 2 (POTENTIAL).
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FT DOMAIN 101 118 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 119 139 3 (POTENTIAL).
FT DOMAIN 140 161 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 162 182 4 (POTENTIAL).
FT DOMAIN 183 204 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 205 225 5 (POTENTIAL).
FT DOMAIN 226 256 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 257 277 6 (POTENTIAL).
FT DOMAIN 278 294 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 295 315 7 (POTENTIAL).
FT DOMAIN 316 353 CYTOPLASMIC (POTENTIAL).
SQ SEQUENCE 353 AA: 39063 MW: F6EBB2DF381084A9 CRC64:

Query Match 96.7%; Score 1763; DB 1; Length 353;
Best Local Similarity 96.0%; Pred. No. 3.5e-95;
Matches 339; Conservative 6; Mismatch 8; Indels 0; Gaps 0;

QY 1 MDLEASLPTGPNASNTSDGPDNLTSAGSPRTGSIYINIMPVFGTICLIGTNGST 60
DB 1 MDLQTSLSLTPGNASNTSDGQDNLTLPGSPRTGSIYINIMPVFGTICLIGTNGST 60
QY VIFAVVKKSLHMCNNVDFIIFINLSYVDLFLGMPFMHQLMGVHFGETMCTLT 120
DB VIFAVVKKSLHMCNSNPDIIFINLSYVDLFLGMPFMHQLMGVHFGETMCTLT 120
QY 61 VIFAVVKKSLHMCNSNPDIIFINLSYVDLFLGMPFMHQLMGVHFGETMCTLT 120
DB 61 VIFAVVKKSLHMCNSNPDIIFINLSYVDLFLGMPFMHQLMGVHFGETMCTLT 120
QY 121 AMDANSOFTSYITLTAMADRTATVHPISSTFRKRSMTLVICLMAISFISIPVWL 180
DB 121 AMDANSOFTSYITLTAMADRTATVHPISSTFRKRSMTLVICLMAISFISIPVWL 180
QY 121 AMDANSOFTSYITLTAMADRTATVHPISSTFRKRSMTLVICLMAISFISIPVWL 180
DB 121 AMDANSOFTSYITLTAMADRTATVHPISSTFRKRSMTLVICLMAISFISIPVWL 180
QY 181 YARLIPPGGAVGGRILPDPDDLYFTLYOFLAFALPFVYTAAYVRIIDORMTSSVA 240
DB 181 YARLIPPGGAVGGRILPDPDDLYFTLYOFLAFALPFVYTAAYVRIIDORMTSSVA 240
QY 181 YARLIPPGGAVGGRILPDPDDLYFTLYOFLAFALPFVYTAAYVRIIDORMTSSVA 240
DB 181 YARLIPPGGAVGGRILPDPDDLYFTLYOFLAFALPFVYTAAYVRIIDORMTSSVA 240
QY 241 PASORSIRLRTKRVTRTAIAICLVFVCMAPYYVQLTQLSISRPILFVYLYNAISLG 300
DB 241 PASORSIRLRTKRVTRTAIAICLVFVCMAPYYVQLTQLSISRPILFVYLYNAISLG 300
QY 301 YANCLNPFYIVICETFRKRLVSVKPAQOGIIRAVNSNOTDEETESKGT 353
DB 301 YANCLNPFYIVICETFRKRLVSVKPAQOGIIRAVNSNOTDEETESKGT 353
QY 301 YANCLNPFYIVICETFRKRLVSVKPAQOGIIRAVNSNOTDEETESKGT 353
DB 301 YANCLNPFYIVICETFRKRLVSVKPAQOGIIRAVNSNOTDEETESKGT 353

RESULT 2
GP24_HUMAN STANDARD; prt; 402 AA.
AC Q99705;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Probable G protein-coupled receptor GPR24 (SLC-1).
GN GPR24 OR SLC1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9131607; PubMed=8977118;
RA Kolakowski L.F., Jr., Jung B.P., Nguyen T., Johnson M.P., Lynch K.R.,
RA Cheng R., Heng H.H.Q., George S.R., O'Dowd B.F.;
RT "Characterization of a human gene related to genes encoding
RT somatostatin receptors."
RT FEBS Lett. 398:253-258(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20057165; PubMed=10591208;
RA Dunham I., Hunt A.R., Collins J.E., Bruskiewich R., Beare D.M.,
RA Clamp M., Smith L.J., Ainscough R., Almeida J.P., Babbage A.K.,
RA Baguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
RA Bird C.P., Blakey S.E., Bridgman A.M., Buck D., Burgess J.,
RA Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,

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RA Dhani P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,
RA Gilbert J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C.,
RA Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,
RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.K., King A.,
RA Laird G.K., Langford C.F., Leverisha M.A., Lloyd C., Lloyd D.M.,
RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,
RA Mcclay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.,
RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,
RA Phillips S.H., Plumb R.W., Ramsey H., Ramsey Y., Rogers L., Ross M.T.,
RA Scott C.E., Senha H.K., Skuce C.D., Smalley S., Smith M.L.,
RA Soderlund C., Spragon L., Stewart C.A., Sulston J.E., Swan R.M.,
RA Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,
RA Williams C.L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
RA Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,
RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyama S.,
RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
RA Dorman A., Pang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.T.,
RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,
RA Phan S., Qi S., Qian Y., Ray L., Ren O., Shaull S., Sloan D., Song L.,
RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
RA Zhan M., Zhang G., Chissos S., Murray J., Miller N., Minx P.,
RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
RA Hinds K., Kemp K., Latreille P., Layman D., Ozerky P., Rohlfing T.,
RA Scheet P., Walker C., Wamsley A., Woldmann P., Pepin K., Nelson R.,
RA Koit I., Bedell J.A., Hillier L., Mardis E., Waterston R., Wilson R.,
RA Emanuel B.S., Shaikh T., Kurahashi H., Saita S., Budarf M.L.,
RA McDermid B.E., Johnson A., Wong A.C.C., Morrow B.E., Edelmann L.,
RA Kim U.J., Shizuya H., Simon M.I., Dumas J.P., Peyraud M., Kedra D.,
RA Seroussi E., Fransson I., Tapia I., Bruder C.E., O'Brien K.P.,
RA Wilkinson P., Bodenteich A., Hartman K., Hu X., Khan A.S., Lane L.,
RA Tikhunov Y., Wright H.,
RT "The DNA sequence of human chromosome 22."
RL Nature 402:489-495(1999).
CC -I- FUNCTION: ORPHAN RECEPTOR. DOES NOT SEEM TO BIND TO SOMATOSTATIN.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- TISSUE SPECIFICITY: GREATEST ABUNDANCE IN BRAIN, PARTICULARLY IN
CC THE FRONTAL CORTEX AND HYPOTHALAMUS. A LOWER LEVEL EXPRESSION IS
CC SEEN IN THE LIVER AND HEART.
CC -I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC SIMILAR TO SOMATOSTATIN RECEPTORS.
CC -----
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CC -----
DR EMBL: U71092; AAC14587.1; -.
DR EMBL: Z86090; CAB62943.1; -.
DR Gene; HGNC:4479; GPR24.
DR MIM: 601751; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR InterPro; IPR004047; MCH1receptor.
DR Pfam; PF00001; 7tm1.1.
DR PRINTS; PR000237; GPCR_RHODOPSIN.
DR PRINTS; PR01507; MCH1RECEPTOR.
DR PROSITE; PS00237; G_PROTEIN_REC_F1.1; FALSE_NEG.
DR PROSITE; PS00262; G_PROTEIN_REC_F1.2; 1.
KW G-protein coupled receptor; transmembrane.
FT DOMAIN 1 94 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 95 115 1 (POTENTIAL).
FT DOMAIN 116 128 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 129 149 2 (POTENTIAL).
FT DOMAIN 150 167 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 168 188 3 (POTENTIAL).
FT DOMAIN 189 210 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 211 231 4 (POTENTIAL).
FT DOMAIN 232 253 EXTRACELLULAR (POTENTIAL).

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FT TRANSMEM 254 274 5 (POTENTIAL).
FT DOMAIN 275 305 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 306 326 6 (POTENTIAL).
FT DOMAIN 327 343 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 344 364 7 (POTENTIAL).
FT DOMAIN 365 402 CYTOPLASMIC (POTENTIAL).
SQ SEQUENCE 402 AA; 44454 MW; 5D24B72E76CF4F82 CRC64;

Query Match 92.8%; Score 1692; DB 1; Length 402;
Best Local Similarity 99.4%; Pred. No. 4,7e-91;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 24 LTSAGSPRTGISISYINIMPSVFGTICLLGIIGNSVIVFAVVKSKLHMCNNVPDIFII 83
DB 73 LLSGSPRTGISISYINIMPSVFGTICLLGIIGNSVIVFAVVKSKLHMCNNVPDIFII 132
QY 84 NLAVYDLFLIGMPFMTIOLMGNGVHMGEMCLITAMANSQFTSTYILITAMADRYL 143
DB 133 NLAVYDLFLIGMPFMTIOLMGNGVHMGEMCLITAMANSQFTSTYILITAMADRYL 192
QY 144 AVHPISSTKRRKPSVATVYICLMLSFISIPVWMLARLPPGAVGCGIRLPNDT 203
DB 193 AVHPISSTKRRKPSVATVYICLMLSFISIPVWMLARLPPGAVGCGIRLPNDT 252
QY 204 DLYWETLYQFFLALFPVYITAAVYIILQMTSSVAPASQSRIRLTKRVTATAICL 263
DB 253 DLYWETLYQFFLALFPVYITAAVYIILQMTSSVAPASQSRIRLTKRVTATAICL 312
QY 264 VFEVCMAPIYVLOLTQISRPITFEYVLAISIGVANSCLNPFYIYLCTFRKRLV 323
DB 313 VFEVCMAPIYVLOLTQISRPITFEYVLAISIGVANSCLNPFYIYLCTFRKRLV 372
QY 324 LSVKPAAGOLRAVSNQTADEERTESKGT 353
DB 373 LSVKPAAGOLRAVSNQTADEERTESKGT 402

RESULT 3
SSR2_HUMAN STANDARD; PRT; 369 AA.
AC P30874;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Somatostatin receptor type 2 (SS2R) (SRIF-1).
GN SS2R.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92108031; PubMed=1346068;
RA Yamada Y., Post S.R., Wang K., Tager H.S., Bell G.I., Selino S.;
RT "Cloning and functional characterization of a family of human and
RT mouse somatostatin receptors expressed in brain, gastrointestinal
RT tract, and kidney.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:251-255(1992).
RN [2]
RP ALTERNATIVE SPLICING.
RX MEDLINE=93236586; PubMed=8386508;
RA Patel Y.C., Greenwood M., Kent G., Panetta R., Srikanth C.B.;
RT "Multiple gene transcripts of the somatostatin receptor SSR2: tissue
RT selective distribution and cAMP regulation.";
RL Biochem. Biophys. Res. Commun. 192:288-294(1993).
RN [3]
RP INTERACTION WITH SHANK1.
RX MEDLINE=20020275; PubMed=10551867;
RA Zitzer H., Hoencel H.-H., Beecher D., Richter D., Kreienkamp H.-J.;
RT "Somatostatin receptor interacting protein defines a novel family of
RT multidomain proteins present in human and rodent brain.";
RL J. Biol. Chem. 274:32997-33001(1999).
CC -1- FUNCTION: RECEPTOR FOR SOMATOSTATINS-14 AND -28. THIS RECEPTOR IS

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CC COUPLED VIA PERTUSSIS TOXIN SENSITIVE G PROTEINS TO INHIBITION OF
CC ADENYLATE CYCLASE. IN ADDITION IT STIMULATES PHOSPHORYLATION
CC PHOSPHATASE AND PLC VIA PERTUSSIS TOXIN INSENSITIVE AS WELL AS
CC SENSITIVE G PROTEINS. IN RIN 5F CELLS, THIS RECEPTOR INHIBITS
CC CALCIUM ENTRY BY SUPPRESSING VOLTAGE DEPENDENT CALCIUM-CHANNELS.
CC -1- SUBUNIT: THE C-TERMINUS INTERACTS WITH SHANK1 PDZ DOMAIN.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A (SHOWN HERE) AND B; ARE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: CEREBRUM AND KIDNEY. IN LESSER AMOUNTS IN
CC JEJUNUM, COLON, AND LIVER.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC
DR EMBL: M81830; AA58248.1; -.
DR PIR: B41795; B41795.
DR HSSE: P02699; 1B0J.
DR GeneW: HGNC:11331; SS2R.
DR MIM: 182452; -.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_REC_F1_1; 1.
DR PROSITE: PS50262; G_PROTEIN_REC_F1_2; 1.
DR KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multi-gene family; Lipoprotein; Palmitate; Alternative splicing.
FT DOMAIN 1 43
FT TRANSMEM 4 67
FT DOMAIN 68 78
FT TRANSMEM 79 103
FT DOMAIN 104 118
FT TRANSMEM 119 138
FT DOMAIN 139 161
FT TRANSMEM 162 181
FT DOMAIN 182 207
FT TRANSMEM 208 229
FT DOMAIN 230 253
FT TRANSMEM 254 278
FT DOMAIN 279 288
FT TRANSMEM 289 303
FT DOMAIN 304 369
FT CARBOHYD 9
FT CARBOHYD 22
FT CARBOHYD 29
FT CARBOHYD 32
FT DISULFID 115
FT LIPID 328
FT VANSPLIC 332
SQ SEQUENCE 369 AA; 41332 MW; 3B5D7D8A9AC446C6 CRC64;

Query Match 29.1%; Score 530.5; DB 1; Length 369;
Best Local Similarity 31.8%; Pred. No. 2.9e-24;
Matches 114; Conservative 75; Mismatches 128; Indels 41; Gaps 8;

QY 2 DLEASILPTGNASNTSGPNDLTASGSPRTGISISYINIMPSVFGTICLLGIIGNSY 61
DB 20 DLNGSVST--NTSQTPPYDILTS-----NAVLFTYVVCILGCGMTLV 64
QY 62 IFAYVVKSKLHMCNNVPDIFIIINLVYDLFLGMPF-----MIHDMGNGVHGEETM 115
DB 65 IYVILRYAKM---KTIWYIILNLAIDELFMLGLPLAMQVALVH-----WPECKAI 114
QY 116 CGLITAMANSQFSTYILITAMADRYLAVYHPSISKRRKPSVATVYICLMLASFIST 175
DB 115 CRVAVTVDGINQFTSIFCLTVMSIDRYLAVVHPITKSAKWRKRPRTAKITMAVGVSLVI 174

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ID	NAME	STANDARD	PRT	368 AA.
SSR2_5	SSR2_BOVIN			
AC	P34939			
DT	01-FEB-1994 (Rel. 28, Created)			
DT	01-FEB-1994 (Rel. 28, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Somatostatin receptor type 2 (SS2R) (SRIF-1).			
GN	SSR2.			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;			
OX	Bovidae; Bovinae; Bos.			
OX	NCBI_TaxID=9913;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RA	Xin W.W., Wong M.-L., Rimland J., Nestler E.J., Duman R.S.;			
RL	Submitted (XXX-1992) to the EMBL/Genbank/DBD databases.			
CC	-1- FUNCTION: RECEPTOR FOR SOMATOSTATINS-14 AND -28. THIS RECEPTOR IS			
CC	COUPLED VIA PERTUSSIS TOXIN SENSITIVE G PROTEINS TO INHIBITION OF			
CC	ADENYLATE CYCLASE. IN ADDITION IT STIMULATES PHOSPHOTYROSINE			
CC	PHOSPHATASE AND PLC VIA PERTUSSIS TOXIN INSENSITIVE AS WELL AS			
CC	SENSITIVE G PROTEINS. IN RIN 5F CELLS, THIS RECEPTOR INHIBITS			
CC	CALCIUM ENTRY BY SUPPRESSING VOLTAGE DEPENDENT CALCIUM-CHANNELS.			
CC	-1- SUBUNIT: The C-terminus interacts with SHANK1 PDZ domain (By			
CC	similarity).			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
CC	-----			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@sib-sib.ch).			
CC	-----			
DR	EMBL; L06613; AAA30764.1; -			
DR	HSSP; P02699; 180J			
DR	InterPro; IPR000276; GPCR_Rhodpsn.			
DR	Pfam; PF00001; 7tm_1.1.			
DR	PRINTS; PR00237; GPCRHOOPS.			
DR	PROSITE; PS00237; G_PROTEIN_REC_P1.1; 1.			
DR	PROSITE; PS00262; G_PROTEIN_REC_P1.2; 1.			
KW	G-protein coupled receptor; Transmembrane; Glycoprotein;			
KW	Multigene family; Lipoprotein; Palmitate.			
FT	DOMAIN 1 42			
FT	TRANSMEM 43 66			
FT	TRANSMEM 67 77			
FT	DOMAIN 78 102			
FT	TRANSMEM 103 137			
FT	DOMAIN 138 137			
FT	TRANSMEM 138 160			
FT	TRANSMEM 161 180			
FT	DOMAIN 181 206			
FT	TRANSMEM 207 228			
FT	DOMAIN 229 252			
FT	TRANSMEM 253 277			
FT	DOMAIN 278 287			
FT	TRANSMEM 288 302			
FT	DOMAIN 303 368			
FT	CARBOHYD 8 8			
FT	CARBOHYD 21 21			
FT	CARBOHYD 28 28			
FT	CARBOHYD 31 31			
FT	DISULFID 114 192			
FT	LIPID 327 327			
FT	PALMITATE (POTENTIAL).			

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SQ      SEQUENCE 368 AA: 41133 MW: 85852262626AB080B CRC64:
Query Match 28.9%; Score 528; DB 1; Length 368;
Best Local Similarity 31.5%; Pred. No. 4e-24;
Matches 116; Conservative 76; Mismatches 134; Indels 42; Gaps 9;

OY      1 MDLASELPLPGPNAS-----NTSDGPDNLTSGSPRTGSIYI---NIMSPVGTIC 51
          ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
DB      1 MDVSELNENQPMULTIPFDLNGSYGANINSQTEP-----YDASANVLFITFPVC 53
OY      52 LLGITGNTVIFAIVKRSKLHMCNNVPDIFINISVDLFLGMPF-----MIHOLMG 105
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      54 IIGCGTFLVIYILRYAKM---KRTITNYIILNLAIDELFMELGPLAMQVALVH--- 106
OY      106 NGVWHEPEMCTPLTAMDANSQTFSTYILTLAIDRYATLAVPSSRKPEKPSVATVLC 165
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      107 ---WPGKALICRVYAVDGINQFTISFCLTQWISIDRYAVVHPKSKMRPRTAMINV 163
OY      166 LLMALSEISTPFWYLARLIPFPGAVGGCIRLPNDTDLX-WETLYQFLAPALPFWVI 224
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      164 AVMGVSLTILVLPIMITYAGLRSMQGRSCCTIWPGESGAWTYGFIYAFILGFLVPLTII 223
OY      225 TAAVRLRLQMTSSVAPASQSRRLRLETKRVPTALICLQVFQOMAPYVYLQTLQSTIS- 283
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      224 CLCLFLFIIVKSSGIRVGSSKRKSEKKVTRMYSIVAVTFPCWDFLYFNWSSVAVI 283
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      284 RPTTFYVLYNAISLGYANSCLNPFVYVLCETPFRKRLVLSVPAAGOLRAVSAQAQ 343
          || : : : : ||||| || : : : : || : : : : || : : : :
DB      284 SPFLALGMDFEVLVLTANSCANPILVAFISDNRK-----SPQNVLCIVKVSQTD 335
OY      344 DEERTESK 351
          | : : : |
DB      336 DGRSDSK 343

RESULT 6
SSR2_PIG ID SSR2_PIG STANDARD; PRT; 369 AA.
AC P34994;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, last sequence update)
DT 15-JUN-2002 (Rel. 41, last annotation update)
DE Somatostatin receptor type 2 (SS2t) (SRF-1).
GN SSR2.
OS Sus scrofa (Pig).
OC Eukaryota; Euteleostomi; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN 11]
RP MEDLINE FROM N.A.
RX MEDLINE-94166590; PubMed-8123072;
RA Matsunoto K., Yokogoshi Y., Fujinaka Y., Zhang C., Saito S.;
RT "Molecular cloning and sequencing of porcine somatostatin receptor
RT 2"
RL Biochem. Biophys. Res. Commun. 199;298-305(1994).
CC -!- FUNCTION: RECEPTOR FOR SOMATOSTATIN-14 AND -28. THIS RECEPTOR IS
CC COUPLED VIA PERTUSSIS TOXIN SENSITIVE G PROTEINS TO INHIBITION OF
CC ADENYLYL CYCLASE. IN ADDITION IT STIMULATES PHOSPHOTYROSINE
CC PHOSPHATASE AND PLC VIA PERTUSSIS TOXIN INSENSITIVE AS WELL AS
CC SENSITIVE G PROTEINS. IN RIN 5F CELLS, THIS RECEPTOR INHIBITS
CC CALCIUM ENTRY BY SUPPRESSING VOLTAGE DEPENDENT CALCIUM-CHANNELS.
CC -!- SUBUNIT: The C-terminus interacts with SHANK1 PDZ domain (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).

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CC -----
EMBL: D21338; BAA04810.1; -.
DR PIR: JC2083; JC2083.
DR HSSP: P02699; 1BOJ.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_RECP_FL_1; 1.
DR PROSITE: PS50262; G_PROTEIN_RECP_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
  Multi-gene family; Lipoprotein; Palmitate
FT DOMAIN 1 43 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 44 67 1 (POTENTIAL).
FT DOMAIN 68 78 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 79 103 2 (POTENTIAL).
FT DOMAIN 104 118 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 119 138 3 (POTENTIAL).
FT DOMAIN 139 161 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 162 181 4 (POTENTIAL).
FT DOMAIN 182 207 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 208 229 5 (POTENTIAL).
FT DOMAIN 230 253 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 254 278 6 (POTENTIAL).
FT DOMAIN 279 288 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 289 303 7 (POTENTIAL).
FT DOMAIN 304 363 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 9 9 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 22 22 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 29 29 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 32 32 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 115 193 BY SIMILARITY.
FT LIPID 328 328 PALMITATE (POTENTIAL).
SQ SEQUENCE 369 AA; 41218 MW; C4C8347764ER2E70 CRC64;

Query Match 28.8%; Score 524.5; DB 1; Length 369;
Best Local Similarity 31.6%; Pred. No. 6.3e-24;
Matches 113; Conservative 75; Mismatches 129; Indels 41; Gaps 8;

QY 2 DLEASLTGPRASNTSGPRLNLSAGSPRTGSIYINIMPEVFGICLLGIGNSTV 61
DB 20 DLNGSVANA--NSSMOTPEPYDLTS-----NAVLITFYVCTIGLCGNLIV 64
QY 62 IFAAVKKSKLHMCNNVPDIFILNLSVDLFLGLGMPF-----MIHOLMGVNHFEETM 115
DB 65 IYVILIRYAKM--KITINIIYILNLAIDELMLGIPFLAMQVALVH-----WPGKAI 114
QY 116 CTLITAMPANDSQFSTYLLTAMADRYATVHPISSTKFRKPSVATLVICLLMALSPISI 175
DB 115 CHVYMTVDGINGQFSTIFCLTWSIDRYLAVVHPKSAKRPRRAKMINAVWGVSLVI 174
QY 176 TPVWLYARLIPPPGAVGCGIRLPMPDIDL-WFTLYOFFLAFALPFVITAAYVRIIQR 234
DB 175 LPIMITYAGIRSNQMGRRSSCTINMPESGAWTGTITVFIILGFLVPLTIIICLCFLIIR 234
QY 235 MTSSVAPASQSRISIRLTKRKTALTAICLVFVCMAPYVLIQLTQLSIS-REPLTEFVLY 293
DB 235 VASSGIRVGSKRKKSEKKEKVTMVSIVAVFEFCWLPYINNVSSVAISPTALKMKE 294
QY 294 NAAISLGANSCLNPFYIVIVLCETPRKRLVLSVKRAAGOLRAVSNQATDEERPREK 351
DB 295 DEVVVLTYSANSCANPLIYAFISDNFK-----SFQNVLCVAKVSGTDGERSDK 344

RESULT 7
SSR2_RAT STANDARD: PRT; 369 AA.
AC P30680;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Somatostatin receptor, type 2 (SSR2) (SRIF-1).
GN SSR2.
OS Rattus norvegicus (Rat).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92262491; PubMed=1374909;
RA Kluxen F.-W., Bruns C., Luebbert H.;
RT "Expression cloning of a rat brain somatostatin receptor cDNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4618-4622(1992).
RN [2]
RP SEQUENCE OF 76-81; 179-189; 294-320 AND 350-358.
RC TISSUE=pituitary;
RX MEDLINE=92231915; PubMed=1348934;
RA Hulmes J.D., Corbett M., Zysk J.R., Boehlen P., Eppeler C.M.;
RT "Partial amino acid sequence of a somatostatin receptor isolated from
  GH4C1 pituitary cells.";
RL Biochem. Biophys. Res. Commun. 184:131-136(1992).
RN [3]
RP ALTERNATIVE SPLICING;
RX MEDLINE=93336586; PubMed=8386508;
RA Patel Y.C., Greenwood M., Kent G., Panetta R., Srikanth C.B.;
RT "Multiple gene transcripts of the somatostatin receptor SSR2: tissue
  selective distribution and cAMP regulation.";
RL Biochem. Biophys. Res. Commun. 192:288-294(1993).
CC -1- FUNCTION: RECEPTOR FOR SOMATOSTATIN-14 AND -28. THIS RECEPTOR IS
  COUPLED VIA PERTUSSIS TOXIN SENSITIVE G PROTEINS TO INHIBITION OF
  ADENYLYL CYCLASE. IN ADDITION IT STIMULATES PHOSPHORYLASE
  PHOSPHATASE AND PLC VIA PERTUSSIS TOXIN INSENSITIVE AS WELL AS
  SENSITIVE G PROTEINS. IN RIN 5F CELLS, THIS RECEPTOR INHIBITS
  CALCIUM ENTRY BY SUPPRESSING VOLTAGE DEPENDENT CALCIUM CHANNELS.
CC -1- SUBUNIT: The C-terminus interacts with SHANK1 PDZ domain (by
  similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A (SHOWN HERE) AND B; ARE
  PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: CORTEX, HIPPOCAMPUS, PITUITARY GLAND, COLON
  ADRENALS, PANCREAS-DERIVED CELL LINE, AND PANCREATIC TUMOR.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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  or send an email to license@sib-sib.ch).
CC -----
EMBL: M96817; AAA42166.1; -.
DR EMBL: M93273; AAA42165.1; -.
DR PIR: A45291; A45291.
DR HSSP: P02699; 1BOJ.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_RECP_FL_1; 1.
DR PROSITE: PS50262; G_PROTEIN_RECP_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
  Multi-gene family; Lipoprotein; Palmitate; Alternative splicing.
FT DOMAIN 1 43 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 44 67 1 (POTENTIAL).
FT DOMAIN 68 78 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 79 103 2 (POTENTIAL).
FT DOMAIN 104 118 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 119 138 3 (POTENTIAL).
FT DOMAIN 139 161 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 162 181 4 (POTENTIAL).
FT DOMAIN 182 207 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 208 229 5 (POTENTIAL).
FT DOMAIN 230 253 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 254 278 6 (POTENTIAL).
FT DOMAIN 279 288 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 289 303 7 (POTENTIAL).

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FT DOMAIN 304 369 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 9 9 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 22 22 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 29 29 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 32 32 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 115 193 BY SIMILARITY.
FT LIPID 328 328 PALMITATE (POTENTIAL).
FT VARSPLIC 332 369 VSGADGERSDSKODKRSKRTORTLNGDLQSI ->
SQ SEQUENCE 369 AA: 41199 MW: 499084898887D19 CRC64:
Query Match 28.8%; Score 524.5; DB 1; Length 369;
Best local Similarity 31.6%; Pred. No. 6.3e-24;
Matches 113; Conservative 75; Mismatches 129; Indels 41; Gaps 8;

QY 2 DLEASLTPTGPNASNTSDGPDMLTSAGSPRRGTSYINIIIMPVSFGICLLIGISTV 61
DB 20 DLNGSLGFS--NQSNOTERYDMTS-----NAVLRTFYVVCVGLGNTLV 64
QY 62 IFAVVKRSLHMCNNVPDIFITILSVLDLELGMF-----MIHOLMGVWHFGETM 115
DB 65 IYVILRYAKM--KITTIYIILNLAIDELFELGLPFLAMQVALVH-----WPEGKAI 114
QY 116 CRLITMDMNSOFTSYITITAMIDRYLATVHPISSTFRKPSVATLVICLLMALSPISI 175
DB 115 CRVMTVDGINDOFTISFCLTVMSIDRYLAVHPKISAKMRPRTRAKMIVAWGVSLVI 174
QY 176 TPVWLVARLIPPGAVGCGIRLPNDPDLX-WFTLYOFLEFALFEVYITAAVRIILOR 234
DB 175 LPMIYVAGRSNOMGRSCTIWMGESGAWYGFITIAFIIIGLPLHICLCYLIILIK 234
QY 235 MNSVAPASORSLRLTKRVTFTALICLFEVVCAPYVYVQLQOLIS-RTLTFLYVLY 293
DB 235 VSSGSRVSSSKRKSSEKVKIVAVAFICWLPYITFNVSVAISAPALRGKF 294
QY 294 NAIISLGVANSCLEPNFYIVLCETFRKRLVLSVKRPAAGOCRAVNSAQTAEERTSK 351
DB 295 DEVFILTVANSCANPILYAFILSDNFKK-----SFQNVLCYKVSAGDEGERSDSK 344

RESULT 8
SSR4_HUMAN
ID SSR4_HUMAN STANDARD; PRT; 388 AA.
AC P31391; Q90IY1;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Somatostatin receptor type 4 (SS4R).
GN SSR4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93290656; PubMed=8512564;
RA Xu Y., Song J., Bruno J.F., Berelowitz M.;
RT Molecular cloning and sequencing of a human somatostatin receptor,
RT hSSR4.
RT Biochem. Biophys. Res. Commun. 193:648-652(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93248256; PubMed=8483934;
RA Rohrer L., Raulf F., Bruns C., Buettner R., Hofstaedter F.,
RA Schuele R.;
RT Cloning and characterization of a fourth human somatostatin
RT receptor.
RT Proc. Natl. Acad. Sci. U.S.A. 90:4196-4200(1993).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=93384611; PubMed=8373420;
RA Yamada Y., Kagimoto S., Kubota A., Yasuda K., Masuya Y.,
RA Ihara Y., Li Q., Imura H., Saino S., Saino Y.;

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RT "Cloning, functional expression and pharmacological characterization
RT of a fourth (hSSR4) and a fifth (hSSR5) human somatostatin receptor
RT subtype".
RT Biochem. Biophys. Res. Commun. 195:844-852(1993).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=93302729; PubMed=8100352;
RA Demehyshyn L.L., Strikant C.B., Sunahara R.K., Kent G., Seeman P.,
RA van Tol H.H.M., Panetta R., Patel Y.C., Niznik H.B.;
RT "Cloning and expression of a human somatostatin-14-selective receptor
RT variant (somatostatin receptor 4) located on chromosome 20."
RT Mol. Pharmacol. 43:894-901(1993).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=21638749; PubMed=11780052;
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grahame D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A., King A., Knights A., Laird G.K., Lawlor S.,
RA Levasailho M.H., Levesha M.A., Lloyd G., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConachie L.J., McKay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Molliken J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkhen R., Sims S.,
RA Skuce C.D., Smith M.T., Soderlund C., Steward C.A., Sultun J.E.,
RA Swann R.M., Symamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20."
RT Nature 414:865-871(2001).
RN [6]
RP RECEPTOR FOR SOMATOSTATIN-14. THE ACTIVITY OF THIS
RN RECEPTOR IS MEDIATED BY G PROTEINS WHICH INHIBITS ADENYLYL
RN CYCLASE. IT IS FUNCTIONALLY COUPLED NOT ONLY TO INHIBITION OF
RN ADENYLYL CYCLASE, BUT ALSO TO ACTIVATION OF BOTH ARACHIDONATE
RN RELEASE AND MITOGEN-ACTIVATED PROTEIN (MAP) KINASE CASCADE.
RN MEDIATES ANTIPROLIFERATIVE ACTION OF SOMATOSTATIN IN TUMOR CELLS.
RN - SUBCELLULAR LOCATION: Integral membrane protein.
RN - TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED IN FETAL AND ADULT
RN BRAIN, LONG TISSUE, STOMACH, AND IN LESSER QUANTITIES IN THE
RN KIDNEY, PITUITARY, AND ADRENALS.
RN - SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
RN -----
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RN or send an email to license@isb-sib.ch).
RN -----
DR EMBL: D16826; BAA04106.1; -
DR EMBL: L14856; AAA36623.1; -
DR EMBL: L07833; AAA60565.1; -
DR EMBL: AL049651; CAB51953.1; -
DR PIR: JN0762; JN0762.
DR PIR: JN0762; JN0762.
DR HSSP: P02699; IBOJ.
DR Gene: HGNC:11333; SSR4.
DR MIM: 162454; -
DR InterPro: IPR00276; GPCR_Rhodpsn.

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CC	FT	TRANSSEM	304	327	7 (POTENTIAL).
CC	FT	DOMAIN	328	391	CYTOPLASMIC (POTENTIAL).
CC	FT	CARBOHYD	4	4	N-LINKED (GLCNAC. . .) (POTENTIAL).
CC	FT	CARBOHYD	44	44	N-LINKED (GLCNAC. . .) (POTENTIAL).
CC	FT	CARBOHYD	48	48	N-LINKED (GLCNAC. . .) (POTENTIAL).
CC	FT	DISULFID	130	208	BY SIMILARITY.
CC	FT	LIPID	339	339	PALMITATE (POTENTIAL).
CC	SO	SEQUENCE	391 AA;	42746 MW;	28ED6E894B72FBF7 CRC64;
CC	Query Match		27.3%;	Score 497.5;	DB 1; Length 391;
CC	Best Local Similarity		32.3%;	pred. No. 2,4e-22;	
CC	Matches 104; Conservative		72;	Mismatches 129;	Indels 17; Gaps 7;
CC	QY	9	PTGNASTNSGCP-----DNLTSAG-SPPRGISYSY---INTIMPSEVGTICLGIIGNS	59	
CC	Db	18	PGGCGEGVCSCPGSGAADGMEEPGRSSQNGTISEGGSAILISFTISVYCVLGLGNS	77	
CC	QY	60	TVFAVAVVKKSLHMCNNVPDFFIINLSVYDLFLFLGMPFMHOLMGVWHFGETMCTLI	119	
CC	Db	78	MVIYVILRYAKMKATN---IYIINLIADDELLMLSVPELVTSFLRH-WPFGALLCRVY	133	
CC	QY	120	TAMDANSOFSTYIILITAMADRYLATVHPISISTFRKRSVATLVICLIMALSFTISIPW	179	
CC	Db	134	LSVDAVNMFTIYICLVISVDRYVAVHPDKAARYRREPTAKVYNLGVWVLSLVILPIV	193	
CC	QY	180	LYARLIPPGAVGGGIRLPNP-DTDLWFLTYOFLFAFLPFVYTAARYILQRMSS	238	
CC	Db	194	VFSRIANSIDGTIVACNMMLPEPAQRMLVGFVLYTFIMGFLPLPGALICLCYVLIANKMV	253	
CC	QY	239	VAPASRSIRLTKRKVTRFTAIALICLVEFCVCAPIYVIOLTOLISRPTLYVLYNMAIS	298	
CC	Db	254	ALKGMQOKRSERKITLMVMMVVAVEVICWMPFVYVQVNVFAEODATVSOI---SVI	310	
CC	QY	299	LGVANSCLNPFYIVICETFERK	320	
CC	Db	311	LGVANSCLNPLIYGLFSLDNFRK	332	
CC	RESULT 11				
CC	SSRL_HUMAN				
CC	ID	SSRL_HUMAN	STANDARD;	PRT;	391 AA.
CC	AC	P30872			
CC	DT	01-JUL-1993	(Rel. 26, Created)		
CC	DT	01-JUL-1993	(Rel. 26, Last sequence update)		
CC	DT	16-OCT-2001	(Rel. 40, Last annotation update)		
CC	DE	Somatostatin receptor type 1 (SSIR) (SRIF-2).			
CC	GN	SSRL.			
CC	OS	Homo sapiens (Human).			
CC	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
CC	OX	NCBI_TaxID=9606;			
CC	RN	[1]			
CC	RP	SEQUENCE FROM N.A.			
CC	RX	MEDLINE=92108031; PubMed=1346068;			
CC	RA	Yanada Y., Post S.R., Wang K., Rager H.S., Bell G.I., Seino S.;			
CC	RT	"Cloning and functional characterization of a family of human and			
CC	RT	mouse somatostatin receptors expressed in brain, gastrointestinal			
CC	RT	tract, and kidney.";			
CC	RL	Proc. Natl. Acad. Sci. U.S.A. 89:251-255(1992).			
CC	CC	-I- FUNCTION: RECEPTOR FOR SOMATOSTATIN WITH HIGHER AFFINITY FOR			
CC	CC	SOMATOSTATIN-14 THAN -28. THIS RECEPTOR IS COUPLED VIA PERTUSSIS			
CC	CC	TOXIN SENSITIVE G PROTEINS TO INHIBITION OF ADENYLYL CYCLASE. IN			
CC	CC	ADDITION IT STIMULATES PHOSPHOTRANSFER OF ADENYLYL CYCLASE AND NA+/H+			
CC	CC	EXCHANGER VIA PERTUSSIS TOXIN INSENSITIVE G PROTEINS.			
CC	CC	-I- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	CC	-I- TISSUE SPECIFICITY: FETAL KIDNEY, FETAL LIVER, AND ADULT PANCREAS,			
CC	CC	BRAIN, LUNG, JEJUNUM, AND STOMACH.			
CC	CC	-I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
CC	CC	-----			
CC	CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	CC	use by non-profit institutions as long as its content is in no			


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DE Somatostatin receptor type 1 (SSIR) (SRIF-2).
GN SSTRI OR SMSTR1.
OS Mus musculus (Mouse).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OK NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92108031; PubMed=1346068;
RA Yamada Y., Post S.R., Wang K., Tager H.S., Bell G.I., Seino S.;
RT "Cloning and functional characterization of a family of human and
RT mouse somatostatin receptors expressed in brain, gastrointestinal
RT tract, and kidney.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:251-255(1992).
CC -1- FUNCTION: RECEPTOR FOR SOMATOSTATIN WITH HIGHER AFFINITY FOR
CC SOMATOSTATIN-14 THAN -28. THIS RECEPTOR IS COUPLED VIA PERTUSSIS
CC TOXIN SENSITIVE G PROTEINS TO INHIBITION OF ADENYLATE CYCLASE. IN
CC ADDITION IT STIMULATES PHOSPHORYLASE KINASE AND NA+/H+
CC EXCHANGER VIA PERTUSSIS TOXIN INSENSITIVE G PROTEINS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: JEJUNUM AND STOMACH.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC -----
DR EMBL; M81831; AAA58255.1; -.
DR PIR; C41795; C41795.
DR MGD; MGI:98327; Smstr1.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECPT_FL1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECPT_FL2; 1.
DR KW G-protein coupled receptor; Transmembrane; Glycoprotein;
DR Multigene family; Lipoprotein; Palmitate.
FT DOMAIN 1 56
FT TRANSMEM 57 84
FT DOMAIN 85 94
FT TRANSMEM 95 120
FT DOMAIN 121 131
FT TRANSMEM 132 153
FT DOMAIN 154 175
FT TRANSMEM 176 196
FT DOMAIN 197 219
FT TRANSMEM 220 244
FT DOMAIN 245 270
FT TRANSMEM 271 296
FT DOMAIN 297 303
FT TRANSMEM 304 327
FT DOMAIN 328 391
FT CARBOHYD 4 4
FT CARBOHYD 44 44
FT CARBOHYD 48 48
FT DISULFID 130 208
FT LIPID 339 339
SQ SEQUENCE 391 AA; 42718 MW; 4461673956F2BD22 CRC64;
Query Match 27.2%; Score 496.5; DB 1; Length 391;
Best Local Similarity 32.5%; Pred. No. 2,7e-22;
Matches 101; Conservative 68; Mismatches 121; Indels 21; Gaps 5;
QY 11 GPAASTSDGPDNLTSAGSEPTGTSIYNIIMPVSFGTCLLIGTNSFVAVVKKSK 70
DB 42 GRNASSONGLTSEGOGSA-----ILSFIYSYCVLGLCGNSMVIYILRYAK 88
QY 71 LHCNVPDFITINLSVVDLLFLMGPEMIHQLMGNGVHHEFTMKTILTADANSQFTS 130

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DB 89 MKTATN---IYIINLAIDELMLSVPELVSTLNRH-WPFGALLCRVLSDAVNMFTS 144
QY 131 TYILTAMADRYLATVPISTFKRPSVATVTCILMALSFSTIPVYLRIPEFG 190
DB 145 IYCLTVLSVDRYVAVHPHKAARVRRPYAKVNVGNWLSLIVILPIYVFSTRANSNG 204
QY 191 AVCCGIRLDRNP-DTDLWFTLLQFLAPLPEVYVTAAYVRLQRTSSVAPASQSRIRL 249
DB 205 TVACNNLMPEPAPQRMVLGVGLVYTFLLMGFLPYGALICLVLLIAKRMVALKAGWQRRR 264
QY 250 RTRRVRTAIALCVFVCGAPYVYVQLNQLSISRPTLFVYLYNMAISIGVANSCLDF 309
DB 265 SEKKITLMMVMYVVICMPEYVQVAVNEAEQDATVSQL---SVILGANSCLNDI 321
QY 310 VYIVLCETPK 320
DB 322 LVGLSDNFKR 332
RESULT 13
SSR4_RAT
ID SSR4_RAT STANDARD; PRT; 384 AA.
AC P30937;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Somatostatin receptor type 4 (SSR4).
GN SSR4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OK NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=93087484; PubMed=1360663;
RA Bruno J.F., Xu Y., Song J., Berelowitz M.;
RT "Molecular cloning and functional expression of a brain-specific
RT somatostatin receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:11151-11155(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Hippocampus;
RX MEDLINE=94230347; PubMed=8175684;
RA Bito H., Mori M., Sakanaka C., Takano T., Honda Z., Gotoh Y.,
RA Nishida E., Shimizu T.;
RT "Functional coupling of SSR4, a major hippocampal somatostatin
RT receptor, to adenylyl cyclase inhibition, arachidonate release and
RT activation of the mitogen-activated protein kinase cascade.";
RL J. Biol. Chem. 269:12722-12730(1994).
CC -1- FUNCTION: RECEPTOR FOR SOMATOSTATIN-14. THE ACTIVITY OF THIS
CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH INHIBITS ADENYLATE
CC CYCLASE. IT IS FUNCTIONALLY COUPLED NOT ONLY TO INHIBITION OF
CC ADENYLATE CYCLASE, BUT ALSO TO ACTIVATION OF BOTH ARACHIDONATE
CC RELEASE AND MITOGEN-ACTIVATED PROTEIN (MAP) KINASE CASCADE.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: BRAIN, LUNGS, HEART AND ISLETS. MODERATE
CC LEVELS IN THE HIPPOCAMPUS, CORTEX, AND OLFACTORY BULB.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL; M96544; AAA42180.1; -.
DR EMBL; U04738; AAA17519.1; -.
DR PIR; A47249; A47249.
DR HSSP; P02699; IBOU.
DR InterPro; IPR000276; GPCR_Rhodopsn.

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DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PROSITE: PS00237; G_PROTEIN_RECPR_F1_1; 1.
DR PROSITE: PS50262; G_PROTEIN_RECPR_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multiene family; Lipoprotein; Palmitate.
FT DOMAIN 1 41 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 42 69 1 (POTENTIAL).
FT DOMAIN 70 79 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 80 105 2 (POTENTIAL).
FT DOMAIN 106 116 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 117 138 3 (POTENTIAL).
FT DOMAIN 139 160 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 161 181 4 (POTENTIAL).
FT DOMAIN 182 203 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 204 228 5 (POTENTIAL).
FT DOMAIN 229 254 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 255 280 6 (POTENTIAL).
FT DOMAIN 281 287 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 288 311 7 (POTENTIAL).
FT DOMAIN 312 384 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 21 21 N-LINKED (GLCNAC. .) (POTENTIAL).
FT DISULFID 115 194 BY SIMILARITY.
FT LIPID 323 323 PALMITATE (POTENTIAL).
SQ SEQUENCE 384 AA; 42087 MW; 044542BA922411B5 CRC64;

Query Match 27.1%; Score 494.5; DB 1; Length 384;
Best Local Similarity 33.0%; Pred. No. 3.5e-22;
Matches 104; Conservative 66; Mismatches 116; Indels 29; Gaps 8;

OY 16 NTSDDPDLTASGSPPTGSGISYINIIIMPVEFGTICLLIGISNVTIFAFAVKKSKLMCN 75
DB 21 NASAPDEEDAVNSDGTGTGAVTI--QCITAYLVCLVGLVGNALVIFVILIRAKMTAT 78
OY 76 NVPDFIINLSVVDLLFLFGMPFI-----HOLMGNGWHFGETMCTLTAMDANSOFT 129
DB 79 N---IYLLNLAVDELFLMVSFASALAH-----NPGFVLCRAVLSVGLNMFT 128
OY 130 SYITLTAADIRYATVPISTKFRKPSVATVYICLMAISFISIPVWLYARLIFPG 189
DB 129 SVECLTVLSVDRYAVVHPLRAATYRPSVAKNLINGWLASLWTLPTFAVFAUTRRARG 188
OY 190 G-AVGCIGIRLPDIDLYM---FTLYQFPLAFALFFVITAAVYRIIORMTSVAPASOR 245
DB 189 GEAVACNLMHPH-----AMSAVFVITFLGLPLVLAIGCYLLIYCKMAVALRAGWQ 244
OY 246 STRLTKRYTRALAIICLVFVGCAPRYVLOLTQISIRPLTFVLYLYNAISIGYANSC 305
DB 245 QRRSEKRTIRLVLMVVVFVLCWMPFYVOLNLFVTSIDAT--VNVHSLILSYANSC 301
OY 306 LNPFIYVLCETFRK 320
DB 302 ANPILIGFLSDNFR 316

RESULT 14
SSR4 MOUSE STANDARD: PRT; 384 AA.
AC P49660; 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Somatostatin receptor type 4 (SS4R).
GN SSTR4 OR SMSSTR4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N. A.
RC STRAIN=129/SVT; TISSUE=Liver;
RX MEDLINE=96194903; PUBMED=8654950;
Schwabe W., Brennan M.B., Hochgeschwender U.;

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RT Isolation and characterization of the mouse (Mus musculus)
RT somatostatin receptor type-4-encoding gene (SMSSTR4).";
RL E-Function: RECEPTOR FOR SOMATOSTATIN-14. THE ACTIVITY OF THIS
CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH INHIBITS ADENYLYL
CC CYCLASE. IT IS FUNCTIONALLY COUPLED NOT ONLY TO INHIBITION OF
CC ADENYLYL CYCLASE, BUT ALSO TO ACTIVATION OF BOTH ARACHIDONATE
CC RELEASE AND MITOGEN-ACTIVATED PROTEIN (MAP) KINASE CASCADE.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U26176; AAA67561.1; -.
DR HSP; P02699; 1BO1.
DR MGD; MGI:105372; SMSSTR4.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PROSITE: PS00237; G_PROTEIN_RECPR_F1_1; 1.
DR PROSITE: PS50262; G_PROTEIN_RECPR_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multiene family; Lipoprotein; Palmitate.
FT DOMAIN 1 41 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 42 69 1 (POTENTIAL).
FT DOMAIN 70 79 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 80 105 2 (POTENTIAL).
FT DOMAIN 106 116 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 117 138 3 (POTENTIAL).
FT DOMAIN 139 160 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 161 181 4 (POTENTIAL).
FT DOMAIN 182 203 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 204 228 5 (POTENTIAL).
FT DOMAIN 229 254 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 255 280 6 (POTENTIAL).
FT DOMAIN 281 287 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 288 311 7 (POTENTIAL).
FT DOMAIN 312 384 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 21 21 N-LINKED (GLCNAC. .) (POTENTIAL).
FT DISULFID 115 194 BY SIMILARITY.
FT LIPID 323 323 PALMITATE (POTENTIAL).
SQ SEQUENCE 384 AA; 42089 MW; 04DB0751481C6BBF CRC64;

Query Match 26.5%; Score 483; DB 1; Length 384;
Best Local Similarity 31.9%; Pred. No. 1.6e-21;
Matches 105; Conservative 69; Mismatches 133; Indels 22; Gaps 8;

OY 1 MDLEASL-----PTGPMNSNTSDGDNLTASGPPRTGSGISYINIIIMPVEFGTICLLGI 55
DB 1 MNAPATLIGVEDPTWTGPNASWAPQEDDAGSGGTAGAVTI--QCITAYLVCLV 58
OY 56 IGNSTVFAVVKSKLHMKNVPDFIINLSVVDLLFLGMPFIHOLMGNGVHFGETM 115
DB 59 VGNALVIFVILIRAKMTATN---IYLLNLAVADEFLMVSF--VNSAALRHMPGAVL 114
OY 116 CTLTAMDANSQTSYIITLMAIDRYATVHISSTKFRKPSVALVYICLMAISFISI 175
DB 115 CRAVLSDYDGLNMFVSCLTVLSVDRYAVVHPLRAATYRPSVAKNLINGWLASLWTL 174
OY 176 TPWLVYARLILPFGG-AVGCIGIRLPDIDLYM---FTLYQFPLAFALFFVITAAVYRI 231
DB 175 LPIAVFADTPRARGEEVACNLMHPH-----AMSASFVITFLGLPLPVLAIGCYLLI 230
OY 232 LQRTSSVAPASORSIRLTKRYTRALAIICLVFVGCAPRYVLOLTQISIRPLTFVY 291
DB 231 VGKRAVALNGWQRRRSSEKRTIRLVLMVVVFVLCWMPFYVOLNLFVTSIDAT--- 287

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OM protein - protein search, using sw model

Run on: February 13, 2003, 13:56:01 ; Search time 12.6809 Seconds

(without alignments)
2676.114 Million cell updates/sec

Title: US-09-885-478-28

Perfect score: 1824
Sequence: 1 MDLEASLPTGPNASNTSDG.....LRAVSNAGTADERTESKGT 353

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08

Maximum Match 100%
Listing first 45 summaries

Database :

PIR.73:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1824	100.0	422	2	JC7080 melanin-concentrat
2	565.5	31.0	340	2	JC7695 G protein-coupled
3	530.5	29.1	369	2	B41795 somatostatin recep
4	529.5	29.0	369	2	D41795 somatostatin recep
5	524.5	28.8	369	2	JC2083 somatostatin recep
6	524.5	28.8	369	2	A45291 somatostatin recep
7	511.5	28.0	346	2	S29248 somatostatin recep
8	505.5	27.7	388	2	JN0605 somatostatin recep
9	504.5	27.7	418	2	A46226 somatostatin recep
10	497.5	27.3	391	2	A39297 somatostatin recep
11	496.5	27.2	391	2	A41795 somatostatin recep
12	496.5	27.2	391	2	C41795 somatostatin recep
13	494.5	27.1	384	2	A47249 somatostatin recep
14	483	26.5	384	2	JC4629 brain-specific som
15	480.5	26.3	428	2	S30508 somatostatin recep
16	478.5	26.2	363	2	I57955 probable G protein
17	478.5	26.2	364	2	JN0763 somatostatin recep
18	472	25.9	428	2	A44021 somatostatin recep
19	470.5	25.8	363	2	I57940 somatostatin recep
20	452.5	24.8	372	2	I38532 delta opioid recep
21	446.5	24.5	372	2	S34592 delta opioid recep
22	444	24.3	392	2	S65693 delta opioid recep
23	444	24.3	400	2	I56553 opiod receptor mu
24	443	24.3	398	2	I56517 mu opiate receptor
25	442.5	24.3	398	2	A57510 mu opioid receptor
26	441	24.2	372	2	B48227 delta opioid recep
27	436	23.9	398	2	I56504 mu opioid receptor
28	433.5	23.8	380	2	JC2338 kappa opioid recep
29	426	23.4	380	2	A55259 kappa opioid recep

30	421	23.1	328	2	I38973 G protein-coupled
31	419	23.0	380	2	A48227 kappa opioid recep
32	419	23.0	380	2	S36143 kappa opioid recep
33	409.5	22.5	333	2	I38974 G protein-coupled
34	408.5	22.4	370	2	S43087 orphan opioid rece
35	408	22.4	380	2	JC2434 kappa opioid recep
36	407	22.3	373	2	JE0087 delta opioid recep
37	406.5	22.3	367	2	I49022 kappa opioid recep
38	406.5	22.3	367	2	JC2421 opiod receptor ho
39	406.5	22.3	367	2	I56520 G protein-coupled
40	372.5	20.4	359	2	I51372 angiotensin II rec
41	368	20.2	362	2	JN0694 angiotensin II rec
42	361	19.8	423	2	JC7677 allatostatin recep
43	347	19.0	371	2	JC5796 probable chemoatr
44	341	18.7	350	2	A42009 N-formyl peptide r
45	341	18.7	359	2	A42656 angiotensin II rec

ALIGNMENTS

RESULT 1

JC7080 melanin-concentrating hormone receptor [validated] - human

N:Alternate names: MCHR; orphan somatostatin-like receptor 1 (SLC-1)

C:Species: Homo sapiens (man)

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 11-May-2000

C:Accession: JC7080

R:Shimomura, Y.; Morl, M.; Sugo, T.; Ishibashi, Y.; Abe, M.; Kurokawa, T.; Onda, H.; Blochem. Biophys. Res. Commun. 261, 622-626, 1999

A:Title: Isolation and identification of melanin-concentrating hormone as the endogen

A:Reference number: JC7080; MUID:99373129; PMID:10441476

A:Accession: JC7080

A:Molecule type: mRNA

A:Residues: 1-422 <SH1>

A>Note: It is uncertain wheather Met-1, Met-6 or Met-70 is the initiation codon

C:Superfamily: neukokinin 1 receptor

C:Keywords: hormone receptor; transmembrane protein

Query Match 100.0%; Score 1824; DB 2; Length 422;

Best Local Similarity 100.0%; Pred. No. 3.5e-152;

Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MDLEASLPTGPNASNTSDGPNLTSSAGSPRTGSISYINIIIMPSEFTLLGIGNST	60
DB	70	MDLEASLPTGPNASNTSDGPNLTSSAGSPRTGSISYINIIIMPSEFTLLGIGNST	129
QY	61	VIFPAVVKSKLHWCNVDPDIFINLSVVDLFLGMPMIHQMGNGVWHRGETMCTLIIT	120
DB	130	VIFPAVVKSKLHWCNVDPDIFINLSVVDLFLGMPMIHQMGNGVWHRGETMCTLIIT	189
QY	121	AMDANSQFTSYILFAMADIRLATVHPISSTKPKKPSVAATLVLCIMALSFIITPWL	180
DB	190	AMDANSQFTSYILFAMADIRLATVHPISSTKPKKPSVAATLVLCIMALSFIITPWL	249
QY	181	YARLIPFGAVGCGIRLPNDTLYMFTLYOFIAFAFLPVPVITAAVRILOMTSSVA	240
DB	250	YARLIPFGAVGCGIRLPNDTLYMFTLYOFIAFAFLPVPVITAAVRILOMTSSVA	309
QY	241	PASQSRILRTKRVTRIAIAICLVFVCGAPYVVLQTLQSTISRPITLFFVLYNAATSLG	300
DB	310	PASQSRILRTKRVTRIAIAICLVFVCGAPYVVLQTLQSTISRPITLFFVLYNAATSLG	369
QY	301	YANSCLNFEVYIVICFEPKRLIVSVPAAGOLRAVSNAGTADERTESKGT	353
DB	370	YANSCLNFEVYIVICFEPKRLIVSVPAAGOLRAVSNAGTADERTESKGT	422

RESULT 2

JC7695 G protein-coupled receptor, SLT receptor - human

C:Species: Homo sapiens (man)

C>Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 22-Oct-2001

C:Accession: JC7695
B:Mori, M.; Harada, M., Terao, Y.; Sugo, T.; Watanabe, T.; Shimomura, Y.; Abe, M.; Shint Biorchim. Biophys. Res. Commun. 283, 1013-1018, 2001

A>Title: Cloning of a novel G protein-coupled receptor, SLT, a subtype of the melanin-co A:Reference number: JC7695; MUID:21255282; PMID:1135873

A:Contents: Hippocampus

A:Accession: JC7695

A:Molecule type: mRNA

A:Residues: 1-340 <MOR>

A:Cross-references: DDBJ:AB060151

C:Comment: This receptor, a second subtype of the melanin-concentrating hormone (MCH) re memory.

C:Genetics:

A:Gene: slt

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; transmembrane protein

```
Query Match          31.0%; Score 565.5; DB 2; Length 340;  
Best Local Similarity 37.0%; Pred. No. 5.5e-42;  
Matches   113; Conservative    62; Mismatches 119; Indels     11; Gaps      4;  
  
Oy       41 IIMPSVFETCLLGLTGNSYIVFAVVKSKSLHMCNNVPDITILNLSVDLFLLGMPMI 100  
           :|::||: ||:||: |::| ::|:: |::||: |:~::~|::|::||: |:  
Db        35 VLPFMIGIICTGTVGNILIFTLIRSRK---KYPDPIICMLAADVHIHYGMFLLI 90  
           :||:||||: |::||:|:|::|::|: ~~~~~|::|::|::||:|  
Oy       101 HOLMGNGWHGEFTCCLTITAMDANSQPTSTYLITAMADLYLATVHPISSTKRKKSSVA 160  
           || ~~~||: ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
Db        91 HDMAGGEMVGEGPLCTITTSIDTCNCNPACSAIMTYMSVDRYEALNVDFRLTRRTTKYT 150  
           || ~~~||: ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
Oy       161 TLVICLLMALSFISTTPWVLARLIPEPGAVGGCIRLPNDPDTLVWFETYQLFLAFALP 220  
           :||: ||||: ||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
Db       151 IRINGLMANASFIIALPWVVYSKIYKFMDGVESCFDLTSPD-DVLMTYLTLTTTFEPFP 209  
           ||||: ||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
Oy       221 FVTIAAAVRIL-----QRMTSVAPASQRSI-RLRTRKRVRFPAICLVFCVCAPAAYV 274  
           :||: ||||: ||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
Db       210 LPLLIVCYILLICYWEHYQQCKDKRCNCPSPYPKORVMKLKMWLVLYVVIISAAPHV 269  
           :||: ||||: ||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
Oy       275 IOLVOLSIISRPLTFEVYLYYNMAISLGYANSCINPFVYIVLCIEPRFKRRLVSVKPPDAQGQL 334  
           :||: ||||: ||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
Db       270 IOLVNLQMGPFLPAYVGYLISTCLSYASSSINPELLYILLSGNCRKRLPOLRRATERKEI 329  
           :||: ||||: ||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
Oy       335 RAASN 339  
           :|  
Db       330 NNNGN 334  
           :|  
  
RESULT 3  
BA1795  
somatostatin receptor 2 - human  
C:Species: Homo sapiens (man)  
C>Date: 31-Dec-1993 #sequence revision 31-Dec-1993 #text change 24-Nov-1999  
C:Accession: BA1795  
R.Yamada, Y.; Acosta, S.R.; Wang, K.; Tagger, H.S.; Bell, G.I.; Selino, S.  
A:Title: Cloning and functional characterization of a family of human and mouse somatos-  
tic reference numbers: AA1795; MUID:92108031; PMID:1346068  
A:Accession: BA1795  
A:Molecule type: DNA  
A:Residues: 1-369 <YANA>  
A:Cross-references: GB:M61830; NID:g307435; PIDN:AAA58248.1; PTD:g307436  
A>Note: sequence extracted from NCBI backbone (NCBIN:74769; NCBP:74770)

C:Genetics:



A:Gene: GDB:SSTR2



A:Cross-references: GDB:I34186; OMTM:182452



A:Map position: I7q24-I7q24



A:Introns: #status absent



C:Superfamily: vertebrate rhodopsin



C:Keywords: G protein-coupled receptor; glycoprotein; hormone receptor; lipoprotein; phn-



F:80-105/Domain: transmembrane #status predicted <TM2>



F:117-138/Domain: transmembrane #status predicted <TM3>



F:158-180/Domain: transmembrane #status predicted <TM4>



F:205-235/Domain: transmembrane #status predicted <TM5>


```

F:254-261/Domain: transmembrane #status predicted <TM6>
F:288-315/Domain: transmembrane #status predicted <TM7>
F:9-22/29_32,351/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:15-193/disulfide bonds: #status predicted
F:250/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status pre
F:328/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match 29.1%; Score 530.5; DB 2; Length 369;
Best Local Similarity 31.8%; Pred. No. 7e-39;
Matches 114; Conservative 75; Mismatches 128; Indels 41; Gaps 8;

D DLEASLLTTPGRNASTSGDPDNLTSAGSPRTGISTYINIIIMPVFGICLIGNSTV 61
|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||
20 DLNGSVST--NTSQTEPPYYDLTS-----NAVLTFIVVCITIGCGMTLV 64
62 IFAVVKSKSLHMCNNVPDIIFILINSVDLLFLGMPF-----MIHOLMGNVHFGETM 115
:::||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
65 IYIIRIRAKM---KITIMIIYLINALADELMGLPIAMQVALVH-----WPGKAI 114
CTLTAMDANDSOGFTSYLLTAADRYLATVHPISSTFKRPSVAITYCLMALSFSTI 175
:::||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db CRYVTMTVGIDQINFTEICTFLTWSIDRYLAVVHPIKSAKRBRPAKMITMAVWGSLVI 174
116 TFWMLIARLIERPBGAVOCGIRLPNDPDL-WFTLYOFPILAPLFVEVITAAYRIOR 234
:::||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Qy I75 LPTMIYAGIRSNQWRSSCTTNWPGESEGAWYGTFFITFIIGFLVPLTLICLFIITIK 234
176 TFWMLIARLIERPBGAVOCGIRLPNDPDL-WFTLYOFPILAPLFVEVITAAYRIOR 234
:::||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db I75 LPTMIYAGIRSNQWRSSCTTNWPGESEGAWYGTFFITFIIGFLVPLTLICLFIITIK 234
235 MTSSVAPASQRISIRTRTKRTALAIQLFEVCAPARYVLQLOLSIS-RPTLIFYLY 293
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 235 VASSGIRGVSSKKRKSEKKVFPMVSIVAVAFICFCLLPYIFNVSVSAISPALKGMF 294
294 NAAISLGANSCLNPFYIVLCETFRKRLVLSVKRAAQOLRAVNSAOTADERESK 351
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 295 DEVVYLTYSANCANPILYAFISDNFKK-----SFQNVLCVLYKVSQTDDGERDSK 344

RESULT 4
D41795
somatostatin receptor 2 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 24-Nov-1999
C:Accession: D41795; I56236
Riyamada, Y.; Post, S.R.; Wang, K.; Tager, H.S.; Bell, G.I.; Selho, S.
Proc. Natl. Acad. Sci. U.S.A. 89, 251-255, 1992
A>Title: Cloning and functional characterization of a family of human and mouse somat
A:Reference number: A41795; MUID:92108031; PMID:1346068
A:Accession: D41795
A>Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-369 <YAN>
A:Cross-references: GB:M8183; NID:g201060; PIDN:AAA58256.1; PTD:g201061
R.Bellotti, D.E.; Metwalli, A.; Blum, A.M.; Sandor, M.; Lynch, R.; Weinstein, J.V.
J. Immunol. 153, 1180-1186, 1994
A>Title: T lymphocytes isolated from the hepatic granulomas of schistosome-infected m
A:Reference number: I56236; MUID:94300079; PMID:7913111
A:Accession: I56236
A:Molecule type: mRNA
A:Molecule type: translated from GB/EMBL/DBJ
A>Status: preliminary;
A:Residues: 99-309 <RES>
A:Cross-references: GB:S71756; NID:g560631
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; hormone receptor; transmembrane protein

Query Match 29.0%; Score 529.5; DB 2; Length 369;
Best Local Similarity 31.8%; Pred. No. 8.6e-39;
Matches 114; Conservative 75; Mismatches 128; Indels 41; Gaps 8;

Qy 2 DLEASLLTTPGRNASTSDGPDNLTSAGSPRTGISTYINIIIMPVFGICLIGNSTV 61
|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||
Db 20 DLNGSLGPS--NGSNQTEPPYYDMTS-----NAVLTFIVVCVAGLGGMTLV 64
62 IFAVVKSKSLHMCNNVPDIIFILINSVDLLFLGMPF-----MIHOLMGNVHFGETM 115
:::||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Qy 62 IFAVVKSKSLHMCNNVPDIIFILINSVDLLFLGMPF-----MIHOLMGNVHFGETM 115
:::||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

[illegible]

RESULT 8

somatostatin receptor 4 - human
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 20-Jun-2000
C:Accession: JN0605; JN0762; D47457
R:Xu, Y.; Song, J.; Bruno, J.F.; Berelowitz, M.
Biochem. Biophys. Res. Commun. 193, 648-652, 1993
A:Title: Molecular cloning and sequencing of a human somatostatin receptor, hSSTR4.
A:Reference number: JN0605; MUID:93290656; PMID:8512564
A:Accession: JN0605
A:Molecule type: DNA
A:Residues: 1-388 <XUY>
A:Cross-references: GB:LI4856; NID:g292499; PIDN:AAA36623.1; PID:g292500
R:Iimada, Y.; Kagiimoto, S.; Kubota, A.; Yasuda, K.; Masuda, K.; Someya, Y.; Ihara, Y.; I
Biochem. Biophys. Res. Commun. 195, 844-852, 1993
A:Title: Cloning, functional expression and pharmacological characterization of a fourth
A:Reference number: JN0762; MUID:93384611; PMID:8373420
A:Accession: JN0762
A:Molecule type: DNA
A:Residues: 1-388 <YAM>
A:Cross-references: GB:D16826; NID:g653907; PIDN:BA04106.1; PID:g653908
R:Kotter, L.; Raulf, F.; Bruns, C.; Buettner, R.; Hofstaedter, F.; Schulte, R.
A:Title: Natl. Acad. Sci. U.S.A. 90, 4196-4200, 1993
A:Title: Cloning and characterization of a fourth human somatostatin receptor.
A:Reference number: A47457; MUID:93248256; PMID:8483934
A:Accession: A47457
A:Molecule type: DNA
A:Residues: 1-82, 'T', 84-364, 'K', 366-388 <ROH>
A:Cross-references: GB:L07833; NID:g307429; PIDN:AAA60565.1; PID:g307430
A:Note: sequence extracted from NCBI backbone (NCBI:n130856, NCBI:p130858)
C:Comment: This protein mediates the diverse actions of the tetradecapide somatostatin
C:Genetics:
A:Gene: GDB:SSTR4
A:Cross-references: GDB:202662; OMIM:182454
A:Map position: 20p11.2-20p11.2
A:Introns: #status absent
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; hormone receptor; lipoprotein; pho
F:47-73/Domain: transmembrane #status predicted <TM1>
F:84-109/Domain: transmembrane #status predicted <TM2>
F:121-142/Domain: transmembrane #status predicted <TM3>
F:162-184/Domain: transmembrane #status predicted <TM4>
F:208-228/Domain: transmembrane #status predicted <TM5>
F:257-284/Domain: transmembrane #status predicted <TM6>
F:291-314/Domain: transmembrane #status predicted <TM7>

F,24/Binding site: carboxylate (asn) (covalent) #status predicted
F,119-198/Disulfide bonds: #status predicted
F,161,253/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status:
F,332/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match

Best Local Similarity 32.0%; Pred. No. 1.2e-36;
Matches 107; Conservative 73; Mismatches 117; Indels 37; Gaps 9,

QY 6 SLDPG-----PAASNTSGPNDLTSGAGSPPTGSGSYINILIMPVFQTLGII 56
 QY 6 SLDPG-----PAASNTSGPNDLTSGAGSPPTGSGSYINILIMPVFQTLGII 56
 Db 5 SLDPGGEGLGTAMPASANAASSAPAEAEVAGPGDARAAG-VAIQCIYALNCTGLV 63
 QY 57 GNSVITAVYAKSKSLHMCNNVPDIFIIINLSVOLLTLGMPFI-----HQLMGNGYWH 110
 Db 64 GNAIVFVLLRYAMKTATN---LYLLINLAADLEPMLSPFPVSAALRHH-----WP 113
 QY 111 FGEIMCETLTAMANDSOFTSTLYLTAMAIDRYLATVHPISSTFKRKPVSATVILCLMAL 170
 Db 114 FGSVLCRAVLVSQGLMNFTEVFCGLTVLSVDYVAAYVHHPLRAATYRRSPVAKILNGVWLA 173
 QY 171 SFISITPVMYLAKLIPPGG-ANGCGIRLNPDTDLXW--FLIYQFLAFMLPRVYITA 226
 Db 174 SLVLTEDIAIFADRPARGGOAACINQWHP-----AMSAVFVYVYFLLGFLIPVLAIGL 229
 QY 227 AYVRLDRMTSSVAPASORSIRLTRKRVYETAALICLFEVFCAPYVYQLTQLSISPT 286
 Db 230 CYLLIVGKMRVAVALRAQMOQRSEKKITRLVLYMVVYVYELCMPPYVYQLLNLVTSID 289
 QY 287 LTFVYLYNAISIGYANSCINPFIYVYLCETFRK 320
 Db 290 AT---VNVHVSLLISYANSCANPILYGLFSIDNEFR 320

RESULT 9

somatostatin receptor 3 - human
 C:Species: Homo sapiens (man)
 C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_Change 24-Nov-1999
 C:Accession: A46226; S32501
 R:Yamada, Y.; Reisine, T.; Law, S.F.; Ihara, Y.; Kubota, A.; Kagimoto, S.; Seino, M.,
 Mol. Endocrinol. 6, 2136-2142, 1992
 A:Title: Somatostatin receptors, an expanding gene family: cloning and functional chan
 A:Reference number: A46226; PMID:93149123; PMID:1337145
 A:Accession: A46226
 A:Molecule type: DNA
 A:Residues: 1-418 <YAM>
 A:Cross-references: GB:M6738; NID:q338498; PIDN:AAA60592.1; PID:q338499
 A:Note: Sequence extracted from NCBI Backbone (NCBI:123665, NCBI:P.123690)
 R:Connors, J.D.; Demchigshyln, L.T.; Seeman, P.; van Tol, H.H.M.; Srikant, C.B.; Kent,
 FEBS Lett. 321, 279-284, 1993
 A:Title: A human somatostatin receptor (SSTR3), located on chromosome 22, displays pr
 A:Reference number: S32501; PMID:93238970; PMID:8094749
 A:Accession: S32501
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-418 <COR>
 C:Genetics:
 A:Gene: GDB:SSTR3
 A:Cross-references: GDB:134187; OMIM:182453
 A:Map position: 22q13.1-22q13.1
 A:Introns: #status absent
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane p
 F:44-70/Domain: transmembrane #status predicted <TM2>
 F:81-106/Domain: transmembrane #status predicted <TM2>
 F:118-139/Domain: transmembrane #status predicted <TM3>
 F:159-181/Domain: transmembrane #status predicted <TM4>
 F:203-233/Domain: transmembrane #status predicted <TM5>
 F:255-282/Domain: transmembrane #status predicted <TM6>
 F:289-316/Domain: transmembrane #status predicted <TM7>
 F:17-30/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:116-191/Disulfide bonds: #status predicted

F:151;251;317;332/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F:251/Binding site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status predicted
F:256/Binding site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status predicted
F:412/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 27.7%; Score 504.5; DB 2; Length 418;
Best Local Similarity 32.5%; Pred. No. 1.5e-36;
Matches 118; Conservative 76; Mismatches 134; Indels 35; Gaps 11;

QY 12 PNASNTSDGPNLTLSAGSP-----PRTGISITINIMESVFGTICLLIGNSTV 61
| : : : | - | : | : | :
6 PSSVTSTSEPNASAMPDPDALTGNVSAGSPSAPGLAVSGVLDIPLYLVWCVGILGNSLV 65
QY IFVAVKKSLTHMCNNVPDIFINTLSVDLFLTMPFIHDMNGV--WHFGETMCTLI 119
| :
Db IYYVLRIHTA---SSSVNIVYLINALDELPMGLPELAAD--NALSYMPFGSLMKRLV 119
QY 120 TAMDANSOFTSYLLITAMADRYLATVHPISSTFKRRPSVATVICTLMALSFISTPPW 179
| :
Db MAVDGINOFSTIFCLTVWSVDRLAVVHPTRSAMRTPARVARTSAVMVASAVVLPVV 179
QY 180 LYARLIRPGGAVCGIRLEPMDIDLYW---FLTLYGFPLALPFPVVIATAVVRILLQMT 236
Db 180 VFSGV---PRMSSTCHMQWPEPA--AKRAGFITTTALALGGFGLVYCICCYLLIYVKVR 234
QY 237 SS----VAPASORSIRLRKTFRRTAIAICLFECVCAPIYVLOLTOLTSIRP--TLTFEYV 291
| :
Db 235 SAGRHWAPSCQR--RSERERTRMVAVVALFVLCCMWPFVLVINNVVCPLEPAPAFG 293
QY 292 LYNNAISLGYSNQLNPVYIVLCETPR--KRVLVSKPAQGQLRAVSNAGADEERT 348
| :
Db 294 LYELVALPYANSCANPIILYGFLSTRFKGRFRRVLRPRSRVRSQEPTVGPEKTEBEDE 353
QY 349 ESK 351
| :
Db 354 EEE 356

RESULT 10
A39297 somatostatin receptor - rat
N:Alternate names: probable G-protein-coupled receptor; SRIF receptor
C:Species: Rattus norvegicus (Norway rat)
C>Date: 03-Aug-1992 #sequence_revision 03-Aug-1992 #text_change 24-Nov-1999
C:Accession: A39297; A45102; S20088
R:Myerhof, W.; Pause, H.J.; Schoenrock, C.; Richter, D.
DNA Cell Biol. 10, 689-694, 1991
A>Title: Cloning of a cDNA encoding a novel putative G-protein-coupled receptor expressed
A:Reference number: A39297; MUID:920960119; PMID:1661559
A:Accession: A39297
A:Molecule type: mRNA
A:Residues: 1-391 <ME>
A:Cross-references: GB:X62314; GB:X61630; NID:g56309; PIDN:CAA4193.1; PID:g56310
A:Experimental source: brain
R:Bli, X.J.; Forte, M.; North, R.A.; Ross, C.A.; Snyder, S.H.
J. Biol. Chem. 267, 21307-21312, 1992
A>Title: Cloning and expression of a rat somatostatin receptor enriched in brain.
A:Reference number: A45102; MUID:93016064; PMID:1400442
A:Accession: A45102
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-391
A:Experimental source: brain
A>Note: Sequence extracted from NCBI backbone (NCBIF:116692)
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; receptor; transmembrane protein

Query Match 27.3%; Score 497.5; DB 2; Length 391;
Best Local Similarity 32.3%; Pred. No. 5.0e-36;
Matches 104; Conservative 72; Mismatches 129; Indels 17; Gaps 7;

9 PTGNASNTSGP-----DNLTSG-SPPRTGSISY--INIMPSVFGTICLLIGINS 59

Dd		: :	:	: :	:	:::	{ } :	{ }
Db	PEGCGEGYCSKPGSGADGMEPEGRNSSQNGTSLSEGGASALLISFIYSVCVLGLCNS	77						
Oy	TIVFAVAKSKRLHMCNNVPDIFIIINLSVDLLFLLGMPFMIHQMGNCVMHGECTCLI	119						
Dd	MVIYIILRAKKMKATN---ITLNLAIADELMIMSVPLVTSTLRH-WFGALLCRLV	133						
Oy	LTMANDNQSFSTYYILLTAAMDRIYLAVTHPDISSTRKRKSRYTYICLLMAISFSIPYW	179						
Dd	LTSDVAWNMTSYTCYTCLLVSDRIVAVVHPILKAIRRPPTAAKNVGWMLGVTLVVLPETV	193						
Oy	IYAARLIPEPGAAGCGIGILPNP-DTDLYMFTLYGFELAFAPFYVTVTAAYRIIQRTSS	238						
Dd	VESFRPAANSDDGTACNMMLPEQAQMVLGEVFYLFIMGELLPVGAICTCYLIAAKMMV	253						
Oy	VAPSQRSRTRLTKRVTRATAICLYFFVCNAPIYVOLDTQLSISRPLLTFVIIYMIAIS	298						
Dd	ALKAWOQRKRERKITLMVMVMVFVICWMPFYVOLVNVEAEDDATVSOL--SVI	310						
Oy	LGYNASCNPFPYIVILECFRK	320						
Dd	LGYNANCPPIIFYGLSDNFRR	332						
RESULT	11							
A:1795	somatostatin receptor 1 - human							
C:Species:	Homo sapiens (man)							
C:Date:	31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 24-Nov-1999							
C:Accession:	A41795							
R:Yamada,Y.; Postl,S.R.; Wang,K.; Tager,H.S.; Bell,G.I.; Selino,S.								
Proc.Natl.Acad.Sci.U.S.A.	89; 1251-1255, 1992							
A:Title:	Cloning and functional characterization of a family of human and mouse somat-							
A:Reference number:	A41795; MUID:92108031; PMID:1346068							
A:Accession:	AA1795							
A:Molecule type:	DNA							
A:Residues:	1-391 <YAM>							
A:Cross-references:	GK:M61829; NID:g307433; PIDN:AAA58247.1; PID:g307434							
A>Note:	sequence extracted from NCBI backbone (NCBIN:74767, NCBP:74768)							
C:Genetics:								
A:Gene:	GDB::SSTR1							
A:Cross-references:	GDB:134185; OMIM:182451							
A:Map position:	14q13-q13							
A:Intons:	#status absent							
C:Subfamily:	vertebrate rhodopsin							
C:Keywords:	G protein-coupled receptor; glycoprotein; hormone receptor; lipoprotein;							
F:58-84/Domain:	transmembrane #status predicted <TM1>							
F:95-120/Domain:	transmembrane #status predicted <TM2>							
F:132-153/Domain:	transmembrane #status predicted <TM3>							
F:173-195/Domain:	transmembrane #status predicted <TM4>							
F:220-250/Domain:	transmembrane #status predicted <TM5>							
F:269-296/Domain:	transmembrane #status predicted <TM6>							
F:302-326/Domain:	transmembrane #status predicted <TM7>							
F:4,44,48,381/Binding site:	carbohydrate (Asn) (covalent) #status predicted							
F:130-208/Dissulfide bonds:	#status predicted							
F:172-Binding site:	phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status pre-							
E:265/Binding site:	phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status pre-							
F:339/Binding site:	palmolate (Cys) (covalent) #status predicted							
Query Match	27.2%; Score 496.5; DB 2; Length 391;							
Best Local Similarity	32.5%; Pred.No. 7,le=36;							
Matches 101; Conservative	68; Mismatches 121; Indels 21; Gaps 5;							
Oy	GNPASNTSDGPDLNLTSAQSPPRTGSITIINIIMPSECTCLLGIINGSIYIFAANKSK	70						
Dd	GNNASONGTSLSEGOGA-----ILISPISVCLVGLGCNSMWIYILRAYK	88						
Oy	LHMCAANNVPDEFIINSYVDLFLGMPPNIHQMGNCVMHGECUTCLITLTMANDNQSTS	130						
Dd	KMTAIN----ITYLNLAIDEMLSYPFLVYSTLRH-WFGALLCRLVLSVDAWNMTS	144						
Oy	TYLTRAMAIDRYLATVHPISSTRFKPSVALVTICLLMALSFISTTPPWILTARIIPPBG	190						

Db 145 IYCLFVLSVDKYVAVVHPKAKARYRRPTVAKVNLGVWVLSLVLPIVESTRFANS DG 204
 QY 191 AVGGCIRLELNP-DTDLVMTLTKOFLFALPFPVITAAVYVILQRMSSVAPASQSRIRL 249
 Db 205 TVACNMLMEPEAPQRMVGVGLTFLMGLPVGALICLCYVILIKMRVVALKAGWQQRK 264
 QY 250 RKRRTVTRTAICLVFEVCMAPYVVLQTLQSLISRPITLFFVLYNAAISLGANSCLNPF 309
 Db 265 SERKITIMAMVAVVFIWCMPEFYVQLVWVFAEDDQDATVSQI---SVILGYANSCANPI 321
 QY 310 VYIVLCETFRK 320
 Db 322 LYGFSLDNFKR 332

RESULT 12

C41795

somatostatin receptor 1 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1993 #sequence_revision 31-Dec-1993 #text_change 24-Nov-1999

C:Accession: C41795

R:Name: Y.; Post, S.R.; Wang, K.; Tager, H.S.; Bell, G.I.; Selino, S.

Proc. Natl. Acad. Sci. U.S.A. 89, 251-255, 1992

A:Title: Cloning and functional characterization of a family of human and mouse somatost

A:Reference number: A41795; MUID:92108031; PMID:1346068

A:Accession: C41795

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-391 <YAM>

A:Cross-References: GB:M81831; NID:9201058; PIDN:AAA58255.1; PID:9201059

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; hormone receptor; transmembrane protein

Query Match

Best Local Similarity 32.5%; Score 496.5; DB 2; Length 391;

Matches 101; Conservative 68; Mismatches 121; Indels 21; Gaps 5;

QY 11 GPNASNTSDGPDNLTSAGSPRTGSIYINIMPSVEFTICLLIGNSTVIFAVVKKSK 70
 Db 42 GRNASQNGTISEGQSA-----ILISFYSVVCVLGCGSNMVIYILRYAK 88
 QY 71 LHMGNVPIPIFINISVVDLFLGMPMIHQMGNGVHMGCTMLITAMANDSQPTS 130
 Db 89 KMTATN--IYTLNLAIDELMLSVPLVSTLIRH-WPFGALLCRVLVSDVAVNETS 144
 QY 131 TYILTAADRYLATVHPISSTKFRKPSVATLVICLMAISFISITFVMTYARLIPPG 190
 Db 145 IYCLFVLSVDKYVAVVHPKAKARYRRPTVAKVNLGVWVLSLVLPIVESTRFANS DG 204
 QY 191 AVGGCIRLELNP-DTDLVMTLTKOFLFALPFPVITAAVYVILQRMSSVAPASQSRIRL 249
 Db 205 TVACNMLMEPEAPQRMVGVGLTFLMGLPVGALICLCYVILIKMRVVALKAGWQQRK 264
 QY 250 RKRRTVTRTAICLVFEVCMAPYVVLQTLQSLISRPITLFFVLYNAAISLGANSCLNPF 309
 Db 265 SERKITIMAMVAVVFIWCMPEFYVQLVWVFAEDDQDATVSQI---SVILGYANSCANPI 321
 QY 310 VYIVLCETFRK 320
 Db 322 LYGFSLDNFKR 332

RESULT 13

A47249

brain-specific somatostatin receptor SSTR-4 - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999

C:Accession: A47249

R:Name: Y.; Xu, Y.; Song, J.; Berelowitz, M.

Proc. Natl. Acad. Sci. U.S.A. 89, 1151-1155, 1992

A:Title: Molecular cloning and functional expression of a brain-specific somatostatin re

A:Reference number: A47249; MUID:93087484; PMID:1360663

A:Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 1-384 <BRD>
 A:Cross-References: GB:M96544; NID:9207072; PIDN:AAA42180.1; PID:9207073
 A:Note: sequence extracted from NCBI backbone (NCBIN:119731, NCBI:119732)
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match

Best Local Similarity 33.0%; Score 494.5; DB 2; Length 384;

Matches 104; Conservative 66; Mismatches 116; Indels 29; Gaps 8;

QY 16 NTSDEPDNLTSAGSPRTGSIYINIMPSVEFTICLLIGNSTVIFAVVKKSKLHMGN 75
 Db 21 NASMAPDEEDAVRSDGTGTAGMTI--QCIYALVCLVGLGNALVFIILRYAKMKATAT 78
 QY 76 NVPDIFIINISVVDLFLGMPMI-----HQLMGNGVHMGCTMLITAMANDSQPT 129
 Db 79 N---IYTLNLAVIDELMLSVPLVSTLIRH-WPFGALLCRVLVSDVAVNETS 144
 QY 130 STYILTAADRYLATVHPISSTKFRKPSVATLVICLMAISFISITFVMTYARLIPPG 189
 Db 129 SVFCLTVSDRYVAVVHPKAKARYRRPTVAKVNLGVWVLSLVLPIVESTRFANS DG 204
 QY 190 G-AVGGCIRLELNP-DTDLVMTLTKOFLFALPFPVITAAVYVILQRMSSVAPASQSR 245
 Db 189 GAVACNMLHMPHP-----AMSAVFYITFLGFLPLVLAIGCTILYGRKRAVALRAGWQ 244
 QY 246 SIKLRTKRVTRTAICLVFEVCMAPYVVLQTLQSLISRPITLFFVLYNAAISLGANSQ 305
 Db 245 QRRESEKKITRLVLMVAVVFIWCMPEFYVQLVWVFAEDDQDATVSQI---VNHVSILTSVANSQ 301
 QY 306 LNPFIYIVLCETFRK 320
 Db 302 ANPILYGFSLDNFKR 316

RESULT 14

JC4629

somatostatin receptor type-4 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 10-Apr-1996 #sequence_revision 24-May-1996 #text_change 24-Nov-1999

C:Accession: JC4629

R:Schwabe, W.; Brennan, M.B.; Hochgeschwender, U.

Gene 168, 233-235, 1996

A:Title: Isolation and characterization of the mouse (Mus musculus) somatostatin rece

A:Reference number: JC4629; MUID:96194903; PMID:8654950

A:Accession: JC4629

A:Molecule type: DNA

A:Residues: 1-384 <SCH>

A:Cross-References: GB:U26176; NID:9833840; PIDN:AAA67561.1; PID:9833841

C:Comment: This protein works through the G-proteins and plays a role in mediating in

C:Genetics:

A:Gene: sstr4

C:Superfamily: vertebrate rhodopsin

C:Keywords: receptor; transmembrane protein

P:46-349/Domain: transmembrane #status predicted <TM>

Query Match

Best Local Similarity 26.5%; Score 483; DB 2; Length 384;

Matches 105; Conservative 69; Mismatches 133; Indels 22; Gaps 8;

QY 1 MDLEASL-----PTGRNASNTSDGPDNLTSAGSPRTGSIYINIMPSVEFTICLLIG 55
 Db 1 NMAPPTLLRGVEDTTPGGINASAPPOEDDAGSDGTGTAGMTI--QCIYALVCLVGL 58
 QY 56 IGNSVIVFAVVKSKLHMGNVPIPIFINISVVDLFLGMPMIHQMGNGVHMGCTM 115
 Db 59 VGNALVIVILRYAKMKATN--IYTLNLAVIDELMLSVPLVSTLIRH-WPFGALLCRVLVSDVAVNETS 144
 QY 116 CTLITAMANDSQPTSTYILTAADRYLATVHPISSTKFRKPSVATLVICLMAISFIS 175
 Db 115 CRAVLSDGLNMTFSVFCILFVLSVDKYVAVVHPKAKARYRRPTVAKVNLGVWVLSLVLP 174

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QY 176 TPWLYARLIPPPG-ANGCGIRLPNPDTLYW---FTLYQFLAFALPFVVITAAYRI 231
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Db 175 LPFAVADPRPARGEAVACNLHMPHP---AMGAVFVIYTFLLGFLPVLAIGLCYLLI 230
QY 232 LQRMSSVAPASQBSIRLTKRVYRTAICLVFEVCMAPYVYLQTLQSLISRPITLFPY 291
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Db 231 VGMKRVVALRGWQQRSEKKITRLVMTVFVLCMPFVYVOLLNLFTVSLDAT--- 287
QY 292 LYNAAISLGYANSCINPFYIVLCETFRK 320
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Db 288 VNHVSLTISYANSCANPILYGFLSDNFR 316
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RESULT 15

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S30508
Probable G protein-coupled receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 11-Jan-2000
C:Accession: S30508
R:Meierhof, W.; Wulfsen, I.; Schoenrock, C.; Fehr, S.; Richter, D.
Proc. Natl. Acad. Sci. U.S.A. 89, 10267-10271, 1992
A:Title: Molecular cloning of a somatostatin-28 receptor and comparison of its expression
A:Reference number: S30508; MUID:93066220; PMID:1279674
A:Accession: S30508
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-428 <MEY>
A:Cross-references: EMBL:X63574; NID:956315; PIDN:CAA45130.1; PID:956316
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein
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Query Match

26.3%; Score 480.5; DB 2; Length 428;

Best Local Similarity 31.3%; Pred. No. 2e-34;

Matches 118; Conservative 73; Mismatches 143; Indels 43; Gaps 11;

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      |::| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 8 SSVPTLDPGNASAMPDLDTSLGNASAGTSLAGLAVSGILISLYLVVGVGLGNSLYI 67
QY 63 FAVYKSKLHMGNPNPDIIFINLSVVDLFLGMEFIHQLMNGV--WHEGETMCTLT 120
      : : : : | | | | | | | | | | | | | | | | | | | | | | |
Db 68 YVYLRHTS---SPSVTSYILNLALADELFMLGLPFLAQ--NALSYMPFGSLMCRLYW 121
QY 121 AMDANSQFTSYTLTAMALDRYATVHPISSTKFRKPSVATLVYCLMALSFISITPVWL 180
      |::| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 122 AVDGINQFTSIFCLTVMSYDRLAVVHPTBSARMTAPVARNVSAVWVASAVVYVLPVYV 181
QY 181 YARLIFFPGAVGCGIRLPNPDTLYW---FTLYQFLAFALPFVVITAAYRIIQRMIS 237
      : : : | | | | | | | | | | | | | | | | | | | | | | |
Db 182 FSGV---PRGMSTCHMQWEPRA--AMRTAIIITTAALGFPGPLVYICLCYLIIVKVR 236
QY 238 SV-----APASQBSIRLTKRVYRTAICLVFEVCMAPYVYLQTLQSLISRP 285
      : : : | | | | | | | | | | | | | | | | | | | | | | |
Db 237 TTRRVAPSCQWQVAPACQRR-RRSERVTRMVAVVALFVLCMPFYLINIVNVCPLP 295
QY 286 -TLTFYLYNAAISLGYANSCINPFYIVLCETFRK-----RLVLSVKAQAGOL 334
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QY 335 RAVSNAQTADERTESK 351
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Search completed: February 13, 2003, 14:01:07
Job time : 13.6809 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 13, 2003, 14:00:22 ; Search time 11.7962 Seconds
(without alignments)
764.550 Million cell updates/sec

Title: US-09-885-478-28

Perfect score: 1824

Sequence: 1 MDLEASLLPTGPNASNTSDG.....LRAVNAQTADDERIESKCT 353

BLOSUM62

Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 140259 segs, 25548876 residues

Total number of hits satisfying chosen parameters: 140259

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1824	100.0	353	10	US-09-925-776-2
2	1824	100.0	353	10	US-09-885-478-28
3	1824	100.0	422	10	US-09-885-478-2
4	1819	99.7	422	10	US-09-885-478-26
5	1819	99.7	422	10	US-09-885-478-27
6	1808	99.1	353	10	US-09-885-686-2
7	1763	96.7	353	10	US-09-885-478-4
8	1692	92.8	402	9	US-09-990-940-19
9	1224	67.1	239	10	US-09-864-761-38414
10	565.5	31.0	340	9	US-09-791-932-117
11	565.5	31.0	340	9	US-09-990-940-2
12	524.5	28.8	369	10	US-09-823-114-9
13	504.5	27.7	418	9	US-09-992-331-17
14	496.5	27.2	391	9	US-09-990-940-20
15	480.5	26.3	428	9	US-09-992-331-16
16	472	25.9	428	9	US-09-992-331-15
17	470.5	25.8	363	9	US-09-992-331-14
18	456	25.0	362	9	US-09-992-331-13
19	456	25.0	370	10	US-09-823-114-21

20	452.5	24.8	372	9	US-10-112-599A-4	Sequence 4, Appl1
21	449	24.6	372	10	US-09-966-871-80	Sequence 80, Appl1
22	449	24.6	372	12	US-10-039-645-80	Sequence 80, Appl1
23	449	24.6	415	10	US-09-823-114-20	Sequence 20, Appl1
24	445.5	24.4	382	10	US-09-993-844-4	Sequence 4, Appl1
25	444	24.3	400	10	US-09-966-871-85	Sequence 85, Appl1
26	444	24.3	400	12	US-10-039-645-85	Sequence 85, Appl1
27	443.5	24.3	405	10	US-09-966-871-84	Sequence 84, Appl1
28	443.5	24.3	405	12	US-10-039-645-84	Sequence 84, Appl1
29	443	24.3	398	10	US-09-823-114-16	Sequence 16, Appl1
30	443	24.3	398	12	US-10-039-645-1	Sequence 1, Appl1
31	443	24.3	398	10	US-09-966-871-1	Sequence 1, Appl1
32	442.5	24.3	390	10	US-09-761-962-25	Sequence 25, Appl1
33	442.5	24.3	391	10	US-09-761-962-26	Sequence 26, Appl1
34	442.5	24.3	382	10	US-09-761-962-19	Sequence 19, Appl1
35	442.5	24.3	388	10	US-09-214-904-2	Sequence 29, Appl1
36	442.5	24.3	398	10	US-09-761-962-29	Sequence 29, Appl1
37	442.5	24.3	398	10	US-09-966-871-83	Sequence 83, Appl1
38	442.5	24.3	398	12	US-10-039-645-83	Sequence 83, Appl1
39	442.5	24.3	401	10	US-09-761-962-20	Sequence 20, Appl1
40	442.5	24.3	409	10	US-09-761-962-27	Sequence 27, Appl1
41	442.5	24.3	438	10	US-09-761-962-17	Sequence 17, Appl1
42	442.5	24.3	444	10	US-09-761-962-28	Sequence 28, Appl1
43	442	24.2	372	10	US-09-823-114-8	Sequence 8, Appl1
44	442	24.2	398	10	US-09-966-871-79	Sequence 79, Appl1
45	442	24.2	398	12	US-10-039-645-79	Sequence 79, Appl1

ALIGNMENTS

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RESULT 1
US-09-925-776-2
; Sequence 2, Application US/09925776
; Patent No. US2002038007A1
; GENERAL INFORMATION:
; APPLICANT: AMES, ROBERT S., JR.
; APPLICANT: SARAU, HENRY M.
; APPLICANT: FOLEY, JAMES J.
; APPLICANT: BERGSMAN, DEBK J.
; APPLICANT: ELITS, CATHERINE E.
; APPLICANT: CHAMBERS, JON K.
; TITLE OF INVENTION: A METHOD OF FINDING AGONIST AND
; TITLE OF INVENTION: ANTAGONIST TO HUMAN 11CB SPLICE VARIANT
; FILE REFERENCE: GP-50003-D2
; CURRENT APPLICATION NUMBER: US/09/925,776
; CURRENT FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/032,763
; PRIOR FILING DATE: 1996-12-11
; PRIOR APPLICATION NUMBER: 08/984,288
; PRIOR FILING DATE: 1997-12-03
; PRIOR APPLICATION NUMBER: 60/073,747
; PRIOR FILING DATE: 1998-02-05
; PRIOR APPLICATION NUMBER: 09/060,504
; PRIOR FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 2
; LENGTH: 353
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-925-776-2

Query Match      100.0%; Score 1824; DB 10; Length 353;
Best Local Similarity 100.0%; Pred. No. 9.8e-162;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 MDLEASLLPTGPNASNTSDGPDNTLSAGSPRRGISTYINIMPSVFGTICLLGIGNST 60
DB      1 MDLEASLLPTGPNASNTSDGPDNTLSAGSPRRGISTYINIMPSVFGTICLLGIGNST 60
OY      61 VIFAVVKKSKLHMCNNVPDIFILMSVVDLFLGLMPFMHQLMGNGVHVFGEETCTLT 120
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Db 61 VIEFAVKKSKLHMCNNVDFIINLSVVDLFLGMPFMIHOLMGNGVWHFGETMCTLIT 120
Qy 121 AMDANSQFTSTYIILTAMADIRYLAIVHISSTKFRKRSVATLVICLMAISFISIPVWL 180
Db 121 AMDANSQFTSTYIILTAMADIRYLAIVHISSTKFRKRSVATLVICLMAISFISIPVWL 180
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Db 181 YARLIPFPGAVGCGIRLPNPDITLQYFELAFALPFFVITAAVRIIQRMTSSVA 240
Qy 241 PASQSRIRLRTKRVTRTAICLVFVCWAPYVYLQTLQISIRPILTFEYLYNNAISLG 300
Db 241 PASQSRIRLRTKRVTRTAICLVFVCWAPYVYLQTLQISIRPILTFEYLYNNAISLG 300
Qy 301 YANSCINPFFVYIVLCETFRKRLVSVKPAAGOLRAVSNQOTADEERTESKGT 353
Db 301 YANSCINPFFVYIVLCETFRKRLVSVKPAAGOLRAVSNQOTADEERTESKGT 353
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RESULT 2

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US-09-885-478-28
; Sequence 28, Application US/09885478
; Patent No. US2002011306A1
; GENERAL INFORMATION:
; APPLICANT: SALON, JOHN A
; APPLICANT: LAZ, THOMAS M
; APPLICANT: MAGORNY, RAISA
; APPLICANT: WILSON, AMY E
; TITLE OF INVENTION: DNA ENCODING A HUMAN MELANIN CONCENTRATING HORMONE RECEPTOR (MCH)
; FILE REFERENCE: 1795/57453-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/885,478
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US99/31169
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 353
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: MUTATED MCH RECEPTOR
US-09-885-478-28
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Query Match 100.0%; Score 1824; DB 10; Length 353;
Best Local Similarity 100.0%; Pred. No. 9, 8e-162;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 241 PASQSRIRLRTKRVTRTAICLVFVCWAPYVYLQTLQISIRPILTFEYLYNNAISLG 300
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RESULT 3

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US-09-885-478-2
; Sequence 2, Application US/09885478
; Patent No. US2002011306A1
; GENERAL INFORMATION:
; APPLICANT: SALON, JOHN A
; APPLICANT: LAZ, THOMAS M
; APPLICANT: MAGORNY, RAISA
; APPLICANT: WILSON, AMY E
; TITLE OF INVENTION: DNA ENCODING A HUMAN MELANIN CONCENTRATING HORMONE RECEPTOR (M
; FILE REFERENCE: 1795/57453-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/885,478
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US99/31169
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 422
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-885-478-2
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Query Match 100.0%; Score 1824; DB 10; Length 422;
Best Local Similarity 100.0%; Pred. No. 1, 2e-161;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 VIEFAVKKSKLHMCNNVDFIINLSVVDLFLGMPFMIHOLMGNGVWHFGETMCTLIT 120
Db 130 VIEFAVKKSKLHMCNNVDFIINLSVVDLFLGMPFMIHOLMGNGVWHFGETMCTLIT 189
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Db 190 AMDANSQFTSTYIILTAMADIRYLAIVHISSTKFRKRSVATLVICLMAISFISIPVWL 249
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Db 310 PASQSRIRLRTKRVTRTAICLVFVCWAPYVYLQTLQISIRPILTFEYLYNNAISLG 369
Qy 301 YANSCINPFFVYIVLCETFRKRLVSVKPAAGOLRAVSNQOTADEERTESKGT 353
Db 370 YANSCINPFFVYIVLCETFRKRLVSVKPAAGOLRAVSNQOTADEERTESKGT 422
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RESULT 4

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US-09-885-478-26
; Sequence 26, Application US/09885478
; Patent No. US2002011306A1
; GENERAL INFORMATION:
; APPLICANT: SALON, JOHN A
; APPLICANT: LAZ, THOMAS M
; APPLICANT: MAGORNY, RAISA
; APPLICANT: WILSON, AMY E
; TITLE OF INVENTION: DNA ENCODING A HUMAN MELANIN CONCENTRATING HORMONE RECEPTOR (M
; FILE REFERENCE: 1795/57453-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/885,478
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US99/31169
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
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; LENGTH: 422
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: MUTATED MCH RECEPTOR
US-09-885-478-26
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Best local Similarity 100.0%; Pred. No. 3.5e-161;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; Sequence 27, Application US/09885478
; Patent No. US2002011306A1
; GENERAL INFORMATION:
; APPLICANT: SALON, JOHN A
; APPLICANT: LAZ, THOMAS M
; APPLICANT: NAGORNY, RAISA
; APPLICANT: WILSON, AMY E
; TITLE OF INVENTION: DNA ENCODING A HUMAN MELANIN CONCENTRATING HORMONE RECEPTOR (MCH1)
; FILE REFERENCE: 1795/57453-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/885,478
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US99/31169
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 422
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: MUTATED MCH RECEPTOR
US-09-885-478-27
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Query Match          99.7%; Score 1819; DB 10; Length 422;
Best local Similarity 100.0%; Pred. No. 3.5e-161;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 71 DEASLILPTGPNASNTSDGPNLTSAGSPRTGTSISYINIMPSVFGTICLLGIGNSTV 130
QY 62 IFAVVKKSKLHMCNNVPDIFIIINLSYVDLFLGLGMPFMIHOLMGVNHGEGTMCITLTA 121
DB 131 IFAVVKKSKLHMCNNVPDIFIIINLSYVDLFLGLGMPFMIHOLMGVNHGEGTMCITLTA 190
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QY 122 MDANSOFTSTYIILTAMADRYLATVHPISSTKFRKPSVATLVICLLMAISFISTPWWLY 181
DB 191 MDANSOFTSTYIILTAMADRYLATVHPISSTKFRKPSVATLVICLLMAISFISTPWWLY 250
QY 182 ARLIPPGAVGCGIRLPNPDIDLYWFTLYQFELAFALPFVYITAAVYRIIQRMTSSVAP 241
DB 251 ARLIPPGAVGCGIRLPNPDIDLYWFTLYQFELAFALPFVYITAAVYRIIQRMTSSVAP 310
QY 242 ASORSIRLTRKRVTRTAIICLVFVCMAPIYVLOLTOLISRPITLFFVLYNMAISIGY 301
DB 311 ASORSIRLTRKRVTRTAIICLVFVCMAPIYVLOLTOLISRPITLFFVLYNMAISIGY 370
QY 302 ANSCLNPFYIYVLCETFRKRLVLSVKPAAGQLRAVSNAGTADEERTESKGT 353
DB 371 ANSCLNPFYIYVLCETFRKRLVLSVKPAAGQLRAVSNAGTADEERTESKGT 422
```

```
RESULT 6
US-09-895-686-2
; Sequence 2, Application US/09895686
; Patent No. US20020106655A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN GPCR PROTEINS
; FILE REFERENCE: PC-0044 CIP
; CURRENT APPLICATION NUMBER: US/09/895,686
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; OTHER INFORMATION: Incyte ID No. US20020106655A1 1459432CD1
US-09-895-686-2
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```
Query Match          99.1%; Score 1808; DB 10; Length 353;
Best local Similarity 99.2%; Pred. No. 3e-160;
Matches 350; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 1 MDLEASLILPTGPNASNTSDGPNLTSAGSPRTGTSISYINIMPSVFGTICLLGIGNST 60
DB 1 MDLEASLILPTGPNASNTSDGPNLTSAGSPRTGTSISYINIMPSVFGTICLLGIGNST 60
QY 61 VIFAVVKKSKLHMCNNVPDIFIIINLSYVDLFLGLGMPFMIHOLMGVNHGEGTMCITLT 120
DB 61 VIFAVVKKSKLHMCNNVPDIFIIINLSYVDLFLGLGMPFMIHOLMGVNHGEGTMCITLT 120
QY 121 AMDANSOFTSTYIILTAMADRYLATVHPISSTKFRKPSVATLVICLLMAISFISTPWWLY 180
DB 121 AMDANSOFTSTYIILTAMADRYLATVHPISSTKFRKPSVATLVICLLMAISFISTPWWLY 180
QY 181 YARLIPPGAVGCGIRLPNPDIDLYWFTLYQFELAFALPFVYITAAVYRIIQRMTSSVA 240
DB 181 YARLIPPGAVGCGIRLPNPDIDLYWFTLYQFELAFALPFVYITAAVYRIIQRMTSSVA 240
QY 241 PASORSIRLTRKRVTRTAIICLVFVCMAPIYVLOLTOLISRPITLFFVLYNMAISIG 300
DB 241 PASORSIRLTRKRVTRTAIICLVFVCMAPIYVLOLTOLISRPITLFFVLYNMAISIG 300
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QY 301 YANSCLNPFYIYVLCETFRKRLVLSVKPAAGQLRAVSNAGTADEERTESKGT 353
DB 301 YANSCLNPFYIYVLCETFRKRLVLSVKPAAGQLRAVSNAGTADEERTESKGT 353
```

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RESULT 7
US-09-885-478-4
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```
; Sequence 4, Application US/09885478
; Patent No. US20020111306A1
; GENERAL INFORMATION:
; APPLICANT: SALON, JOHN A
; APPLICANT: LAZ, THOMAS M
; APPLICANT: MAGORNY, RAISA
; APPLICANT: WILSON, AMY E
; TITLE OF INVENTION: DNA ENCODING A HUMAN MELANIN CONCENTRATING HORMONE RECEPTOR (MCH)
; FILE REFERENCE: 1795/57453-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/885,478
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US99/31169
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 353
; TYPE: PRT
; ORGANISM: RATTUS NORVEGICUS
US-09-885-478-4
```

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Query Match          96.7%; Score 1763; DB 10; Length 353;
Best Local Similarity 96.0%; Pred. No. 4,4e-156;
Matches 339; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 MDLEASLPTGPNASNTSDGPDNLTSAQSPRTGSIYINIMPSVFGTICLGIIGNST 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1 MDLQSTLSLTGTNASNISDGDNLTLPSPRTGSIYINIMPSVFGTICLGIIGNST 60

QY 61 VIEFAVKKSKLHMCNNVDFIINLSYVDLLELLGMPFMIHOMGNGVHFGETMCTLT 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 61 VIEFAVKKSKLHMCNNVDFIINLSYVDLLELLGMPFMIHOMGNGVHFGETMCTLT 120

QY 121 ANDAASQSTSYITLTAADIDRYLATVHPISSTRKRSVAIVYICLLMAISITPWL 180
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 121 ANDAASQSTSYITLTAADIDRYLATVHPISSTRKRSVAIVYICLLMAISITPWL 180

QY 181 VARLIPFGAGVCGIRLPNDPDLVWFLLYQEFLLAFALPFVYITAAVRIILQRMSSVA 240
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 181 VARLIPFGAGVCGIRLPNDPDLVWFLLYQEFLLAFALPFVYITAAVRIILQRMSSVA 240

QY 241 PASORSIRLRKTRKTRTAICLVFECMAPIYVQLTOLISIRPLTFVYLYNNAISIG 300
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 241 PASORSIRLRKTRKTRTAICLVFECMAPIYVQLTOLISIRPLTFVYLYNNAISIG 300

QY 301 YANSCINPFVYIVLCETFRKRLVSVKPAAGQLRAVSNAGTADERTESKGT 353
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 301 YANSCINPFVYIVLCETFRKRLVSVKPAAGQLRAVSNAGTADERTESKGT 353
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```
RESULT 8
US-09-990-940-19
; Sequence 19, Application US/09990940
; Publication No. US20030027252A1
; GENERAL INFORMATION:
; APPLICANT: Tian, Hui
; APPLICANT: Zhao, Jiayang
; APPLICANT: Chen, Jin-Long
; APPLICANT: Cutler, Gene
; APPLICANT: An, Songzhu
; APPLICANT: Dai, Kang
; APPLICANT: Gupta, Janila S.
; TITLE OF INVENTION: NO. US20030027252A1el Receptors
; FILE REFERENCE: 018781-007410US
; CURRENT APPLICATION NUMBER: US/09/990,940
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/252,841
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 60/257,636
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 60/261,377
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; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/279,554
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/280,696
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human melanin-concentrating hormone receptor
; OTHER INFORMATION: (MCHr1)
US-09-990-940-19
```

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Query Match          92.8%; Score 1692; DB 9; Length 402;
Best Local Similarity 99.4%; Pred. No. 2e-149;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 24 LTSAGSPRTGSIYINIMPSVFGTICLGIIGNSTVIFAVYKSKLHMCNNVDFIIT 83
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 73 LTSAGSPRTGSIYINIMPSVFGTICLGIIGNSTVIFAVYKSKLHMCNNVDFIIT 132

QY 84 NLSYVDLLELLGMPFMIHOMGNGVHFGETMCTLTITAMANSQSTSYITLTAADRYL 143
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 133 NLSYVDLLELLGMPFMIHOMGNGVHFGETMCTLTITAMANSQSTSYITLTAADRYL 192

QY 144 ATVHPISSTRKRSVAIVYICLLMAISITPWLVARLIPFGAGVCGIRLPNDPT 203
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 193 ATVHPISSTRKRSVAIVYICLLMAISITPWLVARLIPFGAGVCGIRLPNDPT 252

QY 204 DLYWFLLYQEFLLAFALPFVYITAAVRIILQRMSSVAPASORSIRLRKTRKTRTAICL 263
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 253 DLYWFLLYQEFLLAFALPFVYITAAVRIILQRMSSVAPASORSIRLRKTRKTRTAICL 312

QY 264 VEFVCAPIYVQLTOLISIRPLTFVYLYNNAISIGYANSCINPFVYIVLCETFRKRLV 323
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 313 VEFVCAPIYVQLTOLISIRPLTFVYLYNNAISIGYANSCINPFVYIVLCETFRKRLV 372

QY 324 LSVKPAAGQLRAVSNAGTADERTESKGT 353
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 373 LSVKPAAGQLRAVSNAGTADERTESKGT 402
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```
RESULT 9
US-09-864-761-38414
; Sequence 38414, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE REFERENCE: Aecm1ca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
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; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 38414
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO 286090.10
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.67
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.78
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.74
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.72
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.1
; OTHER INFORMATION: EST HUMAN HIT: BE701073.1, EVALUE 6.00e-44
; OTHER INFORMATION: SWISSPROT HIT: Q99705, EVALUE 0.00e+00
US-09-864-761-38414

Query Match          67.1%; Score 1224; DB 10; Length 239;
Best Local Similarity 100.0%; Pred. No. 2.8e-106;
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 115 MCTLTAMANSOFTSTYLTMTAMADRYLATVHPISSTKRRKPSVATLVICLLMALSFTS 174
DB 1 MCTLTAMANSOFTSTYLTMTAMADRYLATVHPISSTKRRKPSVATLVICLLMALSFTS 60
QY 175 ITPVWLARLIPFGAVGCGIRLPNPDLDLYWFTLYOFLAFALPFEVYTAAYVRIQR 234
DB 61 ITPVWLARLIPFGAVGCGIRLPNPDLDLYWFTLYOFLAFALPFEVYTAAYVRIQR 120
QY 235 MNSVAPASQSRIRLRTKRVTRTAICLVFVVCAPRYVYQLTQLSRTTLTFVYLYN 294
DB 121 MNSVAPASQSRIRLRTKRVTRTAICLVFVVCAPRYVYQLTQLSRTTLTFVYLYN 180
QY 295 AATISLGANSCINPFYIYLCETFRKRLVSVKPAAGQLRAVSNAGTADERTESKGT 353
DB 181 AATISLGANSCINPFYIYLCETFRKRLVSVKPAAGQLRAVSNAGTADERTESKGT 239

RESULT 10
US-09-791-932-117
; Sequence 117, Application US/09791932
; Publication No. US20030003451a1
; GENERAL INFORMATION:
; APPLICANT: Vogel, Gabriel
; APPLICANT: Patodi, Luis A.
; APPLICANT: Hiesch, Ronald R.
; APPLICANT: Lind, Peter
```

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; APPLICANT: Kaytes, Paul S.
; APPLICANT: Ruff, Valerie
; APPLICANT: Huff, Rita M.
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: No. US20030003451a1e1 G Protein-Coupled Receptors Cross-Ref
; FILE REFERENCE: 00325_US1
; CURRENT APPLICATION NUMBER: US/09/791,932
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/184,305
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,304
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,303
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,397
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,247
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/188,880
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/217,369
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/217,370
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/218,492
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: 60/186,810
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/188,064
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: 60/186,457
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: 60/213,861
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/194,344
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: 60/218,337
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: Patentln version 3.0
; SEQ ID NO 117
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-932-117

Query Match          31.0%; Score 565.5; DB 9; Length 340;
Best Local Similarity 37.0%; Pred. No. 5.1e-45;
Matches 113; Conservative 62; Mismatches 119; Indels 11; Gaps 4;

QY 41 IIMPVFETICLLIGNSTVIFAIVKRSKLMWCNNVPDIFIIINLSYVDDLFLGMPFM 100
DB 35 VILPSMIGISTGVLGNILVIFETIISRK----KTPVDIYICMLAVADLVHVGMPFL 90
QY 101 HOLMGNGVHGHEIMCTLTITAMDANSOFTSYLTITAMADRYLATVHPISSTFRKPSVA 160
DB 91 HOLMGNGVHGHEIMCTLTITAMDANSOFTSYLTITAMADRYLATVHPISSTFRKPSVA 150
QY 161 TLVICLLMALSFTSTPYWLARLIPFGAVGCGIRLPNPDLDLYWFTLYOFLAFALP 220
DB 151 IKNNGMAASFTLALPVWVYSKYIKFDGVESCAPDLTSPD-DVLMYTYLYLTTFEFP 209
QY 221 FVYITAAVRII-----ORMTSSVAPASQSRIRLRTKRVTRTAICLVFVVCAPRYV 274
DB 210 LPLILVICYLLICYWEMYQONKDCARCPNPSVPQRQVKKILKMLVLYVVFIIISAAVHV 269
QY 275 LQTLQLSRPTLTFVYLYNNAISIGVANSCLNPFYIYLCETFRKRLVSVKPAAGQL 334
DB 270 IQLVNLMQEPFLATVYGYIYISICLSTVASSINPFYIYILSGNQKRLPDQIRATEKEI 329
QY 335 RAVSN 339
DB 330 NNNGN 334
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; Publication No. US20030022186A1
; GENERAL INFORMATION:
; APPLICANT: FEDER, JOHN N.
; APPLICANT: MINTIER, GABE
; APPLICANT: RAMANATHAN, CHANDRA S.
; APPLICANT: HAWKEN, DONALD R.
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPBMY18,
; TITLE OF INVENTION: EXPRESSED HIGHLY IN PITUITARY GLAND AND COLON CARCINOMA
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: D0048NP
; CURRENT APPLICATION NUMBER: US/09/992,331
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/308,540
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/261,782
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/248,483
; PRIOR FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-992-331-17

Query Match          27.7%; Score 504.5; DB 9; Length 418;
Best Local Similarity 32.5%; Pred. No. 3e-39;
Matches 118; Conservative 76; Mismatches 134; Indels 35; Gaps 11;

QY 12 PNASNTSDGPNLTSAGSP-----PRGSISYINIMPSVFGTICLIGTIGNSTV 61
D 6 PSSVTSTSEPNASAPDPATLGNSAGSPAGLAVSGVLLPYLVVCCVGLGNSTV 65
QY 62 IFAYVKKSKLHMCNNVPDIFILNLSVVDLFLGMPFMHQLMGNGV--WHEGETMCTLI 119
D 66 IYVLRHDA--SPSVNIVYLNLALDELFMGLGFLPAQ--NALSTWPGSLMCTLY 119
QY 120 TAMANQOFTSTYILTMALIDRLAYVHPISSTKFKPSVATLVICLMAISFISTPFW 179
D 120 MAVGINSQFTSIFCLTVASDRYLAVHPRSAKMTAVARTVSAVWVAVVVLEPV 179
QY 180 LYARLIFPPGAGCGIRLPNPDLDYV--FTLYQFLAFALPEVITAATVRILOMT 236
D 180 VESGV---PRGMSCTHQMEPEAA--AMRAGFIITTAALGFGLPLVICGLLVVYVR 234
QY 237 SS----VAPASQSRIRLRTKRYRTAIAICLVFVCWARYVYQLTOLISNP--ILTYV 291
D 235 SAGRRVWAPSCQRR--RRSERRTVMVAVVAVLFLCWMPEFYVLTIVNVCPLEBPAPFG 293
QY 292 LYNAISLGYANSCINPFYIVLCETFR--KRLVLSVRPAAGOLRAVSNQOTADERBT 348
D 294 LYFLVVALPYANSCANILYGLSYRKGQGRFVLLRPSRRVRSQEPYTPGPEKTEEDE 353
QY 349 ESK 351
D 354 EEE 356

RESULT 14
US-09-990-940-20
; Sequence 20, Application US/09990940
; Publication No. US20030027252A1
; GENERAL INFORMATION:
; APPLICANT: Tian, Hui
; APPLICANT: Zhao, Jiagang
; APPLICANT: Chen, Jin-Long
; APPLICANT: Cutler, Gene
; APPLICANT: An, Songzhu
; APPLICANT: Dai, Kang
; APPLICANT: Gupta, Jamila S.
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: NO. US20030027252A1el Receptors

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; FILE REFERENCE: 018781-007410US
; CURRENT APPLICATION NUMBER: US/09/990,940
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/252,841
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 60/257,636
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 60/261,377
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/279,554
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/280,696
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human somatostatin receptor 1 (SSTR1)
US-09-990-940-20

Query Match          27.2%; Score 496.5; DB 9; Length 391;
Best Local Similarity 32.5%; Pred. No. 1.5e-38;
Matches 101; Conservative 68; Mismatches 121; Indels 21; Gaps 5;

QY 11 GPNASNTSDGPNLTSAGSPRTGSISYINIMPSVFGTICLIGTIGNSTVIFAYVKKSK 70
D 42 GRNASQNTLSAQGSA-----ILISITISVCLVGLGNSMVIYIILYAK 88
QY 71 LHCNNVPDIFILNLSVVDLFLGMPFMHQLMGNGVWHEGETMCTLTAMANDSQFTS 130
D 89 MKTATN--IYILNLALDELMLTSVPLVSTLIRH--WPGALLCRLVSVAVNMETS 144
QY 131 TYTLTMAIDRLAYVHPISSTKFKPSVATLVICLMAISFISTPFWIYARLIPPG 190
D 145 IYCLTVLSDRKYAVVHPRKARKRYRTYAKVNLGVWLSLVILTYVFSRKANSQD 204
QY 191 AVGCGIRLNP--DTLDYMETLYQFLAPALPEVITAATVRILOMTSSVAPASQSRIRL 249
D 205 TVACNMIMPEPAQRMVLYGVLTFTFLMGFLPLPGALCICLYVLIIMMMVALLKGMQQR 264
QY 250 RTRKRTVTAIAICLVFVCWARYVYQLTOLISNPRLTFYLYNAISLGYANSCINPF 309
D 265 SERKITLMMAYVMVFCIMPEFYVQLVNVPADQDATVSQ---SVILGYANSCANPI 321
QY 310 VYIVLCETFRK 320
D 322 LYGLFLSDNFKR 332

RESULT 15
US-09-992-331-16
; Sequence 16, Application US/09992331
; Publication No. US20030022186A1
; GENERAL INFORMATION:
; APPLICANT: FEDER, JOHN N.
; APPLICANT: MINTIER, GABE
; APPLICANT: RAMANATHAN, CHANDRA S.
; APPLICANT: HAWKEN, DONALD R.
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPBMY18,
; TITLE OF INVENTION: EXPRESSED HIGHLY IN PITUITARY GLAND AND COLON CARCINOMA
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: D0048NP
; CURRENT APPLICATION NUMBER: US/09/992,331
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/308,540
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/261,782
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/248,483
; PRIOR FILING DATE: 2000-11-14

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Thu Feb 20 11:32:54 2003

us-09-885-478-28.rapb

Page 8

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; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-992-331-16

```

Query Match	26.38;	Score 480.5;	DB 9;	Length 428;
Best Local Similarity	31.38;	Pred. No. 5.2e-37;		
Matches 118;	Conservative 73;	Mismatches 143;	Indels 43;	Gaps 11;

[illegible]

Search completed: February 13, 2003, 14:10:33
Job time : 12.7962 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

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Run on:      February 13, 2003, 13:50:31 ; Search time 33.4921 Seconds
              (without alignments)
              1678.958 Million cell updates/sec
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Title: US-09-885-478-27
Perfect score: 2210
Sequence: 1 MSVGAARKGVGRAVGLGGS.....LRVSNAGTADERTESKGT 422

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Scoring table:	BLOSUM62	
	CanD	CanD
	10	0
	CanD	0
	10	5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Database : A_Geneseq_101002.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2210	100.0	422	21	AA813441	Mutant human MCH1
2	2210	100.0	422	23	AAU75858	Human melanin conc
3	2205	99.8	422	21	AA813440	Mutant human MCH1
4	2205	99.8	422	23	AAU75857	Human melanin conc
5	2200	99.5	422	21	AA813436	Human MCH1 receptor
6	2200	99.5	422	23	AAU75853	Human melanin conc
7	2195	99.3	422	21	AA812779	Human SLC-1 protein
8	2195	99.3	422	22	AAE07330	Human melanin conc
9	2195	99.3	422	22	AA881123	Human melanin conc
10	2195	99.3	422	22	AA896871	Human SLC-1, Homo

11	2195	99.3	422	22	AA197670	Human MCH-R3 protein
12	2195	99.3	422	22	AA8B5894	Human long form MCH-R1 protein
13	2195	99.3	422	23	AAU77541	Human melanin-concentrating hormone receptor
14	2195	99.3	422	23	ABR04941	Human SLC-1 protein
15	2195	99.3	422	23	AA680611	Human SLC-1 protein
16	2185	98.9	422	22	AA8B5898	Human long form/mo
17	2185	98.9	673	22	AA8B5907	Human long form/mo
18	2173	98.3	417	22	AAE07329	Human melanin-concentrating hormone receptor
19	2173	98.3	417	22	AA197669	Human MCH-R2 protein
20	1819	82.3	353	19	AA161370	Human 11CB splice
21	1819	82.3	353	20	AA116570	Amino acid sequence
22	1819	82.3	353	21	AA131442	Truncated human MCH-R1 protein
23	1819	82.3	353	21	AA190258	Human 11CB protein
24	1819	82.3	353	22	AAE07328	Human melanin-concentrating hormone receptor
25	1819	82.3	353	22	AAE04747	Human 11CB protein
26	1819	82.3	353	22	AA197668	Human MCH-R1 protein
27	1819	82.3	353	22	AA8B5895	Human short form MCH-R1 protein
28	1819	82.3	353	23	AAU76883	Human melanin-concentrating hormone receptor
29	1819	82.3	353	23	AAU75859	Human melanin-concentrating hormone receptor
30	1819	82.3	709	22	AB8B5636	TSR- α protein
31	1814	82.1	353	22	AB8B5637	Non- α -melanin-concentrating hormone receptor
32	1813	82.0	353	22	AB8B6297	Non- α -melanin-concentrating hormone receptor
33	1813	82.0	353	22	AB8B6305	Non- α -melanin-concentrating hormone receptor
34	1812	82.0	353	22	AB8B6306	Non- α -melanin-concentrating hormone receptor
35	1809	81.9	353	22	AB8B6301	Non- α -melanin-concentrating hormone receptor
36	1809	81.9	353	22	AB8B6303	Non- α -melanin-concentrating hormone receptor
37	1809	81.9	353	22	AA8B5897	Human short form/mo
38	1809	81.9	604	22	AA8B5906	Human short form/mo
39	1808	81.8	353	22	AB8B6300	Non- α -melanin-concentrating hormone receptor
40	1807	81.8	353	22	AB8B6298	Non- α -melanin-concentrating hormone receptor
41	1806	81.7	353	22	AB8B6302	Non- α -melanin-concentrating hormone receptor
42	1806	81.7	353	22	AB8B6304	Non- α -melanin-concentrating hormone receptor
43	1803	81.6	353	21	AA157284	Human GPCR protein
44	1776	80.4	353	23	AAU76892	Dog melanin-concentrating hormone receptor
45	1758	79.5	353	21	AA127778	Rat SLC-1 protein

ALIGNMENTS

	RESULT	1
ID	AAB13441	
XX	AAB13441 standard; Protein: 422 AA.	
XX		
XX	AAB13441;	
DT	17-NOV-2000	(first entry)
XX		
DE	Mutant human MCHL receptor encoded by plasmid R114.	
KW	Human; MCH1 receptor; melanin concentrating hormone; neuroregulator;	
KW	G-protein coupled; feeding; water balance; energy metabolism; arousal;	
KW	attention; memory; cognitive function; psychiatric disorder; stress;	
KW	sexual activity; hormone disorder; hypertension; diabetes;	
KW	cardiovascular; gastrointestinal; electrolyte balance; respiratory;	
KW	asthma; reproductive function; immune; endocrine; musculoskeletal;	
KW	Alzheimer's disease; sensory modulation; transmission;	
KW	motor coordination; Parkinson's disease; olfaction; urinary; depression	
KW	seizure; pain; schizophrenia; morphine tolerance; opiate addiction;	
KW	migraine; mutant; mutain.	
XX		
OS	Homo sapiens.	
OS	Synthetic.	
XX		
FH	Key	Location/Qualifiers
FT	Misc-difference 6	
FT	/note= "Wild-type Met substituted by Ala"	
FT	Misc-difference 70	
FT	/note= "Wild-type Met substituted by Ala"	
XX		
PN	WO200039279-A2.	
XX		
DD	06-JUL-2000.	

Pf	30-DEC-1999;	99WO-USJ1169.
Xx		
Xx	31-DEC-1998;	98US-0224426.
Pt		
Xx	(SYNA-) SYNAPTIC PHARM CORP.	
Pi	Salon JA, Laz TM, Nagorny R,	Wilson AE;
Dk	WPI: 2000-548644/50.	
Xx		
Xx	Novel nucleic acid encoding human melanin concentrating hormone	
Pt	receptor useful for treating cardiovascular disorders, hypertension and	
Pt	diabetes, whose mutant form is activated by melanin concentrating	
Pt	hormone -	
Xx		
Pf	Claim 9; Fig 14; 173pp; English.	
Xx		
Cc	Neuroregulators modulate communication in the nervous system. Melanin	
Cc	concentrating hormone 1 (MCH) is one such neuroregulator. MCH may serve	
Cc	as an integrative neuropeptide, involved in stress response, feeding	
Cc	regulation and sexual activity. Also, MCH is thought to participate in	
Cc	water balance regulation, energy metabolism, general arousal/attention	
Cc	state, memory and cognitive functions and psychiatric disorders. The	
Cc	present sequence is the mutant human MCH receptor encoded by Plasmid	
Cc	R114. The present sequence is a G-protein coupled receptor. MCH receptor	
Cc	may be used in the therapy for a variety of disorders: steroid or	
Cc	pituitary hormone disorder, epinephrine release disorder,	
Cc	gastrointestinal disorder, cardiovascular disorder, electrolyte balance	
Cc	disorder, hypertension, diabetes, respiratory disorder, asthma,	
Cc	reproductive function disorder, immune disorder, endocrine disorder,	
Cc	muskuloskeletal disorder, neuroendocrine disorder, cognitive disorder,	
Cc	memory disorder e.g. Alzheimer's disease, sensory modulation and	
Cc	transmission disorder, motor coordination disorder, sensory integration	
Cc	disorder, dopaminergic function disorder e.g. Parkinson's disease,	
Cc	olfaction disorder, sympathetic innervation disorder, depression, stress,	
Cc	fluid-limbalance disorder, urinary disorder e.g. urinary incontinence,	
Cc	seizure, pain, psychotic behaviour e.g. schizophrenia, morphine	
Cc	tolerance, opiate addiction or migraine.	
Cc		
SQ	Sequence 422 AA:	
	Query Match 100.0%; Score 2210; DB 21; Length 422;	
	Best Local Similarity 100.0%, Pred. No. 1,4e-22n;	
	Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0.	
Qy	1 MSVGAKKKGRAVVGSGSCGCAATEEDPLPCDGACAPCGGRMRLLPPAWEGSSARL 60	
Dd	1 MSVGAKKKRGVAGRVGGSGSCGCAATEDDPLPDGACAAPCGGRMRLLPPAWEGSSARL 60	
Qy	61 WEQATGTGNADLEASILLPTGPNASNTSDGDNLTSAGSPRRGSISYINIMPSVGTTC 120	
Dd	61 WEQATGTGNADLEASILLPTGPNASNTSDGDNLTSAGSPRRGSISYINIMPSVGTTC 120	
Qy	121 LGITINSNYIVFNVVKSKSLHMCNNNDPFIILSVVDLIFFLGMPFMHLQMGNGVMHF 180	
Dd	121 LGITINSNYIVFNVVKSKSLHMCNNNDPFIILSVVDLIFFLGMPFMHLQMGNGVMHF 180	
Qy	181 GEMTCLTIAMDANSOFTSTYILTAMADIRYIATVHPISSTFKRKSVAATVICTLMALS 240	
Dd	181 GEMTCLTIAMDANSOFTSTYILTAMADIRYIATVHPISSTFKRKSVAATVICTLMALS 240	
Qy	241 FISITPWMLYARLIPPGAVGCGIRLPNPDIDLWFYTLIQFLARALPVTAAVYRI 300	
Dd	241 FISITPWMLYARLIPPGAVGCGIRLPNPDIDLWFYTLIQFLARALPVTAAVYRI 300	
Qy	301 LQMTSSVAPAASORSIKRTKRYTRAIACLVFCVCMABYYVYLQLTOLISRPITLFYV 360	
Dd	301 LQMTSSVAPAASORSIKRTKRYTRAIACLVFCVCMABYYVYLQLTOLISRPITLFYV 360	
Qy	361 LYNAAISLGVANSCLNPEFYIVLCETFRKRVLVSVPKPAOGQLRAYSNAOTADEERTESK 420	
Dd	361 LYNAAISLGVANSCLNPEFYIVLCETFRKRVLVSVPKPAOGQLRAYSNAOTADEERTESK 420	

QY	421	GF	422	
DB	421	GP	422	
RESULT 2				
AAU75858				
ID	AAU75858	standard; Protein; 422	AA.	
XX	AAU75858;			
XX	08-MAY-2002	(first entry)		
DE	Human melanin concentrating hormone receptor, MCH1, R114 mutant.			
KW	Human; melanin concentrating hormone receptor; MCH1; R114;			
KW	steroid hormone disorder; pituitary hormone disorder;			
KW	epinephrine release disorder; gastrointestinal disorder; mutein;			
KW	cardiovascular disorder; hypertension; diabetes; respiratory disorder;			
KW	asthma; reproductive function disorder; immune disorder; mutant;			
KW	musculoskeletal disorder; neuroendocrine disorder; cognitive disorder;			
KW	memory disorder; motor coordination disorder; obesity; eating disorder;			
KW	dopaminergic function disorder; pain; psychosis; opiate addiction;			
XX	affective disorder; migraine; transgenic.			
OS	Homo sapiens.			
OS	Synthetic.			
XX				
FH	Key	Location/Qualifiers		
FT	Misc-difference 6	/note= "Wild-type Met substituted by Ala"		
FT	Misc-difference 70	/note= "Wild-type Met substituted by Ala"		
XX				
XX	WO200202744-A2.			
PD	10-JAN-2002.			
XX				
PF	05-JUL-2001; 2001WO-US21350.			
PR	05-JUL-2000; 2000US-0610635.			
PA	(SYNA-) SYNAPTRIC PHARM CORP.			
XX				
PI	Salon JA, Laz TM, Nagorny R, Wilson AE;			
DR	WPI; 2002-164532/21.			
XX				
PT	purified human melanin concentrating hormone receptor protein and			
PT	polynucleotides for screening modulator useful for treating memory			
PT	disorder, sensory modulation and transmission disorder, motor			
PT	coordination disorder			
XX				
PS	Claim 9; Fig 14; 524pp; English.			
XX				
CC	The invention relates to a purified human melanin concentrating hormone			
CC	(MCH1) receptor protein and its encoding nucleic acid (or mutant			
CC	activated by MCH or its analogue or homologue). Also included are			
CC	expression vectors, probes, transformed insect cells, antisense			
CC	oligonucleotides, anti-MCH1 antibodies, an agent capable of inhibiting			
CC	the binding of the antibody to MCH1, a transgenic animal expressing the			
CC	protein, or a homologous knockout or antisense complementary to the MCH1			
CC	nucleic acid, anti/agonists of MCH1, and methods of isolating chemical			
CC	compounds which activate MCH1. The protein, nucleic acid, antibody,			
CC	anti/agonists and compound are useful for diagnosing and treating a			
CC	steroid or pituitary hormone disorder, an epinephrine release disorder, a			
CC	gastrointestinal disorder, cardiovascular disorder, electrolyte balance			
CC	disorder, hypertension, diabetes, respiratory disorder, asthma,			
CC	reproductive function disorder, immune disorder, endocrine disorder,			
CC	musculoskeletal disorder, neuroendocrine disorder, cognitive disorder,			
CC	memory disorder, sensory modulation and transmission disorder, motor			
CC	coordination disorder, sensory integration disorder, motor integration			

CC disorder, dopaminergic function disorder, sensory transmission disorder,
CC olfaction disorder, sympathetic innervation disorder, pain, psychotic
CC behaviour, morphine tolerance, opiate addiction, affective disorder,
CC stress-related disorder, fluid-balance disorder, seizure disorder or
CC migraine, an eating disorder or obesity. The present sequence
CC represents human MCH1 mutant encoded by plasmid R114, which has a
CC methionine residue mutated to alanine in order to investigate the true
CC start codon of MCH1.
XX

Sequence 422 AA;

Query Match 100.0%; Score 2210; DB 23; Length 422;
Best Local Similarity 100.0%; Pred. No. 1.4e-221;
Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSVGAARKGVRAVGLGGSGCQATEEDPLPDGCACAPGGGRRRLPQPAWEGSSARL 60
DB 1 MSVGAARKGVRAVGLGGSGCQATEEDPLPDGCACAPGGGRRRLPQPAWEGSSARL 60
QY 61 WEQATGTGMADLEASLLPTGPNASNTSDGPDNLTSAGSPRTGSIYINIMPSVFGTIC 120
DB 61 WEQATGTGMADLEASLLPTGPNASNTSDGPDNLTSAGSPRTGSIYINIMPSVFGTIC 120
QY 121 LGGIIGNSTVIFAAYVKKSKLHMCNNVPDIFITINLSVVDLLFLGMPFMIHQLMNGVWHF 180
DB 121 LGGIIGNSTVIFAAYVKKSKLHMCNNVPDIFITINLSVVDLLFLGMPFMIHQLMNGVWHF 180
QY 181 GETMCTLTITAMDANSQFTSTYILTAMADRYLATVHPISSTKRPKPSVATLVICLMAALS 240
DB 181 GETMCTLTITAMDANSQFTSTYILTAMADRYLATVHPISSTKRPKPSVATLVICLMAALS 240
QY 241 FISITPWLXARLIPFPGAVGCGIRLPNDPTDLYWFTLYOFLEAFALPFPVITAAVRI 300
DB 241 FISITPWLXARLIPFPGAVGCGIRLPNDPTDLYWFTLYOFLEAFALPFPVITAAVRI 300
QY 301 LQRTSSVAAPASQSRISRLRKRVTRTAIAICLVFVCWAPYYVQLQLTSLISPTLTFVY 360
DB 301 LQRTSSVAAPASQSRISRLRKRVTRTAIAICLVFVCWAPYYVQLQLTSLISPTLTFVY 360
QY 361 LYNNAISILGYANSCNLPFVYIVLCETFRKRLVSVKPAAGGOLRAVSNAGTAEERTESK 420
DB 361 LYNNAISILGYANSCNLPFVYIVLCETFRKRLVSVKPAAGGOLRAVSNAGTAEERTESK 420
QY 421 GT 422
DB 421 GT 422

RESULT 3

AAB13440 ID AAB13440 standard; Protein; 422 AA.

AC AAB13440;

DT 17-NOV-2000 (first entry)

XX Mutant human MCH1 receptor encoded by plasmid R106.

DE Human: MCH1 receptor; melanin concentrating hormone; neuroregulator;
KW G-protein coupled; feeding; water balance; energy metabolism; arousal;
KW attention; memory; cognitive function; psychiatric disorder; stress;
KW sexual activity; hormone disorder; hypertension; diabetes;
KW cardiovascular; gastrointestinal; electrolyte balance; respiratory;
KW asthma; reproductive function; immune; endocrine; musculoskeletal;
KW Alzheimer's disease; sensory modulation; transmission;
KW motor coordination; Parkinson's disease; olfaction; urinary; depression;
KW seizure; pain; schizophrenia; morphine tolerance; opiate addiction;
KW migraine; mutant; mutein.

XX Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers

FT Misc-difference 70 /note= "Wild-type Met substituted by Ala"
FT
XX
XX WO200039279-A2.
PN
XX 06-JUL-2000.
PD
XX
XX 30-DEC-1999; 99WO-US31169.
PF
XX
XX 31-DEC-1998; 98US-0224426.
PR
XX
XX (SYNA-) SYNAPTIC PHARM CORP.
PA
XX Salton JA, Laz TM, Nagorny R, Wilson AE;
PI WPI; 2000-548644/50.
DR
XX

Novel nucleic acid encoding human melanin concentrating hormone
receptor useful for treating cardiovascular disorders, hypertension and
diabetes, whose mutant form is activated by melanin concentrating
hormone -
XX
XX Claim 8; Fig 13; 173pp; English.

Neuroregulators modulate communication in the nervous system. Melanin
concentrating hormone 1 (MCH1) is one such neuroregulator. MCH may serve
as an integrative neuropeptide, involved in stress response, feeding
regulation and sexual activity. Also, MCH is thought to participate in
water balance regulation, energy metabolism, general arousal/attention
state, memory and cognitive functions and psychiatric disorders. The
present sequence is the mutant human MCH1 receptor encoded by plasmid
R106. The present sequence is a G-protein coupled receptor. MCH1 receptor
may be used in the therapy for a variety of disorders: steroid or
pituitary hormone disorder, epinephrine release disorder,
gastrointestinal disorder, cardiovascular disorder, electrolyte balance
disorder, hypertension, diabetes, respiratory disorder, asthma,
reproductive function disorder, immune disorder, endocrine disorder,
musculoskeletal disorder, neuroendocrine disorder, cognitive disorder,
memory disorder e.g. Alzheimer's disease, sensory modulation and
transmission disorder, motor coordination disorder, sensory integration
disorder, dopaminergic function disorder e.g. Parkinson's disease,
CC olfaction disorder, sympathetic innervation disorder, depression, stress,
CC fluid-balance disorder, urinary disorder e.g. urinary incontinence,
CC seizure, pain, psychotic behaviour e.g. schizophrenia, morphine
CC tolerance, opiate addiction or migraine.

Sequence 422 AA;

Query Match 99.8%; Score 2205; DB 21; Length 422;
Best Local Similarity 99.8%; Pred. No. 4.6e-221;
Matches 421; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSVGAARKGVRAVGLGGSGCQATEEDPLPDGCACAPGGGRRRLPQPAWEGSSARL 60
DB 1 MSVGAARKGVRAVGLGGSGCQATEEDPLPDGCACAPGGGRRRLPQPAWEGSSARL 60
QY 61 WEQATGTGMADLEASLLPTGPNASNTSDGPDNLTSAGSPRTGSIYINIMPSVFGTIC 120
DB 61 WEQATGTGMADLEASLLPTGPNASNTSDGPDNLTSAGSPRTGSIYINIMPSVFGTIC 120
QY 121 LGGIIGNSTVIFAAYVKKSKLHMCNNVPDIFITINLSVVDLLFLGMPFMIHQLMNGVWHF 180
DB 121 LGGIIGNSTVIFAAYVKKSKLHMCNNVPDIFITINLSVVDLLFLGMPFMIHQLMNGVWHF 180
QY 181 GETMCTLTITAMDANSQFTSTYILTAMADRYLATVHPISSTKRPKPSVATLVICLMAALS 240
DB 181 GETMCTLTITAMDANSQFTSTYILTAMADRYLATVHPISSTKRPKPSVATLVICLMAALS 240
QY 241 FISITPWLXARLIPFPGAVGCGIRLPNDPTDLYWFTLYOFLEAFALPFPVITAAVRI 300
DB 241 FISITPWLXARLIPFPGAVGCGIRLPNDPTDLYWFTLYOFLEAFALPFPVITAAVRI 300
QY 301 LQRTSSVAAPASQSRISRLRKRVTRTAIAICLVFVCWAPYYVQLQLTSLISPTLTFVY 360

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|||||
Db 301 LQRTSSVAPASQSRIRLRTKRVTRTAICLVFVCMAPYYVQLQLSISRTLTFFVY 360
Qy 361 LYNAISIGYANSCINLPFVYIVLCETFRKRLVLSVKPAQGLRAVSNAGTADERTESK 420
Db 361 LYNAISIGYANSCINLPFVYIVLCETFRKRLVLSVKPAQGLRAVSNAGTADERTESK 420
Qy 421 GT 422
Db 421 GT 422

RESULT 4
AAU75857
ID AAU75857 standard; Protein; 422 AA.
AC AAU75857;
DE 08-MAY-2002 (first entry)
XX Human melanin concentrating hormone receptor, MCH1, R106 mutant.
DE Human melanin concentrating hormone receptor; MCH1; R106;
KW Human; melanin concentrating hormone receptor; MCH1;
KW steroid hormone disorder; pituitary hormone disorder;
KW epinephrine release disorder; gastrointestinal disorder; mutein;
KW cardiovascular disorder; hypertension; diabetes; respiratory disorder;
KW asthma; reproductive function disorder; immune disorder; mutant;
KW musculoskeletal disorder; neuroendocrine disorder; cognitive disorder;
KW memory disorder; motor coordination disorder; obesity; eating disorder;
KW dopaminergic function disorder; pain; psychosis; opiate addiction;
KW affective disorder; migraine; transgenic.
XX Homo sapiens.
OS Synthetic.
XX Key Location/Qualifiers
FH Misc-difference 70
FT /note= "Wild-type Met substituted by Ala"
FT
XX WO200202744-A2.
XX 10-JAN-2002.
XX 05-JUL-2001; 2001WO-US21350.
XX 05-JUL-2000; 2000US-0610635.
XX (SYNA-) SYNAPTIC PHARM CORP.
XX Salon JA, Laz TM, Nagorny R, Wilson AE;
XX WPI: 2002-164532/21.
XX
XX Purified human melanin concentrating hormone receptor protein and
XX polynucleotides for screening modulator useful for treating memory
XX disorder, sensory modulation and transmission disorder, motor
XX coordination disorder -
XX Claim 8; Fig 13; 524pp; English.
XX
XX The invention relates to a purified human melanin concentrating hormone
XX (MCH1) receptor protein and its encoding nucleic acid (or mutant
XX activated by MCH or its analogue or homologue). Also included are
XX expression vectors, probes, transformed insect cells, antisense
XX oligonucleotides, anti-MCH1 antibodies, an agent capable of inhibiting
XX the binding of the antibody to MCH1, a transgenic animal expressing the
XX protein, or a homologous knockout or antisense complementary to the MCH1
XX nucleic acid, or antagonists of MCH1, and methods of isolating chemical
XX compounds which activate MCH1. The protein, nucleic acid, antibody,
XX ant/agonists and compound are useful for diagnosing and treating a
XX steroid or pituitary hormone disorder, an epinephrine release disorder, a
XX gastrointestinal disorder, cardiovascular disorder, electrolyte balance
XX disorder, hypertension, diabetes, respiratory disorder, asthma,

```

```

CC reproductive function disorder, immune disorder, endocrine disorder,
CC musculoskeletal disorder, neuroendocrine disorder, cognitive disorder,
CC memory disorder, sensory modulation and transmission disorder, motor
CC coordination disorder, sensory integration disorder, motor integration
CC disorder, dopaminergic function disorder, sensory transmission disorder,
CC olfaction disorder, sympathetic innervation disorder, pain, psychotic
CC behaviour, morphine tolerance, opiate addiction, affective disorder,
CC stress-related disorder, fluid-balance disorder, seizure disorder or
CC migraine, an eating disorder or obesity. The present sequence
CC represents human MCH1 mutant encoded by plasmid R106, which has a
CC methionine residue mutated to alanine in order to investigate the true
CC start codon of MCH1.
XX
SQ Sequence 422 AA;
Query Match 99.8%; Score 2205; DB 23; Length 422;
Best Local Similarity 99.8%; Pred. No. 4,6e-221;
Matches 421; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MSYGAARKGYGRAVGLGGSGCATDEDPDPCGACAPQGGRRRLPQPAWEGSSARL 60
Db 1 MSYGAARKGYGRAVGLGGSGCATDEDPDPCGACAPQGGRRRLPQPAWEGSSARL 60
Qy 61 WEQATGTGMADLEASLLPTGPNASNTSDGPDMLTSAGSPRTGSISYINIMPSVFGTIC 120
Db 61 WEQATGTGMADLEASLLPTGPNASNTSDGPDMLTSAGSPRTGSISYINIMPSVFGTIC 120
Qy 121 LLGIIIGNSYIVFVAVKSKSLHMCNNPDPIFINLSVVDLLFLGMPFMHOLMGCVHMF 180
Db 121 LLGIIIGNSYIVFVAVKSKSLHMCNNPDPIFINLSVVDLLFLGMPFMHOLMGCVHMF 180
Qy 181 GETMCTLTITAMDNSQFTSYITLTAIDRYLATVPISSFRKRSVATLYICLMALS 240
Db 181 GETMCTLTITAMDNSQFTSYITLTAIDRYLATVPISSFRKRSVATLYICLMALS 240
Qy 241 FISITPVMYLARLIPPGGAVGCGIRLPNPDDLYFTLYQFFLAFLPFVYITAYARI 300
Db 241 FISITPVMYLARLIPPGGAVGCGIRLPNPDDLYFTLYQFFLAFLPFVYITAYARI 300
Qy 301 LQRTSSVAPASQSRIRLRTKRVTRTAICLVFVCMAPYYVQLQLSISRTLTFFVY 360
Db 301 LQRTSSVAPASQSRIRLRTKRVTRTAICLVFVCMAPYYVQLQLSISRTLTFFVY 360
Qy 361 LYNAISIGYANSCINLPFVYIVLCETFRKRLVLSVKPAQGLRAVSNAGTADERTESK 420
Db 361 LYNAISIGYANSCINLPFVYIVLCETFRKRLVLSVKPAQGLRAVSNAGTADERTESK 420
Qy 421 GT 422
Db 421 GT 422

RESULT 5
AAB13436
ID AAB13436 standard; Protein; 422 AA.
AC AAB13436;
DE 17-NOV-2000 (first entry)
XX
XX Human MCH1 receptor.
DE Human MCH1 receptor.
XX Human; MCH1 receptor; melanin concentrating hormone; neuroregulator;
XX G-protein coupled; PKXJ-HR-TL231; feeding; water balance;
XX energy metabolism; arousal; attention; memory; cognitive function;
XX psychiatric disorder; stress; sexual activity; hormone disorder;
XX hypertension; diabetes; cardiovascular; asthma; reproductive function;
XX electrolyte balance; respiratory; seizure; Alzheimer's disease;
XX immune; endocrine; musculoskeletal; motor coordination;
XX sensory modulation; transmission; motor coordination;
XX Parkinson's disease; olfaction; urinary; depression; seizure; pain;
XX schizophrenia; morphine tolerance; opiate addiction; migraine.
XX

```



```
OS Homo sapiens.
XX Key
FH Region
FT 110..135
FT /label= Transmembrane_region_1
FT 149..169
FT /label= Transmembrane_region_2
FT 193..208
FT /label= Transmembrane_region_3
FT 228..262
FT /label= Transmembrane_region_4
FT 274..301
FT /label= Transmembrane_region_5
FT 323..349
FT /label= Transmembrane_region_6
FT 358..383
FT /label= Transmembrane_region_7
XX
XX WO200039279-A2.
XX
XX 06-JUL-2000.
XX
XX 30-DEC-1999; 99WO-US31169.
XX
XX 31-DEC-1998; 98US-0224426.
XX
XX (SYNA-) SYNAPTIC PHARM CORP.
XX
XX Salon JA, Laz TM, Nagorny R, Wilson AE;
XX
XX WPI: 2000-548644/50.
XX
XX N-PSDB; AAA63240.
XX
XX Novel nucleic acid encoding human melanin concentrating hormone
XX receptor useful for treating cardiovascular disorders, hypertension and
XX diabetes, whose mutant form is activated by melanin concentrating
XX hormone -
XX
XX Claim 7; Fig 2; 173pp; English.
XX
XX Neuroregulators modulate communication in the nervous system. Melanin
XX concentrating hormone 1 (MCH1) is one such neuroregulator. MCH may serve
XX as an integrative neuropeptide, involved in stress response, feeding
XX regulation and sexual activity. Also, MCH is thought to participate in
XX water balance regulation, energy metabolism, general arousal/attention
XX state, memory and cognitive functions and psychiatric disorders. The
XX present sequence is the human MCH1 receptor. The present sequence is a
XX G-protein coupled receptor and has 7 transmembrane regions. MCH1 receptor
XX may be used in the therapy for a variety of disorders: steroid or
XX pituitary hormone disorder, epinephrine release disorder,
XX gastrointestinal disorder, cardiovascular disorder, electrolyte balance
XX disorder, hypertension, diabetes, respiratory disorder, asthma,
XX reproductive function disorder, immune disorder, endocrine disorder,
XX musculoskeletal disorder, neuroendocrine disorder, cognitive disorder,
XX memory disorder e.g. Alzheimer's disease, sensory modulation and
XX transmission disorder, motor coordination disorder, sensory integration
XX disorder, dopaminergic function disorder e.g. Parkinson's disease,
XX olfaction disorder, sympathetic innervation disorder, depression, stress,
XX fluid-imbalance disorder, urinary disorder e.g. urinary incontinence,
XX seizure, pain, psychotic behaviour e.g. schizophrenia, morphine
XX tolerance, opiate addiction or migraine. The coding sequence for the
XX present protein is also contained in plasmid pMXJ-HR-1L231 (ATCC 203197).
XX
XX Sequence 422 AA:
XX
XX Query Match 99.5%; Score 2200; DB 21; Length 422;
XX Best Local Similarity 99.5%; Pred. No. 1.5e-220;
XX Matches 420; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 61 WEQATGTGMADLEASLLPTGPNASNTSDGPDNLTSAGSPPTGSIYINIMPSYFGTIC 120
DB 61 WEQATGTGMADLEASLLPTGPNASNTSDGPDNLTSAGSPPTGSIYINIMPSYFGTIC 120
QY 121 LIGIIGNSTVIFAIVYKSKLHMCNNVPDIFITNLAVDILLFLGMPFKIHLMGNCVWHF 180
DB 121 LIGIIGNSTVIFAIVYKSKLHMCNNVPDIFITNLAVDILLFLGMPFKIHLMGNCVWHF 180
QY 181 GETMCTLTITAMANDANSOFSTYITLTAMAIDRYLATVHPISSTFKRPSVATVIICLMALS 240
DB 181 GETMCTLTITAMANDANSOFSTYITLTAMAIDRYLATVHPISSTFKRPSVATVIICLMALS 240
QY 241 FTSITPWWLYARLIPPGGAVGCGIRLPNPDITLYWFTLYOFEALPFWITAAVRI 300
DB 241 FTSITPWWLYARLIPPGGAVGCGIRLPNPDITLYWFTLYOFEALPFWITAAVRI 300
QY 301 LDRMTSSVAPASORSIRLTKRVTFAIALICLFVFCMAPYYVLOLTOLISRPITLTVY 360
DB 301 LDRMTSSVAPASORSIRLTKRVTFAIALICLFVFCMAPYYVLOLTOLISRPITLTVY 360
QY 361 LYNAAISLGYANSCLNPFYIYLCEFFRRRLVLSVPAAGOLRAVSNQTADEERTESK 420
DB 361 LYNAAISLGYANSCLNPFYIYLCEFFRRRLVLSVPAAGOLRAVSNQTADEERTESK 420
QY 421 GT 422
DB 421 GT 422
XX
XX RESULT 6
XX AAU75853
XX ID AAU75853 standard; Protein; 422 AA.
XX
XX AAU75853;
XX
XX 08-MAY-2002 (first entry)
XX
XX Human melanin concentrating hormone receptor, MCH1.
XX
XX DE
XX
XX Human; melanin concentrating hormone receptor; MCH1;
XX steroid hormone disorder; pituitary hormone disorder;
XX epinephrine release disorder; gastrointestinal disorder;
XX cardiovascular disorder; hypertension; diabetes; respiratory disorder;
XX asthma; reproductive function disorder; immune disorder;
XX musculoskeletal disorder; neuroendocrine disorder; cognitive disorder;
XX memory disorder; motor coordination disorder; obesity; eating disorder;
XX dopaminergic function disorder; pain; psychosis; opiate addiction;
XX affective disorder; migraine; transgenic.
XX
XX OS Homo sapiens.
XX
XX PN WO200202744-A2.
XX
XX 10-JAN-2002.
XX
XX 05-JUL-2001; 2001WO-US21350.
XX
XX PR 05-JUL-2000; 2000US-0610635.
XX
XX (SYNA-) SYNAPTIC PHARM CORP.
XX
XX Salon JA, Laz TM, Nagorny R, Wilson AE;
XX
XX WPI: 2002-164532/21.
XX
XX N-PSDB; ABR14548.
XX
XX Purified human melanin concentrating hormone receptor protein and
XX polynucleotides for screening modulator useful for treating memory
XX disorder, sensory modulation and transmission disorder, motor
XX coordination disorder -
XX
XX Example; Fig 2; 524pp; English.
XX
```

CC The invention relates to a purified human melanin concentrating hormone
 CC (MCH1) receptor protein and its encoding nucleic acid (or mutant
 CC activated by MCH or its analogue or homologue). Also included are
 CC expression vectors, probes, transformed insect cells, antisense
 CC oligonucleotides, anti-MCH1 antibodies, an agent capable of inhibiting
 CC the binding of the antibody to MCH1, a transgenic animal expressing the
 CC protein, or a homologous knockout or antisense complementary to the MCH1
 CC nucleic acid, ant/agonists of MCH1, and methods of isolating chemical
 CC compounds which activate MCH1. The protein, nucleic acid, antibody,
 CC ant/agonists and compound are useful for diagnosing and treating a
 CC steroid or pituitary hormone disorder, an ephrine release disorder, a
 CC gastrointestinal disorder, cardiovascular disorder, electrolyte balance
 CC disorder, hypertension, diabetes, respiratory disorder, asthma,
 CC reproductive function disorder, immune disorder, endocrine disorder,
 CC musculoskeletal disorder, neuroendocrine disorder, cognitive disorder,
 CC memory disorder, sensory modulation and transmission disorder, motor
 CC coordination disorder, sensory integration disorder, motor integration
 CC disorder, dopaminergic function disorder, sensory transmission disorder,
 CC olfaction disorder, sympathetic innervation disorder, pain, psychotic
 CC behaviour, morphine tolerance, opiate addiction, affective disorder,
 CC stress-related disorder, fluid-balance disorder, seizure disorder or
 CC migraine, an eating disorder or obesity. The present sequence
 CC represents human MCH1.

CC Sequence 422 AA;

Query Match 99.5%; Score 2200; DB 23; Length 422;
 Best Local Similarity 99.5%; Pred. No. 1.5e-220;
 Matches 420; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSVGAARKGVGRAVGLGGSGCATTEEDPLPCGACAPGGGRRMRLLQPAWEGSSARL 60
 DB 1 MSVGAARKGVGRAVGLGGSGCATTEEDPLPCGACAPGGGRRMRLLQPAWEGSSARL 60
 QY 61 WEQATGTGMADLEASILPTGPNASNTSDGPNLTSAGSPRTGSIYINIIMPVSFETIC 120
 DB 61 WEQATGTGMADLEASILPTGPNASNTSDGPNLTSAGSPRTGSIYINIIMPVSFETIC 120
 QY 121 LGGIIGNSTVFAVVKSKLHMCNNVPDFFIINLSVVDLFLGMPMIHOLMGNGVWHF 180
 DB 121 LGGIIGNSTVFAVVKSKLHMCNNVPDFFIINLSVVDLFLGMPMIHOLMGNGVWHF 180
 QY 181 GETMCTLTAMDANSOFTSTYILTAADRYLATVHPISSTFKRPSVATLVICLMAALS 240
 DB 181 GETMCTLTAMDANSOFTSTYILTAADRYLATVHPISSTFKRPSVATLVICLMAALS 240
 QY 241 FISTPVMYLARLIPPGGAVGCGIRLPNPDLDYWFLLYOFELAFALPVPVITAAYRI 300
 DB 241 FISTPVMYLARLIPPGGAVGCGIRLPNPDLDYWFLLYOFELAFALPVPVITAAYRI 300
 QY 301 LQRMSSVAPASORSIRLRTKRVTRTAICLVFVCMAPYYVQLTOLISRPFLTFVY 360
 DB 301 LQRMSSVAPASORSIRLRTKRVTRTAICLVFVCMAPYYVQLTOLISRPFLTFVY 360
 QY 361 LYNAISIGTANSCNLPVYIVLCETFRKRLVLSVKPAAGQQLRAVNSNAOTADEERTESK 420
 DB 361 LYNAISIGTANSCNLPVYIVLCETFRKRLVLSVKPAAGQQLRAVNSNAOTADEERTESK 420
 QY 421 GT 422
 DB 421 GT 422

RESULT 7

AA012779 standard; Protein: 422 AA.

XX AA012779;
 AC
 XX
 XX 22-NOV-2000 (first entry)
 XX Human SLC-1 protein sequence SEQ ID NO:11.
 XX

KW SLC-1; MHC; melanin concentrating hormone; screening; eating;
 KW appetite stimulator; appetite regulator; period pain; atonic bleeding;
 KW caesarean section; milk congestion; antioleptic agent; drug;
 KW foetal asphyxia; cervical rupture; premature birth; uterine rupture;
 KW Prader-Willi syndrome; anorectic; gynaecological; abortifacient;
 KW antaemia; anabolic; orphan G protein-couple receptor protein.
 OS Homo sapiens.
 PN WO200040725-A1.
 XX 13-0UL-2000.
 XX 27-DEC-1999; 99WO-JP07336.
 XX 28-DEC-1998; 98JP-0374454.
 PR 28-APR-1999; 99JP-0122688.
 PR 02-SEP-1999; 99JP-0249300.
 XX (TAKE) TAKEDA CHEM IND LTD.
 PA
 XX
 PI Mori M, Shimomura Y, Takekawa S, Sugo T, Ishibashi Y, Kitada C;
 PI Suzuki N;
 DR WPI: 2000-475832/41.
 DR N-PSDB; AAA72918.

PT Screening methods for compounds as SLC-1 (ant)agonists useful in the
 PT treatment of eating disorders and as preventives and remedies for e.g.
 PT atonic bleeding and Prader-Willi syndrome
 PS Claim 6; Page 111-113; 123pp; Japanese.

CC The present invention describes a method for screening components (I) or
 CC their salts that can alter the binding properties of melanin-
 CC concentrating hormone (MCH) or its derivative or salt to SLC-1 or its
 CC salt. Compounds identified by (I) are useful as SLC-1 (ant)agonists in
 CC eating disorders and as preventives and remedies for e.g. period pains,
 CC uterine recovery failure, caesarean section, artificial interruption of
 CC pregnancy, galactosistis, tonic uterine contraction, foetal asphyxia,
 CC rupture of uterus, cervical rupture, premature birth and Prader-Willi
 CC syndrome. The present sequence represents the human SLC-1 protein
 CC sequence, which is used in an example from the present invention.

CC Sequence 422 AA;

Query Match 99.3%; Score 2195; DB 21; Length 422;
 Best Local Similarity 99.3%; Pred. No. 5.1e-220;
 Matches 419; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSVGAARKGVGRAVGLGGSGCATTEEDPLPCGACAPGGGRRMRLLQPAWEGSSARL 60
 DB 1 MSVGAARKGVGRAVGLGGSGCATTEEDPLPCGACAPGGGRRMRLLQPAWEGSSARL 60
 QY 61 WEQATGTGMADLEASILPTGPNASNTSDGPNLTSAGSPRTGSIYINIIMPVSFETIC 120
 DB 61 WEQATGTGMADLEASILPTGPNASNTSDGPNLTSAGSPRTGSIYINIIMPVSFETIC 120
 QY 121 LGGIIGNSTVFAVVKSKLHMCNNVPDFFIINLSVVDLFLGMPMIHOLMGNGVWHF 180
 DB 121 LGGIIGNSTVFAVVKSKLHMCNNVPDFFIINLSVVDLFLGMPMIHOLMGNGVWHF 180
 QY 181 GETMCTLTAMDANSOFTSTYILTAADRYLATVHPISSTFKRPSVATLVICLMAALS 240
 DB 181 GETMCTLTAMDANSOFTSTYILTAADRYLATVHPISSTFKRPSVATLVICLMAALS 240
 QY 241 FISTPVMYLARLIPPGGAVGCGIRLPNPDLDYWFLLYOFELAFALPVPVITAAYRI 300
 DB 241 FISTPVMYLARLIPPGGAVGCGIRLPNPDLDYWFLLYOFELAFALPVPVITAAYRI 300
 QY 301 LQRMSSVAPASORSIRLRTKRVTRTAICLVFVCMAPYYVQLTOLISRPFLTFVY 360
 DB 301 LQRMSSVAPASORSIRLRTKRVTRTAICLVFVCMAPYYVQLTOLISRPFLTFVY 360

```

OY 361 LYNAAISIGYANSCINPFIYIVLCETFRKRLVLSVKPAAGQLRAVSNADADEERTESK 420
   |||||||
DB 361 LYNAAISIGYANSCINPFIYIVLCETFRKRLVLSVKPAAGQLRAVSNADADEERTESK 420
OY 421 GT 422
   ||
DB 421 GT 422

RESULT 8
AAE07330
ID AAE07330 standard; Protein: 422 AA.
XX
XX AAE07330;
AC
XX
XX 06-NOV-2001 (first entry)
DT
XX
XX Human melanin-concentrating hormone receptor variant #3.
DE
XX
XX Human; melanin-concentrating hormone; MCH analogue; signal transduction;
KM appetite; therapy; anorexia; acquired immune deficiency syndrome; AIDS;
KM wasting; cachexia; frail elderly; weight maintenance; cancer; anorectic;
KM pain reduction; stress reduction; sexual dysfunction; variant.
XX
XX Homo sapiens.
OS
XX Synthetic.
PN WO200157070-A1.
XX
XX 09-AUG-2001.
PD
XX
XX 01-FEB-2001; 2001WO-US03293.
PF
XX
XX 03-FEB-2000; 2000US-0179967.
PR
XX
XX (MERI ) MERCK & CO INC.
PA
XX
XX Bednarek M.
PI
XX
XX WPI: 2001-483416/52.
DR
XX N-PSDB; AAD13654.
XX
XX Novel peptide encoding a melanin-concentrating hormone analog useful
PT for increasing weight or appetite -
XX
XX Disclosure: Page 35-36; 66pp; English.
XX
XX The present invention relates to truncated melanin-concentrating hormone
CC (MCH) analogues active at the MCH receptor. The truncated MCH analogues
CC are optionally modified peptide derivatives of mammalian MCH. The MCH
CC analogues can bind to the MCH receptor and bring about signal
CC transduction. The MCH agonists can be used to facilitate a weight gain,
CC maintenance of weight and/or an appetite increase. The MCH agonists can
CC also be used to treat disorders such as anorexia, acquired immune
CC deficiency syndrome (AIDS), wasting, cachexia and frail elderly. The MCH
CC antagonists can be used to facilitate weight loss, appetite decrease,
CC weight maintenance, cancer treatment, pain reduction, stress reduction
CC and/or treatment of sexual dysfunction. The present sequence is a human
CC MCH receptor variant.
XX
XX Sequence 422 AA:

Query Match 99.3%; Score 2195; DB 22; Length 422;
Best Local Similarity 99.3%; Pred. No. 5;le-220;
Matches 419; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 1 MSYGAKKGVRAVGLGGSGGCAATEEDPLPDCCGACAGGGRMRRLPQPAWVGSSARL 60
   |||||||
DB 1 MSYGAKKGVRAVGLGGSGGCAATEEDPLPDCCGACAGGGRMRRLPQPAWVGSSARL 60
OY 61 WEQATGTGMADLEASILPTGPNAASNTSDGPDNLTSAGSPPTGCSIXYINIMPSVEFTIC 120
   |||||||

```

```

DB 61 WEQATGTGMADLEASILPTGPNAASNTSDGPDNLTSAGSPPTGCSIXYINIMPSVEFTIC 120
OY 121 ILGIIGNSTVIFAAYKSKSLHMCNNVDPFIINISYVDLLFLIGMPMIHQMGNGVWHP 180
   |||||||
DB 121 ILGIIGNSTVIFAAYKSKSLHMCNNVDPFIINISYVDLLFLIGMPMIHQMGNGVWHP 180
OY 181 GETMCTLTITAMDANSQFTSYIILTAMADRYLATVHPISSTKFRKPSVATLVICLMALS 240
   |||||||
DB 181 GETMCTLTITAMDANSQFTSYIILTAMADRYLATVHPISSTKFRKPSVATLVICLMALS 240
OY 241 FISTTPWMLYARLIPFGGAVCGGIRLPNPTDIYKFTLVQFLAPLPPVYITAAVRI 300
   |||||||
DB 241 FISTTPWMLYARLIPFGGAVCGGIRLPNPTDIYKFTLVQFLAPLPPVYITAAVRI 300
OY 301 LQRTSSVAPASQSRISIRLRTKRTATAICLAFVFCMAPYVYLQTLQSLISRPITLFEVY 360
   |||||||
DB 301 LQRTSSVAPASQSRISIRLRTKRTATAICLAFVFCMAPYVYLQTLQSLISRPITLFEVY 360
OY 361 LYNAAISIGYANSCINPFIYIVLCETFRKRLVLSVKPAAGQLRAVSNADADEERTESK 420
   |||||||
DB 361 LYNAAISIGYANSCINPFIYIVLCETFRKRLVLSVKPAAGQLRAVSNADADEERTESK 420
OY 421 GT 422
   ||
DB 421 GT 422

RESULT 9
AAB81123
ID AAB81123 standard; Protein: 422 AA.
XX
XX AAB81123;
AC
XX
XX 05-JUL-2001 (first entry)
DT
XX
XX Human melanin concentrating hormone receptor (SLC-1).
DE
XX
XX Melanin concentrating hormone; MCH; antagonist; diamine compound;
KM anorectic; antidiabetic; ophthalmological; neuroprotective; nephrotropic;
KM antiarteriosclerotic; antiarthritic; obesity; diabetes; arteriosclerosis;
KM arthritis; melanin concentrating hormone receptor; SLC-1; human.
XX
XX Homo sapiens.
OS
XX
XX WO200121169-A1.
PN
XX
XX 29-MAR-2001.
PD
XX
XX 19-SEP-2000; 2000WO-JP06376.
PF
XX
XX 20-SEP-1999; 99JP-0266278.
PR
XX 17-JUL-2000; 2000JP-0221055.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
PA
XX
XX Kato K, Mori M, Suzuki N, Shimomura Y, Takekawa S, Choh N;
PI
XX WPI: 2001-328055/34.
DR
XX N-PSDB; AAF86229.
XX
XX Melanin concentrating hormone antagonists comprise new and known
PT diamine compounds for treating obesity -
XX
XX Examples: Page 271-273; 284pp; Japanese.
XX
XX This invention relates to melanin concentrating hormone (MCH)
CC antagonists, comprising a diamine compound or its prodrug and/or salt.
CC use of the MCH antagonists can result in anorectic, antidiabetic,
CC ophthalmological, neuroprotective, nephrotropic, antiarteriosclerotic,
CC and antiarthritic activity. Melanin concentrating hormone (MCH)
CC antagonists can be used for treating obesity (e.g. exogenous obesity,
CC hypophyseal adiposity, hypothalamic obesity and hyperphagia) and
CC associated disorders such as diabetes, diabetic complications (such as

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CC diabetic retinopathy, diabetic neuropathy and diabetic nephropathy),
 CC arteriosclerosis and arthritis in the knees. The present sequence
 CC represents the human melanin concentrating hormone receptor (SLC-1). The
 CC SLC-1 cDNA is used in examples to demonstrate the use of the antagonists
 CC of the invention.

XX Sequence 422 AA:

Query Match 99.3%; Score 2195; DB 22; Length 422;
 Best Local Similarity 99.3%; Pred. No. 5.1e-220;
 Matches 419; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSYGAKKGVRAVGLGGSGCGATDEDPDPCGACAPGGGRRMRLLQPAAWEGSSARL 60
 DB 1 MSYGAKKGVRAVGLGGSGCGATDEDPDPCGACAPGGGRRMRLLQPAAWEGSSARL 60
 QY 61 WEQATGTGMADLEASLPTGPNASNTSDGPNLTSAGSPRTGSIYINIMPSVGTIC 120
 DB 61 WEQATGTGMADLEASLPTGPNASNTSDGPNLTSAGSPRTGSIYINIMPSVGTIC 120
 QY 121 LGIIGNSTVIFAVYKSKLHMCNNVPDIFINLSVDLLEFLGMPMIHQMGNGVMHP 180
 DB 121 LGIIGNSTVIFAVYKSKLHMCNNVPDIFINLSVDLLEFLGMPMIHQMGNGVMHP 180
 QY 181 GETMCTLTITAMDANSOFTSTYILITAMADRYLATVHPISSTKFRKPSVATLVICLMALS 240
 DB 181 GETMCTLTITAMDANSOFTSTYILITAMADRYLATVHPISSTKFRKPSVATLVICLMALS 240
 QY 241 FISTPFWLVARLIPFPGAVGCGIRLPNDTDLWFTLYQFLAFALPFWVITAAVYRI 300
 DB 241 FISTPFWLVARLIPFPGAVGCGIRLPNDTDLWFTLYQFLAFALPFWVITAAVYRI 300
 QY 301 LQRMSSVAPASORSIRLRTKRVRTAIAICLVFVCMAPYYVQLTOLISRPRTLTFY 360
 DB 301 LQRMSSVAPASORSIRLRTKRVRTAIAICLVFVCMAPYYVQLTOLISRPRTLTFY 360
 QY 361 LYNAISLGYANSCINPYYIVLICETFRKRLVLSVKPAAGQLRAVSNAGTADERTESK 420
 DB 361 LYNAISLGYANSCINPYYIVLICETFRKRLVLSVKPAAGQLRAVSNAGTADERTESK 420
 QY 421 GT 422
 DB 421 GT 422

RESULT 10
 AAB96871
 ID AAB96871 standard; Protein: 422 AA.
 XX
 AC AAB96871;
 XX
 DT 06-JUL-2001 (first entry)
 XX
 DE Human SLC-1.
 XX
 KW Rat; human: SLC-1; MCH receptor; melanin-concentrating hormone;
 KW obesity; diabetes; hypertension; arteriosclerosis; hyperphagia;
 KW emotional disorder; reproductive disorder; memory disorder;
 KW dementia; hormonal disorder; gonitis.
 XX
 OS Homo sapiens.
 XX
 PN WO200121577-A2.
 XX
 PD 29-MAR-2001.
 XX
 PF 19-SEP-2000; 2000WO-JP06375.
 XX
 PR 20-SEP-1999; 99JP-0266298.
 PR 16-DEC-1999; 98JP-0357889.
 PR 20-APR-2000; 2000JP-0126272.
 XX
 PA (TAKE) TAKEADA CHEM IND LTD.

XX Kato K, Terauchi J, Mori M, Suzuki N, Shimomura Y, Takekawa S;
 PI Ishihara Y;
 XX
 DR WPI: 2001-354775/37.
 XX
 DR N-PSDB: AAF86975.
 XX

PT New aromatic compounds are melanin concentrating hormone antagonists,
 PT useful as anorectic agents, for treating or preventing obesity, also
 PT memory or hormonal disorders or diabetes
 XX
 PS Examples; Page 358-360; 363pp; English.

CC The present invention describes aromatic compounds capable of acting as
 CC melanin-concentrating hormone (MCH) antagonists. Melanin-concentrating
 CC hormone is an appetite control factor and antagonists were expected to be
 CC useful as anti-obesity agents. They can be used in the treatment of
 CC obesity, including malignant mastocytosis, exogenous, hyperinsular,
 CC hypoplasmic, hypothyroid, hypothalamic, symptomatic, infantile, upper
 CC body, alimentary, hypogonadal, simple and central obesity, systemic
 CC mastocytosis and hypophyseal adiposity, hypertension, arteriosclerosis,
 CC hyperphagia, emotional disorders, reproductive function disorders, memory
 CC disorders, dementia, hormonal disorders, diabetes and gonitis. MCH binds
 CC to the SLC-1 receptor. The present sequence is the human SLC-1 protein
 CC sequence.

XX Sequence 422 AA:

Query Match 99.3%; Score 2195; DB 22; Length 422;
 Best Local Similarity 99.3%; Pred. No. 5.1e-220;
 Matches 419; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSYGAKKGVRAVGLGGSGCGATDEDPDPCGACAPGGGRRMRLLQPAAWEGSSARL 60
 DB 1 MSYGAKKGVRAVGLGGSGCGATDEDPDPCGACAPGGGRRMRLLQPAAWEGSSARL 60
 QY 61 WEQATGTGMADLEASLPTGPNASNTSDGPNLTSAGSPRTGSIYINIMPSVGTIC 120
 DB 61 WEQATGTGMADLEASLPTGPNASNTSDGPNLTSAGSPRTGSIYINIMPSVGTIC 120
 QY 121 LGIIGNSTVIFAVYKSKLHMCNNVPDIFINLSVDLLEFLGMPMIHQMGNGVMHP 180
 DB 121 LGIIGNSTVIFAVYKSKLHMCNNVPDIFINLSVDLLEFLGMPMIHQMGNGVMHP 180
 QY 181 GETMCTLTITAMDANSOFTSTYILITAMADRYLATVHPISSTKFRKPSVATLVICLMALS 240
 DB 181 GETMCTLTITAMDANSOFTSTYILITAMADRYLATVHPISSTKFRKPSVATLVICLMALS 240
 QY 241 FISTPFWLVARLIPFPGAVGCGIRLPNDTDLWFTLYQFLAFALPFWVITAAVYRI 300
 DB 241 FISTPFWLVARLIPFPGAVGCGIRLPNDTDLWFTLYQFLAFALPFWVITAAVYRI 300
 QY 301 LQRMSSVAPASORSIRLRTKRVRTAIAICLVFVCMAPYYVQLTOLISRPRTLTFY 360
 DB 301 LQRMSSVAPASORSIRLRTKRVRTAIAICLVFVCMAPYYVQLTOLISRPRTLTFY 360
 QY 361 LYNAISLGYANSCINPYYIVLICETFRKRLVLSVKPAAGQLRAVSNAGTADERTESK 420
 DB 361 LYNAISLGYANSCINPYYIVLICETFRKRLVLSVKPAAGQLRAVSNAGTADERTESK 420
 QY 421 GT 422
 DB 421 GT 422

RESULT 11
 AAY97670
 ID AAY97670 standard; Protein: 422 AA.
 XX
 AC AAY97670;
 XX
 DT 08-MAY-2001 (first entry)
 XX

DE Human MCH-R3 protein sequence.
XX
KW Human; melanin-concentrating hormone receptor; MCH-R1; MCH-R2; MCH-R3;
KW weight loss; weight gain; cancer; pain; diabetes; stress; therapy;
KW sexual dysfunction.
XX
OS Homo sapiens.
XX
FN WO200105947-A1.
XX
PD 25-JAN-2001.
XX
PF 10-JUL-2000; 2000WO-US18733.
XX
PR 14-JUL-1999; 99US-0143706.
XX
PA (MERI) MERCK & CO INC.
XX
PI Howard AD;
XX
DR WPI: 2001-159528/16.
DR N-PSDB; AAA91189, AAA91192.
XX
PT Melanin-concentrating hormone receptor polypeptides for increasing or
PT decreasing appetite, reducing stress and to screen for compounds that
PT bind to the receptor -
XX
PS Claim 21; Page 23; 43pp; English.
XX
CC This sequence is a melanin-concentrating hormone (MCH) receptor
CC protein of the invention, designated MCH-R3. MCH receptor fragments and
CC polypeptides are useful in assays to screen for compounds that bind to
CC the MCH receptor and modulate the activity of the receptor. MCH Receptor
CC activity is modulated to achieve weight loss, weight gain, to treat
CC cancer (e.g. colon or breast), reduce pain, treat diabetes, reduce stress
CC or treat sexual dysfunction. Nucleic acid coding for the MCH receptor can
CC be used to cause an increase in appetite and to create a test system
CC (e.g. a transgenic animal) for screening for compounds affecting MCH
CC receptor expression. Inhibition of MCH receptor nucleic acid activity is
CC useful to inhibit appetite or stress.
XX
XX
SQ Sequence 422 AA;

Query Match 99.3%; Score 2195; DB 22; Length 422;
Best Local Similarity 99.3%; Pred. No. 5.1e-220;
Matches 419; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSVGAARKGVRAVGLGGSGCOATEEDPDPDGCACAPGGGRRRLPQPAWVEGSSARL 60
Db 1 MSVGAARKGVRAVGLGGSGCOATEEDPDPDGCACAPGGGRRRLPQPAWVEGSSARL 60
QY 61 WEQATGTGMADLEASLLPTGPNASNTSDGPNLTSAGSPRTGISTYNIIMPVFGTIC 120
Db 61 WEQATGTGMADLEASLLPTGPNASNTSDGPNLTSAGSPRTGISTYNIIMPVFGTIC 120
QY 121 LGGTIGNSTVFAVYKSKLHMCNNVPDIFIINLSYVDLFLDMPFMIHQLMGNGVWHF 180
Db 121 LGGTIGNSTVFAVYKSKLHMCNNVPDIFIINLSYVDLFLDMPFMIHQLMGNGVWHF 180
QY 181 GETMCTLTITANDANSOFTSTYITLAMAIDRLATVHPSSTKFRKPSVATVITCLMAWS 240
Db 181 GETMCTLTITANDANSOFTSTYITLAMAIDRLATVHPSSTKFRKPSVATVITCLMAWS 240
QY 241 FISTTPWVLARLIPFGAGVCGIRLPNDPTDLYWFTLYOFLAFALPFVVIITAAVYRI 300
Db 241 FISTTPWVLARLIPFGAGVCGIRLPNDPTDLYWFTLYOFLAFALPFVVIITAAVYRI 300
QY 301 LQRTSSVAASQSRISLRKRVTRTAIAICLVFVCWAPYVILQTLQSLISRTLTFVY 360
Db 301 LQRTSSVAASQSRISLRKRVTRTAIAICLVFVCWAPYVILQTLQSLISRTLTFVY 360
QY 361 LYNAAISLGYANSCINPFYIVLCETFRKRLVLSVKPAAGQLRAVNAQTADEERTESK 420
Db 361 LYNAAISLGYANSCINPFYIVLCETFRKRLVLSVKPAAGQLRAVNAQTADEERTESK 420

Db 361 LYNAAISLGYANSCINPFYIVLCETFRKRLVLSVKPAAGQLRAVNAQTADEERTESK 420
QY 421 GT 422
Db 421 GT 422

RESULT 12
AAB85894
ID AAB85894 standard; Protein; 422 AA.
XX
AC AAB85894;
XX
DT 30-NOV-2001 (first entry)
XX
DE Human long form MCHIR sequence.
XX
KW Melanin concentrating hormone receptor; MCHIR; MCH; chimeric; fusion;
KW fluorescent polypeptide; orexigenic; anabolic; food intake; MCHIR.
XX
OS Homo sapiens.
XX
FN WO200168706-A1.
XX
PD 20-SEP-2001.
XX
PF 14-MAR-2001; 2001WO-US08071.
XX
PR 15-MAR-2000; 2000US-0189698.
XX
PA (MERI) MERCK & CO INC.
XX
PI Marsh DJ;
XX
DR WPI: 2001-565791/63.
DR N-PSDB; AAH47297.
XX
PT Fusion proteins comprising melanin concentrating hormone receptor
PT peptides and fluorescent proteins, useful for identifying appetite
PT stimulants -
XX
PS Claim 1; Page 12-13; 71pp; English.
XX
CC The invention provides melanin concentrating hormone (MCH) receptor
CC (MCHIR) chimeric and fusion proteins. The MCHIR chimeric proteins comprise
CC MCHIR polypeptide regions from different species. The MCHIR fusion protein
CC comprise MCHIR polypeptide region and a fluorescent polypeptide region
CC joined directly, or via a linker, to the carboxy side of the MCHIR
CC polypeptide region. The MCHIR fusion proteins can be expressed by standard
CC recombinant methodology. MCH action promotes feeding (orexigenic) and up
CC regulation of MCH activity stimulates food intake. The present sequence
CC represents a human long form MCHIR protein sequence.
XX
XX
SQ Sequence 422 AA;

Query Match 99.3%; Score 2195; DB 22; Length 422;
Best Local Similarity 99.3%; Pred. No. 5.1e-220;
Matches 419; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSVGAARKGVRAVGLGGSGCOATEEDPDPDGCACAPGGGRRRLPQPAWVEGSSARL 60
Db 1 MSVGAARKGVRAVGLGGSGCOATEEDPDPDGCACAPGGGRRRLPQPAWVEGSSARL 60
QY 61 WEQATGTGMADLEASLLPTGPNASNTSDGPNLTSAGSPRTGISTYNIIMPVFGTIC 120
Db 61 WEQATGTGMADLEASLLPTGPNASNTSDGPNLTSAGSPRTGISTYNIIMPVFGTIC 120
QY 121 LGGTIGNSTVFAVYKSKLHMCNNVPDIFIINLSYVDLFLDMPFMIHQLMGNGVWHF 180
Db 121 LGGTIGNSTVFAVYKSKLHMCNNVPDIFIINLSYVDLFLDMPFMIHQLMGNGVWHF 180
QY 181 GETMCTLTITANDANSOFTSTYITLAMAIDRLATVHPSSTKFRKPSVATVITCLMAWS 240
Db 181 GETMCTLTITANDANSOFTSTYITLAMAIDRLATVHPSSTKFRKPSVATVITCLMAWS 240

Db 181 GETMCTLTITAMANDANSQFTSTYIITAMAIIDRYLATVHPISSTKFRKPSVATLVICLLMALIS 240
QY 241 FISTPFWLYARLIPFGGAVGCGIRLPNPDLDYWFLLYQFFLAFLPFWVITAAYVRI 300
Db 241 FISTPFWLYARLIPFGGAVGCGIRLPNPDLDYWFLLYQFFLAFLPFWVITAAYVRI 300
QY 301 LQRMSSVAPASORSIRLTKRVRTTAIAICLVFVCWAPYVYLQTLQISRPPLTFVY 360
Db 301 LQRMSSVAPASORSIRLTKRVRTTAIAICLVFVCWAPYVYLQTLQISRPPLTFVY 360
QY 361 LYNAAISLGYANSCNLPFVYIVLCETFRKRLVLSVKPAAGQLRAVSNAGTADERTESK 420
Db 361 LYNAAISLGYANSCNLPFVYIVLCETFRKRLVLSVKPAAGQLRAVSNAGTADERTESK 420
QY 421 GT 422
Db 421 GT 422

RESULT 13
AAU7541
ID AAU7541 standard; Protein; 422 AA.
XX
AC AAU7541;
XX
DT 05-JUN-2002 (first entry)
XX
DE Human melanin concentrating hormone receptor, SLC-1.
XX
KW G protein-coupled orphan; receptor; SLC; melanin-concentrating hormone;
KW MCH; appetite-stimulating agent; obesity; malignant mastocytosis;
KW exogenous obesity; hyperinsular obesity; sexual function disorder;
KW overpowering intermittent pain; still born; uterus rupture;
KW premature birth; Prader-Willi syndrome; SLC-1; human.
XX
OS Homo sapiens.
XX
PN WO200203070-A1.
XX
PD 10-JUN-2002.
XX
PF 04-JUL-2001; 2001WO-JP05809.
XX
PR 05-JUL-2000; 2000JP-0208254.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Mori M, Shimomura Y, Harada M, Sugo T, Shintani Y;
PI N-PSDB; ABR10854.
DR WPI; 2002-164552/21.
XX
PT Screening for compounds or salts which alter affinity of
PT melanin-concentrating hormone with its receptor to provide agonists as
PT appetite-stimulating agents and its antagonist for preventing or
PT treating obesity, uses a protein or hormone -
XX
PS Disclosure; Page 103-105; 112pp; Japanese.
XX
CC The invention describes a method of screening for compounds or their
CC salts that can change affinity of melanin-concentrating hormone (MCH)
CC with its G protein-coupled orphan receptor protein, SLC. The screened
CC MCH receptor agonists are useful as appetite-stimulating agents and its
CC antagonist for preventing or treating obesity e.g. malignant
CC mastocytosis, exogenous obesity and hyperinsular obesity, and also
CC for treating sexual function disorders, overpowering intermittent pains,
CC still borns, uterus rupture, premature birth and Prader-Willi syndrome.
CC This is the amino acid sequence of the human melanin concentrating
CC hormone SLC-1, described in the invention.
XX
SQ Sequence 422 AA;
Query Match 99.3%; Score 2195; DB 23; Length 422;

Best Local Similarity 99.3%; Pred. No. 5; le-220;
Matches 419; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 MSVGAAKKGVGRANGVGGGSCCATTEEDPLPDGACAPGGGGRWRLPQAWEGSSARL 60
Db 1 MSVGAAKKGVGRANGVGGGSCCATTEEDPLPDGACAPGGGGRWRLPQAWEGSSARL 60
QY 61 WEQATGTGMADLEASLLPTGPNASNTSDGPDNLTSAGSPRTGSIYINIMPSVEGTTIC 120
Db 61 WEQATGTGMADLEASLLPTGPNASNTSDGPDNLTSAGSPRTGSIYINIMPSVEGTTIC 120
QY 121 LIGIIGNSTVIFAVYKRSKLTMCNPNVDIFILNLSVVDLLFLGMPMIHQMGNGVWHR 180
Db 121 LIGIIGNSTVIFAVYKRSKLTMCNPNVDIFILNLSVVDLLFLGMPMIHQMGNGVWHR 180
QY 181 GETMCTLTITAMANDANSQFTSTYIITAMAIIDRYLATVHPISSTKFRKPSVATLVICLLMALIS 240
Db 181 GETMCTLTITAMANDANSQFTSTYIITAMAIIDRYLATVHPISSTKFRKPSVATLVICLLMALIS 240
QY 241 FISTPFWLYARLIPFGGAVGCGIRLPNPDLDYWFLLYQFFLAFLPFWVITAAYVRI 300
Db 241 FISTPFWLYARLIPFGGAVGCGIRLPNPDLDYWFLLYQFFLAFLPFWVITAAYVRI 300
QY 301 LQRMSSVAPASORSIRLTKRVRTTAIAICLVFVCWAPYVYLQTLQISRPPLTFVY 360
Db 301 LQRMSSVAPASORSIRLTKRVRTTAIAICLVFVCWAPYVYLQTLQISRPPLTFVY 360
QY 361 LYNAAISLGYANSCNLPFVYIVLCETFRKRLVLSVKPAAGQLRAVSNAGTADERTESK 420
Db 361 LYNAAISLGYANSCNLPFVYIVLCETFRKRLVLSVKPAAGQLRAVSNAGTADERTESK 420
QY 421 GT 422
Db 421 GT 422

RESULT 14
ABB04941
ID ABB04941 standard; Protein; 422 AA.
XX
AC ABB04941;
XX
DT 14-MAR-2002 (first entry)
XX
DE Human SLC-1 protein SEQ ID NO:9.
XX
KW Human; SLC-1; melanin concentrating hormone antagonist; obesity;
KW anorectic; antidiabetic; hypotensive; antiarteriosclerotic;
KW diabetes; hypertension; arteriosclerosis.
XX
OS Homo sapiens.
XX
PN WO200182925-A1.
XX
PD 08-NOV-2001.
XX
PF 26-APR-2001; 2001WO-JP03614.
XX
PR 28-APR-2000; 2000JP-0134295.
XX
PR 13-DEC-2000; 2000JP-0384897.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Ishihara Y, Suzuki N, Takekawa S;
PI N-PSDB; ABA92411.
DR WPI; 2002-075131/10.
XX
PT Melanin aggregating hormone antagonist for treating obesity -
XX
PS Example; Page 210-212; 223pp; Japanese.
CC The present invention describes a melanin aggregating hormone antagonist

CC (1). (1) has anorectic, antidiabetic, antiarteriosclerotic and
CC hypotensive. (1) can be used in the treatment and prevention of obesity.
CC It may be combined with treatments for diabetes, hypertension or
CC arteriosclerosis. The present sequence represents human SLC-1, which is
CC used the exemplification of the present invention.

Sequence 422 AA;

Query Match 99.3%; Score 2195; DB 23; Length 422;
Best Local Similarity 99.3%; Pred. No. 5.1e-220;
Matches 419; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSVGAARKGVGRVAVGLGGSGCOATEEDPLPDGACAPGOGGRWRRLPOPAMWEGSSARL 60
DB 1 MSVGAARKGVGRVAVGLGGSGCOATEEDPLPDGACAPGOGGRWRRLPOPAMWEGSSARL 60
QY 61 WEOATGTGMDEASLLPTGPNASNTSDGPNLTSAGSPRTGSIYINIMPSVEGTIC 120
DB 61 WEOATGTGMDEASLLPTGPNASNTSDGPNLTSAGSPRTGSIYINIMPSVEGTIC 120
QY 121 LGGIIGNSTVIFAVVKKSKLHMCCNNVPDIFITINSVDLFLGMPMHIQLMGNGVWHF 180
DB 121 LGGIIGNSTVIFAVVKKSKLHMCCNNVPDIFITINSVDLFLGMPMHIQLMGNGVWHF 180
QY 181 GETMCTLTITAMANDANSOFTSTYILITAMADRYLATVHPISSTKFKKPSVATLVICLLMALS 240
DB 181 GETMCTLTITAMANDANSOFTSTYILITAMADRYLATVHPISSTKFKKPSVATLVICLLMALS 240
QY 241 FISITPVMLYARLIFPGGAVGCCGIRLPNPTDLYWFTLYOFELAFALPFAVITAAYVRI 300
DB 241 FISITPVMLYARLIFPGGAVGCCGIRLPNPTDLYWFTLYOFELAFALPFAVITAAYVRI 300
QY 301 IQRMNTSSVAPASQORSIRLRTKRVRTAICLVFVVCAPRYVQLTQLSISRPTLTFVY 360
DB 301 IQRMNTSSVAPASQORSIRLRTKRVRTAICLVFVVCAPRYVQLTQLSISRPTLTFVY 360
QY 361 LYNAASISLGYANSCINPFIYIVLCETFFKRLVLSVPAQOQLRAVSNAGTADEERTESK 420
DB 361 LYNAASISLGYANSCINPFIYIVLCETFFKRLVLSVPAQOQLRAVSNAGTADEERTESK 420
QY 421 GT 422
DB 421 GT 422

RESULT 15
AAG80611
ID AAG80611 standard: Protein: 422 AA.
AC AAG80611;
XX 28-FEB-2002 (first entry)
DE Human SLC-1 protein.
XX
KW SLC-1; melanin-concentrating hormone antagonist; anorectic; depression;
KW antidiabetic; hypotensive; antiarteriosclerotic; antilipidemic; obesity;
KW antiarthritic; antidepressant; tranquilizer; malignant mastocytosis;
KW hypophyseal adiposity; hypothyroid obesity; hyperphagia; diabetes;
KW hypertension; arteriosclerosis; hyperlipidaemia; arthritis; anxiety;
KW human.
XX
OS Homo sapiens.
XX
PN WO200187834-A1.
XX
PD 22-NOV-2001.
XX
PF 15-MAY-2001; 2001WO-JP04015.
XX
PR 16-MAY-2000; 2000JP-0148674.
XX
PR 13-APR-2001; 2001JP-0116219.
XX

PA (TAKE) TAKEDA CHEM IND LTD.

XX Ishihara Y, Terauchi J, Suzuki N, Takekawa S, Aso K;

XX WPI; 2002-055668/07.

DR N-PSDB; AA169442.

PT Use of new and known amine derivatives as melanin concentrating hormone
PT antagonists for treating e.g. obesity, diabetes, hypertension and
PT arteriosclerosis

PS Disclosure: Page 252-254; 283pp; Japanese.

XX This invention describes a novel use of an amine derivative (1) as a
XX melanin concentrating hormone antagonist which has anorectic,
XX antidiabetic, hypotensive, antiarteriosclerotic, antilipidemic,
XX antiarthritic, antidepressant and tranquilizer activity. The products of
XX the invention can be used as melanin concentrating hormone antagonists
XX for treating and preventing obesity (including malignant mastocytosis,
XX hypophyseal adiposity, hypothyroid obesity, infantile obesity and
XX hyperphagia), diabetes, hypertension and arteriosclerosis as well as
XX diabetic complications, hyperlipidaemia, arthritis, depression and
XX anxiety. This sequence represents the human melanin-concentrating hormone
XX SLC-1 gene described in the method of the invention.

Sequence 422 AA;

Query Match 99.3%; Score 2195; DB 23; Length 422;
Best Local Similarity 99.3%; Pred. No. 5.1e-220;
Matches 419; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSVGAARKGVGRVAVGLGGSGCOATEEDPLPDGACAPGOGGRWRRLPOPAMWEGSSARL 60
DB 1 MSVGAARKGVGRVAVGLGGSGCOATEEDPLPDGACAPGOGGRWRRLPOPAMWEGSSARL 60
QY 61 WEOATGTGMDEASLLPTGPNASNTSDGPNLTSAGSPRTGSIYINIMPSVEGTIC 120
DB 61 WEOATGTGMDEASLLPTGPNASNTSDGPNLTSAGSPRTGSIYINIMPSVEGTIC 120
QY 121 LGGIIGNSTVIFAVVKKSKLHMCCNNVPDIFITINSVDLFLGMPMHIQLMGNGVWHF 180
DB 121 LGGIIGNSTVIFAVVKKSKLHMCCNNVPDIFITINSVDLFLGMPMHIQLMGNGVWHF 180
QY 181 GETMCTLTITAMANDANSOFTSTYILITAMADRYLATVHPISSTKFKKPSVATLVICLLMALS 240
DB 181 GETMCTLTITAMANDANSOFTSTYILITAMADRYLATVHPISSTKFKKPSVATLVICLLMALS 240
QY 241 FISITPVMLYARLIFPGGAVGCCGIRLPNPTDLYWFTLYOFELAFALPFAVITAAYVRI 300
DB 241 FISITPVMLYARLIFPGGAVGCCGIRLPNPTDLYWFTLYOFELAFALPFAVITAAYVRI 300
QY 301 IQRMNTSSVAPASQORSIRLRTKRVRTAICLVFVVCAPRYVQLTQLSISRPTLTFVY 360
DB 301 IQRMNTSSVAPASQORSIRLRTKRVRTAICLVFVVCAPRYVQLTQLSISRPTLTFVY 360
QY 361 LYNAASISLGYANSCINPFIYIVLCETFFKRLVLSVPAQOQLRAVSNAGTADEERTESK 420
DB 361 LYNAASISLGYANSCINPFIYIVLCETFFKRLVLSVPAQOQLRAVSNAGTADEERTESK 420
QY 421 GT 422
DB 421 GT 422

Search completed: February 13, 2003, 13:58:01
Job time : 34.4921 secs

Gencore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 13, 2003, 14:00:22 : Search time 14.1019 Seconds

(without alignments)
764.550 Million cell updates/sec

Title: US-09-885-478-27

Perfect score: 2210

Sequence: 1 MSVGAARKGVGRAVLGGGS.....LRAVSNAGTADERTESKGT 422

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 140259 seqs, 25548876 residues

Total number of hits satisfying chosen parameters: 140259

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA:*

1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	2205	99.8	422	10	US-09-885-478-26
3	2200	99.5	422	10	US-09-885-478-2
4	1819	82.3	353	10	US-09-925-776-2
5	1819	82.3	353	10	US-09-885-478-28
6	1803	81.6	353	10	US-09-885-686-2
7	1758	79.5	353	10	US-09-885-478-4
8	1696	76.7	402	9	US-09-990-940-19
9	1224	55.4	239	10	US-09-864-761-88414
10	565.5	25.6	340	9	US-09-990-940-2
11	565.5	25.6	340	9	US-09-990-940-17
12	548	24.8	100	10	US-09-885-478-17
13	537	24.3	100	10	US-09-885-478-16
14	525	23.8	369	10	US-09-823-114-9
15	519	23.5	391	9	US-09-990-940-20
16	504.5	22.8	418	9	US-09-992-331-17
17	487	22.0	91	10	US-09-864-761-38421
18	480.5	21.7	428	9	US-09-992-331-16
19	472	21.4	428	9	US-09-992-331-15

20	470.5	21.3	363	9	US-09-992-331-14	Sequence 14, Appl
21	459	20.8	405	10	US-09-966-871-84	Sequence 84, Appl
22	459	20.8	405	12	US-10-039-645-84	Sequence 84, Appl
23	456.5	20.7	370	10	US-09-823-114-21	Sequence 21, Appl
24	456	20.6	362	9	US-09-992-331-13	Sequence 13, Appl
25	455	20.6	382	10	US-09-993-844-4	Sequence 4, Appl1
26	453.5	20.5	390	10	US-09-761-962-25	Sequence 25, Appl
27	453.5	20.5	391	10	US-09-761-962-26	Sequence 26, Appl
28	453.5	20.5	391	10	US-09-761-962-19	Sequence 19, Appl
29	453.5	20.5	398	10	US-09-761-962-29	Sequence 29, Appl
30	453.5	20.5	398	10	US-09-966-871-83	Sequence 83, Appl
31	453.5	20.5	398	12	US-10-039-645-83	Sequence 83, Appl
32	453.5	20.5	401	10	US-09-761-962-20	Sequence 20, Appl
33	453.5	20.5	409	10	US-09-761-962-27	Sequence 27, Appl
34	453.5	20.5	438	10	US-09-761-962-17	Sequence 17, Appl
35	453.5	20.5	444	10	US-09-761-962-28	Sequence 28, Appl
36	453	20.5	372	9	US-10-112-559A-4	Sequence 4, Appl1
37	453	20.5	415	10	US-09-823-114-20	Sequence 20, Appl
38	452.5	20.5	398	10	US-09-823-114-16	Sequence 16, Appl
39	452.5	20.5	398	10	US-09-966-871-1	Sequence 1, Appl
40	452.5	20.5	398	12	US-10-039-645-1	Sequence 1, Appl1
41	451.5	20.4	398	10	US-09-966-871-79	Sequence 79, Appl
42	451.5	20.4	398	12	US-10-039-645-79	Sequence 79, Appl
43	449.5	20.3	372	10	US-09-966-871-80	Sequence 80, Appl
44	449.5	20.3	372	12	US-10-039-645-80	Sequence 80, Appl
45	448.5	20.3	398	10	US-09-214-904-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1

US-09-885-478-27

Sequence 27, Application US/09885478

Patent No. US20020111306A1

GENERAL INFORMATION:

APPLICANT: SALON, JOHN A

APPLICANT: LAZ, THOMAS M

APPLICANT: MAGORNY, RAISA

APPLICANT: WILSON, AYE E

TITLE OF INVENTION: DNA ENCODING A HUMAN MELANIN CONCENTRATING HORMONE RECEPTOR (M

FILE REFERENCE: 1795/57453-A-PCT-US

CURRENT APPLICATION NUMBER: US/09/885,478

CURRENT FILING DATE: 2001-09-24

PRIOR APPLICATION NUMBER: PCT/US99/31169

PRIOR FILING DATE: 1999-12-30

NUMBER OF SEQ ID NOS: 28

SOFTWARE: PatentIn version 3.1

SEQ ID NO 27

LENGTH: 422

TYPE: PRT

ORGANISM: ARTIFICIAL SEQUENCE

FEATURE:

OTHER INFORMATION: MUTATED MCH RECEPTOR

US-09-885-478-27

Query Match

Best Local Similarity 100.0%; Score 2210; DB 10; Length 422;

Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSVGAARKGVGRAVLGGSGCOATEEDPLPDGCACAPGGGRRWRLOPAWVGSSARL 60

DB 1 MSVGAARKGVGRAVLGGSGCOATEEDPLPDGCACAPGGGRRWRLOPAWVGSSARL 60

QY 61 WEQATGTGADLEASLLPTGPNASNTSDGPDNLTSAGSPRTGSIYINIMPSVFCTIC 120

DB 61 WEQATGTGADLEASLLPTGPNASNTSDGPDNLTSAGSPRTGSIYINIMPSVFCTIC 120

QY 121 LLSIGNSTVFAYAVKRSKSLHMCNNVPDIFINLSYVDLFLGLGMPHIQGLMGNGVWRF 180

DB 121 LLSIGNSTVFAYAVKRSKSLHMCNNVPDIFINLSYVDLFLGLGMPHIQGLMGNGVWRF 180

Thu Feb 20 11:32:35 2003

us-09-885-478-27.rapb

Page 2

OY	181	GEMCGLITLAMDANSQTSSTYLITLMAIDRYLATVHPISSTRKRSKVATIVCLIMALS	240
Db	181	GETMCTLTITAMANDASQTSSTYLITLMAIDRYLATVHESISSTRKRSKVATIVCLIMALS	240
OY	241	FISTIPWVLARLIPEFGAGAVGCGIRLPNBDTDLMYETLOFPLALPFPVTAAVVR	300
Db	241	FISTIPWVLARLIPEFGAGAVGCGIRLPNDTDLYMTLVQFLPALPFPVTAAVVR	300
OY	301	LQRMSSVAAPASORSIRLRTRRVTRTAICLVFPVCWMARYVVOULTOLSIISRPILTIFY	360
Db	301	LQRMSSVAAPASORSIRLRTRRVTRTAICLVFPVCWMARYVVOULTOLSIISRPILTIFY	360
OY	361	LYNNAISIGYANSCINFPFYIIVLCETPERKLJVSVKPAAGQLRAVNSNAQTADERTESK	420
Db	361	LYNNAISIGYANSCINFPFYIIVLCETPERKLJVSVKPAAGQLRAVNSNAQTADERTESK	420
OY	421	GT 422	
Db	421	GT 422	

```

RESULT 2
US-09-885-478-26
; Sequence 26, Application US/09885478
; Patent No. US20020111306A1
; GENERAL INFORMATION:
; APPLICANT: SALON, JOHN A
; APPLICANT: LAZ, THOMAS M
; APPLICANT: NAGORNY, RAISA
; APPLICANT: WILSON, AMY E
; TITLE OF INVENTION: DNA ENCODING A HUMAN MELANIN CONCENTRATING HORMONE RECEPTOR (MCH1)
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 1795/57453-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/885,478
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US99/31169
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 422
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: MUTATED MCH RECEPTOR
US-09-885-478-26

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Query Match	99.8%;	Score 2205;	DB 10;	Length 422;
Best Local Similarity	99.8%;	Pred. No. 9.9e-181;		
Matches 421; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

QY 1 MSVGAARKGVRAVAGLGGSGCCQAT EEDBPJLDCGACAPGGGRRMRLLPQPAWEGSSARL 60

Db 1 MSVGAARKGVRAVAGLGGSGCCQATEEDBPJLDCGACAPGGGRRMRLLPQPAWEGSSARL 60

QY 61 WQOAGCTGMADLEASLPTGPNASNTSDGPNLTLASAPRTGSIYSINIMPSVGTTC 120

Db 61 WQOAGCTGMADLEASLPTGPNASNTSDGPNLTLASAPRTGSIYSINIMPSVGTTC 120

QY 121 LGGIINGSTVIFVAAYKKSKKLHMCNNVPDIFILNLSYVDLFLGLMPMHIQGLNGNGVMEH 180

Db 121 LGGIINGSTVIFVAAYKKSKKLHMCNNVPDIFILNLSYVDLFLGLMPMHIQGLNGNGVMEH 180

QY 181 GETMCTLLTAMDANSQFTSYLYTLMAAIDRYLATVHPISSTKFKKPSVATVLCILMALSS 240

Db 181 GETMCTLLTAMDANSQFTSYLYTLMAAIDRYLATVHPISSTKFKKPSVATVLCILMALSS 240

QY 241 FTSITPVMVLYARLIFPGGAVGCCGIRLPNPTDLWYPTLVOFLAPLAPPVVITAAVVR1 3000

Db 241 FTSITPVMVLYARLIFPGGAVGCCGIRLPNPTDLWYPTLVOFLAPLAPPVVITAAVVR1 3000

QY 301 LDRMTSSVAPASQSRIRLRTRKVTATAICLVEFVCWAPYYVQLQALSSIRPLTFEYV 3600

Db	301	LQRMTSVAPASQSRILRTKRVTRTALAIQVHFCVCMAPYVQLQSLISKPTLFVY	360
QY	361	LYNNAISLIGYANSCINPVIYVILCETPKRKYLSYKRAAQQLRAVNAQTADERTSK	420
Db	361	LYNNAISLIGYANSCINPVIYVILCETPKRKYLSYKRAAQQLRAVNAQTADERTSK	420
QY	421	GT 422	
Db	421	GT 422	

```

      RESULT 3
      US-09-885-478-2
      ; Sequence 2, Application US/09885478
      ; Patent No. US2002011306A1
      ; GENERAL INFORMATION:
      ; APPLICANT: SALON, JOHN A
      ; APPLICANT: LAZ, THOMAS M
      ; APPLICANT: NAGORNY, RAISA
      ; APPLICANT: WILSON, AMY E
      ; TITLE OF INVENTION: DNA ENCODING A HUMAN MELANIN CONCENTRATING HORMONE RECEPTOR (M
      ; TITLE OF INVENTION: USES THEREOF
      ; FILE REFERENCE: 1795/57453-A-PCT-US
      ; CURRENT APPLICATION NUMBER: US/09/885,478
      ; CURRENT FILING DATE: 2001-09-24
      ; PRIOR APPLICATION NUMBER: PCT/US99/31169
      ; PRIOR FILING DATE: 1999-12-30
      ; NUMBER OF SEQ ID NOS: 28
      ; SOFTWARE: PatentIn version 3.1
      ; SEQ ID NO 2
      ;
      ; LENGTH: 422
      ;
      ; TYPE: PRT
      ;
      ; ORGANISM: HOMO SAPIENS
      ;
      US-09-885-478-2

```

Query Match	99.5%	Score 2200;	DB 10;	Length 422;
Best Local Similarity	99.5%;	Pred. No. 2.6e-180;		
Matches 420; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0.

QY	1	MSVGAKKGVGRAVIGGGSCGQATEBDPLPDCGACAPQGGRRRLPQPAVDEGSSARL	60
Db	1	MSVGAKKGVGRAVIGGGSCQATEBDPLPCGACAPQGGRRRLPQPAVDEGSSARL	60
QY	61	WEGATGTGNADLEASLLPTGPNAASNTSDGPDNLTSGSPPTGSIYINIIMPSVGTIC	120
Db	61	WEGATGTGNADLEASLLPTGPNAASNTSDGPDNLTSGSPPTGSIYINIIMPSVGTIC	120
QY	121	LLGIIGNSTYVIEAVYKRSKILHWCNNVPDIFIINLSYVDLLFLGMPFMIHOLMGWME	180
Db	121	LLGIIGNSTYVIEAVYKRSKILHWCNNVPDIFIINLSYVDLLFLGMPFMIHOLMGWME	180
QY	181	GEFMCLLTITAMDNOSQFTSYTLTAMADRYLATVHPISSTKFRKRSVATIVICLIMALS	240
Db	181	GEFMCLLTITAMDNOSQFTSYTLTAMADRYLATVHPISSTKFRKRSVATIVICLIMALS	240
QY	241	FISITFVWLTYARLIPPPGAVGCGIRLPNPDYDLWFTLYQEFIALPFPVVTAAVYRI	300
Db	241	FISITFVWLTYARLIPPPGAVGCGIRLPNPDYDLWFTLYQEFIALPFPVVTAAVYRI	300
QY	301	LQRMSTSSVAPASORSIRLRTKRYTRTALAIQVFEFCMAPIYVLOLTOLISRPULTFEY	360
Db	301	LQRMSTSSVAPASORSIRLRTKRYTRTALAIQVFEFCMAPIYVLOLTOLISRPULTFEY	360
QY	361	LYNAAISLGVANCLNPEVYIVLCETFRKRLVSVKPAAGOLRAVSNMQTADERTESK	420
Db	361	LYNAAISLGVANCLNPEVYIVLCETFRKRLVSVKPAAGOLRAVSNMQTADERTESK	420
QY	421	GT 422	
Db	421	GT 422	

```
US-09-925-776-2
; Sequence 2, Application US/09925776
; Patent No. US20020038007A1
; GENERAL INFORMATION:
; APPLICANT: AMES, ROBERT S., JR.
; APPLICANT: SARAU, HENRY M.
; APPLICANT: FOLEY, JAMES J.
; APPLICANT: BERGSMAN, DEREK J.
; APPLICANT: ELLIS, CATHERINE E.
; APPLICANT: CHAMBERS, JON K.
; TITLE OF INVENTION: A METHOD OF FINDING AGONIST AND
; TITLE OF INVENTION: ANTAGONIST TO HUMAN 11CB SPLICED VARIANT
; FILE REFERENCE: GP-50003-D2
; CURRENT FILING DATE: 2001-08-09
; PRIOR FILING DATE: 2001-08-09
; PRIOR FILING DATE: 1996-12-11
; PRIOR FILING DATE: 1997-12-03
; PRIOR FILING DATE: 1997-12-03
; PRIOR FILING DATE: 1998-02-05
; PRIOR FILING DATE: 1998-02-05
; PRIOR FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 353
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-925-776-2

Query Match      82.3%; Score 1819; DB 10; Length 353;
Best Local Similarity 100.0%; Pred. No. 7.1e-148;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 71 DLEASLPTGPNASNTSDGPNLTSSAGSPRTGSIYINIMPSVFTCLLGIIGNSTV 130
DB 2 DLEASLPTGPNASNTSDGPNLTSSAGSPRTGSIYINIMPSVFTCLLGIIGNSTV 61
QY 131 IFVAVKSKLHMKNVDPIDFIIINLSVVDLFLGMPFMHQLMGNGVHGFETMCTLITA 190
DB 62 IFVAVKSKLHMKNVDPIDFIIINLSVVDLFLGMPFMHQLMGNGVHGFETMCTLITA 121
QY 191 MDANSQFTSTYILTAMADRYLATVHPISSTKFRKPSVATLVICLLMAISFISTPVWLX 250
DB 122 MDANSQFTSTYILTAMADRYLATVHPISSTKFRKPSVATLVICLLMAISFISTPVWLX 181
QY 251 ARLIFPGGAVGCGIRLPNPTDLYWFTLYQFLAFALPFPVITAAVRLIQRMTSSVAP 310
DB 182 ARLIFPGGAVGCGIRLPNPTDLYWFTLYQFLAFALPFPVITAAVRLIQRMTSSVAP 241
QY 311 ASORSIRLRTKRVTRTAIAICLVFVCWAPYVYLQTLQLSISRTLTFFVLYNAALSLGY 370
DB 242 ASORSIRLRTKRVTRTAIAICLVFVCWAPYVYLQTLQLSISRTLTFFVLYNAALSLGY 301
QY 371 ANSCINPFPVYIVLCETFRKRLVLSVKRPAAGQLRAVSNAGTADBERESKGT 422
DB 302 ANSCINPFPVYIVLCETFRKRLVLSVKRPAAGQLRAVSNAGTADBERESKGT 353

RESULT 5
US-09-885-478-28
; Sequence 28, Application US/09885478
; Patent No. US20020111306A1
; GENERAL INFORMATION:
; APPLICANT: SALON, JOHN A
; APPLICANT: LAZ, THOMAS M
; APPLICANT: NAGORNY, RAISA
; APPLICANT: WILSON, AMY E
; TITLE OF INVENTION: DNA ENCODING A HUMAN MELANIN CONCENTRATING HORMONE RECEPTOR (MCH)
; FILE REFERENCE: 1795/57453-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/885,478
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; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US99/31169
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 353
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: MUTATED MCH RECEPTOR
US-09-885-478-28

Query Match      82.3%; Score 1819; DB 10; Length 353;
Best Local Similarity 100.0%; Pred. No. 7.1e-148;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 71 DLEASLPTGPNASNTSDGPNLTSSAGSPRTGSIYINIMPSVFTCLLGIIGNSTV 130
DB 2 DLEASLPTGPNASNTSDGPNLTSSAGSPRTGSIYINIMPSVFTCLLGIIGNSTV 61
QY 131 IFVAVKSKLHMKNVDPIDFIIINLSVVDLFLGMPFMHQLMGNGVHGFETMCTLITA 190
DB 62 IFVAVKSKLHMKNVDPIDFIIINLSVVDLFLGMPFMHQLMGNGVHGFETMCTLITA 121
QY 191 MDANSQFTSTYILTAMADRYLATVHPISSTKFRKPSVATLVICLLMAISFISTPVWLX 250
DB 122 MDANSQFTSTYILTAMADRYLATVHPISSTKFRKPSVATLVICLLMAISFISTPVWLX 181
QY 251 ARLIFPGGAVGCGIRLPNPTDLYWFTLYQFLAFALPFPVITAAVRLIQRMTSSVAP 310
DB 182 ARLIFPGGAVGCGIRLPNPTDLYWFTLYQFLAFALPFPVITAAVRLIQRMTSSVAP 241
QY 311 ASORSIRLRTKRVTRTAIAICLVFVCWAPYVYLQTLQLSISRTLTFFVLYNAALSLGY 370
DB 242 ASORSIRLRTKRVTRTAIAICLVFVCWAPYVYLQTLQLSISRTLTFFVLYNAALSLGY 301
QY 371 ANSCINPFPVYIVLCETFRKRLVLSVKRPAAGQLRAVSNAGTADBERESKGT 422
DB 302 ANSCINPFPVYIVLCETFRKRLVLSVKRPAAGQLRAVSNAGTADBERESKGT 353

RESULT 6
US-09-895-686-2
; Sequence 2, Application US/09895686
; Patent No. US2002010665A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN GPCR PROTEINS
; FILE REFERENCE: PC-004 CIP
; CURRENT APPLICATION NUMBER: US/09/895,686
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc:feature
; OTHER INFORMATION: incyte ID No. US2002010665A1 145943ZCD1
US-09-895-686-2

Query Match      81.6%; Score 1803; DB 10; Length 353;
Best Local Similarity 99.1%; Pred. No. 1.6e-146;
Matches 349; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 71 DLEASLPTGPNASNTSDGPNLTSSAGSPRTGSIYINIMPSVFTCLLGIIGNSTV 130
DB 2 DLEASLPTGPNASNTSDGPNLTSSAGSPRTGSIYINIMPSVFTCLLGIIGNSTV 61
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RESULT 9
US-09-864-761-38414
; Sequence 38414, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmca-x-1
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 38414
; LENGTH: 239
; TYPE: prt
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO 286090.10
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.67
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.78
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.74
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.72
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.1
; OTHER INFORMATION: EST_HUMAN HIT: BE701073.1, EVALUE 6.00e-44
; OTHER INFORMATION: SWISSPROT HIT: Q99705, EVALUE 0.00e+00
US-09-864-761-38414
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Query Match 55.4%; Score 1224; DB 10; Length 239;
Best Local Similarity 100.0%; Pred. No. 2.7e-97;

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Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 184 MCTLTADANDANQFSTYITLTMADIRLATVPHVHSSKFRKPSVATVLCIMAAISFIS 243
|((((((((((((((((((((((((((((((((((((((((((((((((((((((((
Db 1 MCTLTADANDANQFSTYITLTMADIRLATVPHVHSSKFRKPSVATVLCIMAAISFIS 60
QY 244 TPVWLVYARLTPFGGAVGCGIRLPPNPTDLYWFTLYQFLAFALPFWITAAVRIIQR 303
|((((((((((((((((((((((((((((((((((((((((((((((((((((((((
Db 61 TPVWLVYARLTPFGGAVGCGIRLPPNPTDLYWFTLYQFLAFALPFWITAAVRIIQR 120
QY 304 MTSVAPASQSRIRLRTKRVRTAIALICLVFVCGMAPYVYLQLSISRPTLTFYLYN 363
|((((((((((((((((((((((((((((((((((((((((((((((((((((((((
Db 121 MTSVAPASQSRIRLRTKRVRTAIALICLVFVCGMAPYVYLQLSISRPTLTFYLYN 180
QY 364 AATISGVYNSCINPFVYIVLCETFEKKRLVLSVKPRAOQGLRAVSNAGTADERTESKGT 422
|((((((((((((((((((((((((((((((((((((((((((((((((((((((((
Db 181 AATISGVYNSCINPFVYIVLCETFEKKRLVLSVKPRAOQGLRAVSNAGTADERTESKGT 239
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RESULT 10
US-09-791-932-117
; Sequence 117, Application US/09791932
; Publication No. US20030003451A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Parodi, Luis A.
; APPLICANT: Hiedsch, Ronald R.
; APPLICANT: Lind, Peter
; APPLICANT: Kayles, Paul S.
; APPLICANT: Ruff, Valerie
; APPLICANT: Huff, Rita M.
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: No. US20030003451A1el G protein-coupled Receptors Cross-Refere
; FILE REFERENCE: 00325.US1
; CURRENT APPLICATION NUMBER: US/09/791,932
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/184,305
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,304
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,303
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,397
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,247
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/188,880
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/217,369
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/217,370
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/218,492
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: 60/186,810
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/188,064
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: 60/186,457
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: 60/213,861
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/194,344
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: 60/218,337
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 117
; LENGTH: 340
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-791-932-117
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;; TITLE OF INVENTION: USES THEREOF
;; FILE REFERENCE: 1795/57453-A-PCT-US
;; CURRENT APPLICATION NUMBER: US/09/885,478
;; CURRENT FILING DATE: 2001-09-24
;; PRIOR APPLICATION NUMBER: PCT/US99/31169
;; PRIOR FILING DATE: 1999-12-30
;; NUMBER OF SEQ ID NOS: 28
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 16
;; LENGTH: 100
;; TYPE: PRT
;; ORGANISM: ARTIFICIAL SEQUENCE
;; OTHER INFORMATION: MUTATION CLONE
US-09-885-478-16

Query Match 24.3%; Score 537; DB 10; Length 100;
Best Local Similarity 98.0%; Pred. No. 4,2e-39;
Matches 98; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 MSVGAKKGVRAVGLGGSGCCATBEDPLPCGACAPGGGGRMRLLPQPAWEGSSARL 60
Db 1 MSVGAAMKGVGTAVGLGGSGCCATBEDPLPCGACAPGGGGRMRLLPQPAWEGSSARL 60
OY 61 WEQATGTGMADLEASLLPTGPNASNTSDGPDNLTSAGSP 100
Db 61 WEQATGTGMADLEASLLPTGPNASNTSDGPDNLTSAGSP 100

RESULT 14

US-09-823-114-9
; Sequence 9, Application US/09823114
; Patent No. US20020061554A1

GENERAL INFORMATION:

APPLICANT: EVANS, CHRISTOPHER J.

KEITH, DUANE B.

TITLE OF INVENTION: OPIOID RECEPTOR GENES

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER

STREET: 2000 PENNSYLVANIA AVENUE, NW, Suite 5500

CITY: WASHINGTON

STATE: DC

COUNTRY: USA

ZIP: 20006-1888

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/823,114

FILING DATE: 29-Mar-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/148,351

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: MORASHIGE, KATE H.

REGISTRATION NUMBER: 29,959

REFERENCE/DOCKET NUMBER: 2000-20526.22

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 887-1500

TELEFAX: (202) 887-0763

TELEX: 90-4030 MRSNROERSWSH

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 369 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-823-114-9

Query Match 23.8%; Score 525; DB 10; Length 369;
Best Local Similarity 31.5%; Pred. No. 2,2e-37;
Matches 117; Conservative 76; Mismatches 133; Indels 46; Gaps 10;

OY 62 EOATGTG-WA-----DEASLLPTGPNASNTSDGPDNLTSAGSPPTGSSISYINIIMPVSF 116
Db 6 EQFGSQWVIRSPFDNLGSLGPS--NGSNQTEBYDMTS-----NAVLTFEYI 50
OY 117 GTICLLIGNSYVIRFVAVKSKLHMCNNVPDFFITNLSVVDLPLFGMP-----MIH 170
Db 51 FVVCVGLCGNTLVTVILKTKM--KTTNITYILNLAIDELMLGPIFAMQVALVH 107
OY 171 QLMGNGVWHFETMCTLTAMDANSQFTSYIYLTANAIDRYLATVHPISSTFRKPSVAT 230
Db 108 -----WPFKAIICRVVMVDGINDQTSIFCLTVMSIDRYLAIVHPISAKWRRPRAK 160
OY 231 LVYCLLMAISFISTTPWYLAFLIPPGGAVGCGILPDPDILY-WFTLYQFLAFLAP 289
Db 161 MINVAVGSLVILPLMAYLAGLRSMQWGRSSCTIMWPESGAMYGFIYAFILGLVP 220
OY 290 FVVTAAVYVRIQMTSSVAPASQSRIRLTKRKYPTATAICLVFVCWAPYYVLQTL 349
Db 221 LTIICLCYLFILIKVSSGIRVGSKRKSEKVTBMSIVAVFICWLPFYINVSAY 280
OY 350 SIS-RPTLTVYLYNAISIGYANSCINPEVYIVLCETFRKRLVLSYKPAAGOLRAVSN 408
Db 281 SVALSPPALKGMFDEVVILTVANSCANPLIVAFISDNFK-----SFGNVCLVKV 332
OY 409 AQTADERTESK 420
Db 333 SGADGERSDSK 344

RESULT 15

US-09-990-940-20
; Sequence 20, Application US/09990940
; Publication No. US20030027252A1

GENERAL INFORMATION:

APPLICANT: Tian, Hui

APPLICANT: Chen, Jia-Liang

APPLICANT: Chen, Jin-Long

APPLICANT: Cutler, Gene

APPLICANT: An, Songzhu

APPLICANT: Dai, Kang

APPLICANT: Gupta, Jamila S.

APPLICANT: Tularik Inc.

TITLE OF INVENTION: No. US20030027252A1el Receptors

FILE REFERENCE: 018781-007410US

CURRENT APPLICATION NUMBER: US/09/990,940

PRIOR FILING DATE: 2001-11-21

PRIOR APPLICATION NUMBER: US 60/252,841

PRIOR FILING DATE: 2000-11-22

PRIOR APPLICATION NUMBER: US 60/257,636

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: US 60/261,377

PRIOR FILING DATE: 2001-01-12

PRIOR APPLICATION NUMBER: US 60/279,554

PRIOR FILING DATE: 2001-03-28

PRIOR APPLICATION NUMBER: US 60/280,696

PRIOR FILING DATE: 2001-03-29

NUMBER OF SEQ ID NOS: 54

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 20

LENGTH: 391

TYPE: PRT

ORGANISM: Homo sapiens

OTHER INFORMATION: human somatostatin receptor 1 (SSTR1)

US-09-990-940-20

Query Match 23.5%; Score 519; DB 9; Length 391;
Best Local Similarity 30.9%; Pred. No. 7,6e-37;

Matches 112; Conservative 70; Mismatches 136; Indels 44; Gaps 7;

```
OY 29 PLPCGACAPGCGGRMRLLPQPAWEGSSARLMEQATGTGWADLEASILPTGPNASNTSD 88
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 14 PSPSPGSCGEGGGR-----GPGAGAAD---GMEERGRIASQNGT 50
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 89 GPDNLTSAGSPPTGSIYINIMPSVGTICLLIGIGNSTVIFAVYKSKLHWCNVDP 148
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 51 LSEGGGSA-----ILISFIYVCLVGLCGNSMVIYIILRYAKMKTATN--- 94
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 149 IFIINLSVVDLLFLGMFPMIHQLMNGVWHFGETMCTLITAMDANSQFTSTYILLTAMAI 208
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 95 IYILMLAIADLMLSVPLVLTSLRH-WPFGALLCRLVSDAVNMFTSIYCLTVLSV 153
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 209 DRYLATVHPISSTKFRKPSVATLVICLMAISFISITPVMLYARLIIPPGGAVGCGIRLP 268
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 154 DRYAVAVHPIKAKYRRPTAKVNLGAVLSLVILPIYFESRTAANSDDGTVACNMMLP 213
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 269 NP-DTDLWFTLYOFFLAFALPEVYITAAVYRILOQMTSSVAPASQSRIRLRTKRVPTA 327
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 214 EPAQRMLVGFVLYTFMLMGFLTPVGAICLCYVLIKMRMVALKGMQQRKRSERKITLMV 273
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 328 IAIQVFFVCMAPYVVLQTLQISRPITLFEYLYNAAISIGYANSCINPFYIYICETF 387
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 274 MMVVMVFVICMMPFTYVQLVNVFAEQDDATVSQ---SVIIGYANSCANPILYGFLSDNF 330
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 388 RK 389
   | |
Db 331 KR 332
```

Search completed: February 13, 2003, 14:10:32
Job time : 15.1019 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 13, 2003, 13:56:01 ; Search time 15.1596 Seconds
(Without alignments)
2676.114 Million cell updates/sec

Title: US-09-885-478-27

Perfect score: 2210
Sequence: 1 MSVGARKKGVRAVGLGGGS.....LRAVNAQTADERTESKGT 422

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 segs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	2195	99.3	422	2	JC7080 melanin-concentrat
2	565.5	25.6	340	2	JC7695 G protein-coupled
3	532	24.1	369	2	DA1795 somatostatin recep
4	530.5	24.0	369	2	BA1795 somatostatin recep
5	525	23.8	369	2	AA5291 somatostatin recep
6	524.5	23.7	369	2	JC2083 somatostatin recep
7	519	23.5	391	2	AA1795 somatostatin recep
8	514	23.3	346	2	S29248 somatostatin recep
9	513.5	23.2	388	2	JN0605 somatostatin recep
10	513	23.2	391	2	CA1795 somatostatin recep
11	504.5	22.8	418	2	AA6226 somatostatin recep
12	500	22.6	391	2	A39297 brain-specific som
13	494.5	22.4	384	2	AA7249 somatostatin recep
14	485	21.9	384	2	JC4629 somatostatin recep
15	480.5	21.7	428	2	S30508 probable G protein
16	478.5	21.7	363	2	I57955 somatostatin recep
17	478.5	21.7	364	2	JN0763 somatostatin recep
18	472	21.4	428	2	AA4021 somatostatin recep
19	470.5	21.3	363	2	I57940 somatostatin recep
20	453.5	20.5	398	2	AA5510 mu opioid receptor
21	453	20.5	372	2	I38532 delta opioid recep
22	452.5	20.5	398	2	I56517 mu opioid receptor
23	450.5	20.4	372	2	S34592 delta opioid recep
24	448	20.3	400	2	I56553 mu opiate receptor
25	447	20.2	392	2	SE6593 opioid receptor mu
26	443.5	20.2	398	2	I56504 mu opioid receptor
27	443.5	20.1	372	2	BA8227 delta opioid recep
28	440.5	19.9	380	2	JC2338 kappa opioid recep
29	432.5	19.6	380	2	AA5259 kappa opioid recep

30	420.5	19.0	380	2	AA8227 kappa opioid recep
31	420	19.0	328	2	I38973 G protein-coupled
32	419	19.0	380	2	S36143 kappa opioid recep
33	413	18.7	370	2	S43087 orphan opioid rece
34	410.5	18.6	367	2	I49022 kappa opioid recep
35	410.5	18.6	367	2	JC2421 opioid receptor ho
36	409.5	18.5	333	2	I38974 G protein-coupled
37	409.5	18.5	367	2	I56520 G protein-coupled
38	409.5	18.5	380	2	JC2434 kappa opioid recep
39	407	18.4	373	2	JE0087 delta opioid recep
40	372.5	16.9	359	2	I51372 angiotensin II rec
41	368	16.7	362	2	JN0694 angiotensin II rec
42	361	16.3	423	2	JC7677 allostastatin recep
43	347	15.7	371	2	JC5796 probable chemotatr
44	341	15.4	350	2	N-formyl peptide r
45	341	15.4	359	2	AA2656 angiotensin II rec

ALIGNMENTS

RESULT 1

JC7080
melanin-concentrating hormone receptor [validated] - human
N:Alternate names: MCHR, orphan somatostatin-like receptor 1 (SLC-1)
C:Species: Homo sapiens (man)
C:Date: 03-Dec-1999 #sequence, revision 03-Dec-1999 #text, change 11-May-2000
C:Accession: JC7080
R:Shinomura, Y.; Mori, M.; Sugo, T.; Ishibaashi, Y.; Abe, M.; Kurokawa, T.; Onda, H.;
Biochem. Biophys. Res. Commun. 261, 622-626, 1999
A:Title: Isolation and identification of melanin-concentrating hormone as the endoge
A:Reference number: JC7080; MUID:99373129; PMID:10441476
A:Accession: JC7080
A:Molecule type: mRNA
A:Residues: 1-422 <SH1>
A>Note: It is uncertain whether Met-1, Met-6 or Met-70 is the initiation codon
C:Superfamily: neurokinin 1 receptor
C:Keywords: hormone receptor; transmembrane protein

Query Match 99.3%; Score 2195; DB 2; Length 422;

Best Local Similarity 99.3%; Pred. No. 1.2e-174;
Matches 419; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY	1	MSVGAARKKGVRAVGLGGSGCQATEEDPLDPCGACAPGGRMRLLQPAMVGGSSARL	60
DB	1	MSVGAARKKGVRAVGLGGSSGQATEEDPLDPCGACAPGGRMRLLQPAMVGGSSARL	60
QY	61	WEQATGTGMADLEASLLPTGPNAWTFSDGPDNLTSAGSPRTGSIYINIMPSVEGTIC	120
DB	61	WEQATGTGMADLEASLLPTGPNAWTFSDGPDNLTSAGSPRTGSIYINIMPSVEGTIC	120
QY	121	LGIIIGNSTVIVPAVYKSKSLHWCNNVPDIFITINLSVDLLFLGMPFIHOLMGNGWHF	180
DB	121	LGIIIGNSTVIVPAVYKSKSLHWCNNVPDIFITINLSVDLLFLGMPFIHOLMGNGWHF	180
QY	181	GETMCTLTAMDANSQFTSYTLTMAIDRYLAIVHPISSTFKRPSVAATLVICLMAALS	240
DB	181	GETMCTLTAMDANSQFTSYTLTMAIDRYLAIVHPISSTFKRPSVAATLVICLMAALS	240
QY	241	FISITPVMVLYARLPPPGAVGCGIRLPNPDLDLWFLTYQFPLAFALPFAVITAAVRI	300
DB	241	FISITPVMVLYARLPPPGAVGCGIRLPNPDLDLWFLTYQFPLAFALPFAVITAAVRI	300
QY	301	LQRMSSVAPASORSIRLTKRVTATAICLVFVCNAPYYVLQOLSTSRPTLFFVY	360
DB	301	LQRMSSVAPASORSIRLTKRVTATAICLVFVCNAPYYVLQOLSTSRPTLFFVY	360
QY	361	LYNAASISLGYANCLNPFFVYLCEFPFRRLVLSKPPAAQGLRAVNAQTADERTESK	420
DB	361	LYNAASISLGYANCLNPFFVYLCEFPFRRLVLSKPPAAQGLRAVNAQTADERTESK	420
QY	421	GT 422	
DB	421	GT 422	

Db 421 GT 422

RESULT 2

JC7695

G:protein-coupled receptor, SLT receptor - human

C:Species: Homo sapiens (man)

C>Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 22-Oct-2001

C:Accession: JC7695

C:Accession: JC7695

Biochem. Biophys. Res. Commun. 283, 1013-1018, 2001

A:Title: Cloning of a novel G protein-coupled receptor, SLT, a subtype of the melanin-concentrating hormone (MCH) receptor

A:Reference number: JC7695; MUID:21255282; PMID:11355873

A:Contents: Hippocampus

A:Accession: JC7695

A:Molecule type: mRNA

A:Residues: 1-340 <MOR>

A:Cross-references: DDBJ:AB060151

C:Comment: This receptor, a second subtype of the melanin-concentrating hormone (MCH) receptor.

C:Genetics:

A:Gene: slt

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 25.68; Score 565.5; DB 2; Length 340;

Best Local Similarity 37.0%; Pred. No. 2,1e-39;

Matches 113; Conservative 62; Mismatches 119; Indels 11; Gaps 4;

QY 110 IIMPSVFGTICLLIGNSTVIFAVYKSKLHMCNNVPDIFINLSVVDLFLGMPMT 169

Db 35 VILPMSIGISTGLVGNILVETFIIRSK----KTPVDIYICMLAVADLHIVGMPFLI 90

QY 170 HOLMNGVHGEHMCITLTAMDANSQTSYIITLAMAIDRYLATVHPISSTKRRKPSVA 229

Db 91 HOWMAGWVEGEGPLCTITTSIDTCNPFACSAIMTWSVDYRFALVDFRLTRKTRKYT 150

QY 230 TIVICLLMALSFISTPWLVARLIPPGAGVCGIRLPNPDYLYWFTLYOFELAPALP 289

Db 151 IRIINGLMAASTILALPWWYISKVIFKDGVESCAFDLTSPD-DLVMTLTLVLTITTFEPF 209

QY 290 FVYITAAVYRII-----QRMSTVAPASORSI-RLTKRVTRTALVGLVFCVCAPIYV 343

Db 210 LPLILVICYLILCYTWMYQONKDKARCCNPSPVKQKRWKLTVMVLVAVVILSLAAPHV 269

QY 344 IQLTQLSIRPLTFVYLYNMAISGVANSCNLPVYIVLCETFEKRLVLSKPAQGL 403

Db 270 IQLVNLQMEQPTLAFYGVYISICLSTVASSINPFLYTLDSGNFQKRLPQIQRATEKEI 329

QY 404 RAVSN 408

Db 330 NNMGN 334

RESULT 3

DA1795

somatostatin receptor 2 - mouse

C:Species: Mus musculus (house mouse)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 24-Nov-1999

C:Accession: DA1795; I56236

C:Accession: DA1795; I56236

R.Yamada, Y.; Post, S.R.; Wang, K.; Tager, H.S.; Bell, G.I.; Seino, S.

Proc. Natl. Acad. Sci. U.S.A. 89, 251-255, 1992

A:Title: Cloning and functional characterization of a family of human and mouse somatostatin receptors

A:Reference number: AA1795; MUID:92108031; PMID:1346068

A:Accession: DA1795

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-369 <YAM>

A:Cross-references: GB:M81832; NID:9201060; PIDN:AA58256.1; PID:9201061

R.Bliott, D.E.; Metwalli, A.; Blum, A.M.; Sandor, M.; Lynch, R.; Weinstein, J.V.

J. Immunol. 153, 1180-1186, 1994

A:Title: T lymphocytes isolated from the hepatic granulomas of schistosoma-infected mice

A:Reference number: I56236; MUID:94300079; PMID:7913111

A:Accession: I56236

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 99-309 <RES>

A:Cross-references: GB:S71756; NID:9560631

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; hormone receptor; transmembrane protein

Query Match 24.1%; Score 532; DB 2; Length 369;

Best Local Similarity 31.7%; Pred. No. 1.4e-36;

Matches 118; Conservative 76; Mismatches 132; Indels 46; Gaps 10;

QY 62 EQATGTG-WA----DLKASLPTGPNASNTSDGPNLTGASGPPRTGISYINIMPSVF 116

Db 6 EQLNSQVWVSSPFDLNGSLGPS--NGSNQTPYYDMTS-----NAVITPIY 50

QY 117 GTICLLIGTIGNSTVIFAVYKSKLHMCNNVPDIFINLSVVDLFLGMPF-----MII 170

Db 51 FVVCVGLGNTLVYIVLIRYAKM--KTTIYIILNLALADELMLGLPFLAMQVALVH 107

QY 171 QLMNGVHGEHMCITLTAMDANSQTSYIITLAMAIDRYLATVHPISSTKRRKPSVAT 230

Db 108 -----WPGKALICVWMTVDGINFTISFCLTWSIDRYLAIVHPIKSAKRPRTRAK 160

QY 231 LVICLLMALSFISTPWLVARLIPPGAGVCGIRLPNPDYLY-WFTLYOFELAPALP 289

Db 161 MIVAVWCVSLVLIPLIMYAGIRSNOMGRSCITIMMPGEGAWYTGFIYAFILGLVLP 220

QY 290 FVYITAAVYRIIORMSVAPASORSIRLTKRVTRTALVGLVFCVCAPIYVLTQL 349

Db 221 LTIICLCYPLTIKIVASSGIRGSSKRKSEKVTWMSIVAVFIPLLPYIINVS 280

QY 350 SIS-RPTLTFVYLYNMAISGVANSCNLPVYIVLCETFEKRLVLSKPAQGLRANSN 408

Db 281 SVASIPPLAKGMEFVYVILTYANSCANPLIYAFISDNFKF-----SFQNLVLKYV 332

QY 409 AQTADERETSK 420

Db 333 SCTEDGERSDSK 344

RESULT 4

DA1795

somatostatin receptor 2 - human

C:Species: Homo sapiens (man)

C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 24-Nov-1999

C:Accession: DA1795

C:Accession: DA1795

R.Yamada, Y.; Post, S.R.; Wang, K.; Tager, H.S.; Bell, G.I.; Seino, S.

Proc. Natl. Acad. Sci. U.S.A. 89, 251-255, 1992

A:Title: Cloning and functional characterization of a family of human and mouse somatostatin receptors

A:Reference number: AA1795; MUID:92108031; PMID:1346068

A:Accession: DA1795

A:Molecule type: DNA

A:Residues: 1-369 <YAM>

A:Cross-references: GB:M81830; NID:9307435; PIDN:AA58248.1; PID:9307436

A:Note: sequence extracted from NCBI backbone (NCBIN:74769, NCBIIP:74770)

C:Genetics:

A:Gene: GDB:SSTR2

A:Cross-references: GDB:134186; OMIM:182452

A:Map position: 17q24-17q24

A:Introns: #status absent

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; glycoprotein; hormone receptor; lipoprotein;

F:44-69/Domain: transmembrane #status predicted <TM1>

F:80-105/Domain: transmembrane #status predicted <TM2>

F:117-138/Domain: transmembrane #status predicted <TM3>

F:158-180/Domain: transmembrane #status predicted <TM4>

F:205-235/Domain: transmembrane #status predicted <TM5>

F:234-281/Domain: transmembrane #status predicted <TM6>

F:288-315/Domain: transmembrane #status predicted <TM7>

F:9,22,29,32,351/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:115-193/Disulfide bonds: #status predicted

F:250/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status pre

A:Title: Isolation and characterization of the mouse (Mus musculus) somatostatin receptor
A:Reference number: J04629; MUID:96194903; PMID:8654950
A:Accession: J04629
A:Molecule type: DNA
A:Residues: 1-384 <SCH>
A:Cross-references: GB:026176; NID:9833840; PIDN:AAA67561.1; PID:9833841
C:Comment: This protein works through the G-proteins and plays a role in mediating interactions with the G-protein-coupled receptor.
A:Gene: str4
C:Superfamily: vertebrate rhodopsin
C:Keywords: receptor; transmembrane protein
F:46-349/Domain: transmembrane #status predicted <TM>

Query Match 21.9%; Score 485; DB 2; Length 384;
Best Local Similarity 29.9%; Pred. No. 1,2e-32;
Matches 102; Conservative 69; Mismatches 134; Indels 36; Gaps 8;

QY 53 VEGSARLMDEGATGTGNADLEASLLPTGPNASNTSDGPDNLTSGSPPRGISYINIM 112
Db 8 LRGVEDITWTGIANASNA-----PREDAMKSDGRTGDM-----VTI 46
QY 113 PSVEGTICLLGIQNSVTYFAVVKSKILHMCNNVPDIFIINLSVVDLFLGMPMIHQL 172
Db 47 QCITALVCLVGLVGNALVIFILRYAKKKTATN---TYLLMLAADELFMLSYEP-VRSA 102
QY 173 MGNQVMHGEIMCULITAMDANSOFTSYITLTAIDRYLATVTPISSTKFKSPVATLV 232
Db 103 AALHWPFGAVLCRAVLSDGLNMFETSVFCLTLVSDRYAVVAPHLRATYRRSPVAKLI 162
QY 233 ICLMLALSFISITVWVLYARLIFPPGG-AYCGGIRLNPDTLYW---FTIYQFLAFAL 288
Db 163 NLGWLASLVTLYLPIAFADTRPARGEAVACNLHWP---AMSAYEIVTYTLGFLP 218
QY 289 PFVITAAVYVILQMTSSVAPASQSRIRLTKRVTYRTAICLFFVQWAPVYVLDLTQ 348
Db 219 PVLAIGLCYLLIYGMRAVALRGGMQRRESEKITRLLVAVVYFVLCWMPFVYQDLN 278
QY 349 LSIISPFITFVYLYNAAISLGYANSCLNPFYIYLCETFEK 369
Db 279 LEVTSLDAT---VMHVSLLISYANSCANPILYGLFSDMFR 316

RESULT 15
S30508
Probable G protein-coupled receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 13-Jan-1995 #sequence, revision 13-Jan-1995 #text, change 11-Jan-2000
C:Accession: S30508
R:Myerhoff, W.; Wulfsen, I.; Schoenrock, C.; Fehr, S.; Richter, D.
A:Title: Molecular cloning of a somatostatin-28 receptor and comparison of its expression with that of the somatostatin receptor.
A:Reference number: S30508; MUID:93066220; PMID:1279674
A:Accession: S30508
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-428 <EMB>
A:Cross-references: EMBL:X63574; NID:956315; PIDN:CAA5130.1; PID:956316
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 21.7%; Score 480.5; DB 2; Length 428;
Best Local Similarity 31.3%; Pred. No. 3.2e-32;
Matches 118; Conservative 73; Mismatches 143; Indels 43; Gaps 11;

QY 75 SLPTGPNASNTSDG---PDNLTSGSPPRGISYINIMPSVEGTICLLGIQNSVTY 131
Db 8 SSVPTTLDPGNASSAMPIDTSLGNASACTSLAGLAVSGILISLYLVAVCVGLGNSLVI 67
QY 132 FAYVKKSLHMCNNVPDIFIINLSVVDLFLGMPMIHOLMGNV---MHGCEMCTLIT 189
Db 68 YVVLNHTS---SPSVTSYIILMLADELFMLIGLFLAAQ---NALSTWPGSLMCRLVK 121
QY 190 AMDANSOFTSYIITLTAIDRYLATVHPISSTKFKSPVATLVICLMLALSFISITPVWL 249

[illegible]

Search completed: February 13, 2003, 14:01:06
Job time : 16.1596 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 13, 2003, 13:50:36 ; Search time 13.7494 Seconds
(without alignments)
1273.004 Million cell updates/sec

Title: US-09-885-478-27

Perfect score: 2210
Sequence: 1 MSVGAKKGVGRAVLGGGS.....LRVSNAGTADERTESKGT 422

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	ID	Description
1	1758	79.5	353	1	GP24_RAT
2	1696	76.7	402	1	GP24_HUMAN
3	1532	24.1	369	1	SSR2_MOUSE
4	530.5	24.0	369	1	SSR2_HUMAN
5	525	23.8	369	1	SSR2_RAT
6	524.5	23.7	369	1	SSR2_PIG
7	523.5	23.7	368	1	SSR2_BOVIN
8	519	23.5	391	1	SSR1_HUMAN
9	513.5	23.2	388	1	SSR4_HUMAN
10	513	23.2	391	1	SSR1_MOUSE
11	504.5	22.8	418	1	SSR3_HUMAN
12	500	22.6	391	1	SSR1_RAT
13	494.5	22.4	384	1	SSR4_MOUSE
14	485	21.9	384	1	SSR4_MOUSE
15	480.5	21.7	428	1	SSR3_RAT
16	478.5	21.7	364	1	SSR5_HUMAN
17	472	21.4	428	1	SSR3_MOUSE
18	470.5	21.3	363	1	SSR5_RAT
19	458	20.7	401	1	OPRM_BOVIN
20	456	20.6	362	1	SSR5_MOUSE
21	453.5	20.5	398	1	OPRM_MOUSE
22	453	20.5	401	1	OPRM_PIG
23	451.5	20.4	372	1	OPRD_HUMAN
24	451.5	20.4	398	1	OPRM_RAT
25	451	20.4	400	1	OPRM_MACMU
26	450.5	20.4	372	1	OPRD_RAT
27	448	20.3	400	1	OPRM_HUMAN
28	443.5	20.1	372	1	OPRD_MOUSE
29	440.5	19.9	380	1	OPRK_HUMAN
30	432.5	19.6	380	1	OPRK_CAVPO
31	426	19.3	370	1	OPRX_CAVPO
32	420.5	19.0	380	1	OPRK_MOUSE
33	420	19.0	328	1	OPR7_HUMAN

34	419	19.0	380	1	OPRK_RAT	P34975	rattus norv
35	413	18.7	370	1	OPRX_HUMAN	P41146	homo sapien
36	410.5	18.6	367	1	OPRX_MOUSE	P35377	mus musc
37	409.5	18.5	333	1	OPRX_HUMAN	P48146	homo sapien
38	409.5	18.5	367	1	OPRX_RAT	P35370	rattus norv
39	398	18.0	370	1	OPRX_PIG	P79292	sus scrofa
40	372.5	16.9	359	1	AG2R_CHICK	P79785	gallus gall
41	372.5	16.9	359	1	AG2R_MELEA	P33396	meleagris g
42	370	16.7	363	1	AG2S_XENLA	P35373	xenopus lae
43	368	16.7	362	1	AG2R_XENLA	P32303	xenopus lae
44	359.5	16.3	352	1	P2Y7_HUMAN	O15722	homo sapien
45	350	15.8	353	1	CKR8_MOUSE	P56484	mus musc

ALIGNMENTS

```

RESULT 1
GP24_RAT
ID GP24_RAT STANDARD: PRT: 353 AA.
AC P97639.
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Probable G protein-coupled receptor GPR24 (SLC-1).
GN GPR24 OR SLC1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98193144; PubMed=9531978;
RA Lakaye B., Minet A., Zorzi W., Grisar T.;
RT "Cloning of the rat brain cDNA encoding for the SLC-1 G protein-
RL Biochim. Biophys. Acta 1401:216-220(1998).
[2]
SEQUENCE OF 143-300 FROM N.A.
RX MEDLINE=97131607; PubMed=8977118;
RA Kolakowski L.F., Jr., Jung B.P., Nguyen T., Johnson M.P., Lynch K.R.,
RT Cheng R., Heng H.H.O., George S.R., O'Dowd B.F.;
RT "Characterization of a human gene related to genes encoding
RT somatostatin receptors."
RL FEBS Lett. 398:253-258(1996).
CC -1- FUNCTION: ORPHAN RECEPTOR. DOES NOT SEEM TO BIND TO SOMATOSTATIN.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC SIMILAR TO SOMATOSTATIN RECEPTORS.
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EMBL: AF008650; AAC27977.1; -.
EMBL: U77953; AAC14588.1; -.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR InterPro: IPR004047; MCH1receptor.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PRINTS: PR01507; MCH1RECEPTOR.
DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; FALSE_NEG.
DR PROSITE: PS50262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane.
FT DOMAIN 1 45 66
FT TRANSMEM 46 66
FT DOMAIN 67 79
FT TRANSMEM 67 79
FT DOMAIN 80 100
FT TRANSMEM 80 100
2 (POTENTIAL).

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FT DOMAIN 101 118 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 119 139 3 (POTENTIAL).
FT TRANSSEM 140 161 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 162 182 4 (POTENTIAL).
FT TRANSSEM 183 204 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 205 225 5 (POTENTIAL).
FT TRANSSEM 226 256 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 257 277 6 (POTENTIAL).
FT TRANSSEM 278 294 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 295 315 7 (POTENTIAL).
FT TRANSSEM 316 353 CYTOPLASMIC (POTENTIAL).
SO SEQUENCE 353 AA; 39063 MW; F6EBB2DF381084A9 CRC64;

Query Match 79.5%; Score 1758; DB 1; Length 353;
Best Local Similarity 96.0%; Pred. No. 4e-91;
Matches 338; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 71 DLEASLPTGPNASNTSDGPNLTSGSPRTGSIYINIMPSVFETGLLGIINSYV 130
DB 2 DLQSLSTGPNASINISDQDNLTLPSPRTGSIYINIMPSVFETGLLGIINSYV 61
QY 131 IFVAVKRSKILHWCNNVDIFILINISVDLFLGMPMIHQMGNGYWHFGEIMCTILTA 130
DB 62 IFVAVKRSKILHWCNNVDIFILINISVDLFLGMPMIHQMGNGYWHFGEIMCTILTA 121
QY 191 MDANSQSFSTYILTAIDRLATVHPISSTFKRPSVATVITGLMALSFISTPVMWLY 250
DB 122 MDANSQSFSTYILTAIDRLATVHPISSTFKRPSVATVITGLMALSFISTPVMWLY 161
QY 251 ARLPEFGAVGCGIRLPNDPTDLYWFTLYXOFALFALFPVVTAAVRYILQRMSSVAP 310
DB 182 ARLPEFGAVGCGIRLPNDPTDLYWFTLYXOFALFALFPVVTAAVRYILQRMSSVAP 241
QY 311 ASQSRIRKTRKVRRTAIALICLVFVCMAPYVYQLQOLISRTPLFVLYNAISLG 370
DB 242 ASQSRIRKTRKVRRTAIALICLVFVCMAPYVYQLQOLISRTPLFVLYNAISLG 301
QY 371 ANSCINPFYVYVLCETFEKRLVLSYKPAQOGLRAVSNAGTADERTESKGT 422
DB 302 ANSCINPFYVYVLCETFEKRLVLSYKPAQOGLRAVSNAGTADERTESKGT 353

RESULT 2
GP24_HUMAN STANDARD; PRT; 402 AA.
ID GP24_HUMAN
AC 099705;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Probable G protein-coupled receptor GPR24 (SLC-1).
GN GPR24 OR SLC1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97131607; PubMed=8977118;
RA Kolakowski L.F., Jr., Jung B.P., Nguyen T., Johnson M.P., Lynch K.R.,
RA Cheng R., Heng H.H.Q., George S.R., O'Dowd B.F.;
RT "Characterization of a human gene related to genes encoding
RT somatostatin receptors."
RL FEBS Lett. 398:253-258(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20057165; PubMed=10591208;
RA Dunham I., Hunt A.R., Collins J.E., Bruskewich R., Beare D.M.,
RA Clump M., Smith L.J., Ainscough R., Almeida J.P., Babbage A.K.,
RA Baguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
RA Bird C.P., Blakey S.E., Bridgman A.M., Buck D., Burgess J.,
RA Buttliff W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,

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RA Dhani P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,
RA Gilbert J.G.R., Goward M.E., Grahame D.V., Griffiths M.N.D., Hall C.,
RA Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,
RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
RA Laird G.K., Langford C.F., Leverisha M.A., Lloyd C., Lloyd D.M.,
RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., McCann O.T.,
RA Mcclay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.,
RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,
RA Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,
RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,
RA Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,
RA Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,
RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilmington L.,
RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
RA Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,
RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyama S.,
RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,
RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L.,
RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
RA Zhan M., Zhang G., Chiscoe S., Murray J., Miller N., Mix P.,
RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
RA Hinds K., Kemp K., Latreille P., Layman D., Ozerisky P., Rohlfing T.,
RA Scheet P., Walker C., Wamsley A., Wohlmann P., Pepin K., Nelson J.,
RA Korf I., Bedell J.A., Hillier L., Mardis E., Waterston R., Wilson R.,
RA Emanuel B.S., Shalk T., Kurahashi H., Saita S., Budarf M.L.,
RA McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E., Edelmann L.,
RA Kim U.J., Shizuya H., Simon M.I., Dunanski J.P., Peyrard M., Kedra D.,
RA Seroussi E., Franssen I., Tapia I., Bruder C.E., O'Brien K.B.,
RA Wilkerson P., Bodenleitch A., Hartman K., Hu X., Khan A.S., Lane L.,
RA Tilihoun Y., Wright H.;
RT "The DNA sequence of human chromosome 22."
RU Nature 402:489-495(1999).
CC -1- FUNCTION: ORPHAN RECEPTOR. DOES NOT SEEM TO BIND TO SOMATOSTATIN.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: GREATEST ABUNDANCE IN BRAIN, PARTICULARLY IN
CC THE FRONTAL CORTEX AND HYPOTHALAMUS. A LOWER LEVEL EXPRESSION IS
CC SEEN IN THE LIVER AND HEART.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC SIMILAR TO SOMATOSTATIN RECEPTORS.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: U71092; AAC14587.1; -.
CC EMBL: Z86090; CAB62943.1; -.
CC GeneW: HGNC:4479; GPR24.
CC MIM: 601751; -.
CC InterPro: IPR000276; GPCR_Rhodopsn.
CC InterPro: IPR004047; MCH1receptor.
CC Pfam: PF00001; 7tm_1; 1.
CC PRINTS: PR00237; GPCR_RHODOPSIN.
CC PRINTS: PR01507; MCH1RECEPTOR.
CC PROSITE: PS00237; G_PROTEIN_RECPT_FL_1; FALSE_NEG.
CC PROSITE: PS02622; G_PROTEIN_RECPT_FL_2; 1.
CC G-protein coupled receptor; Transmembrane.
CC DOMAIN 1 94 EXTRACELLULAR (POTENTIAL).
CC TRANSSEM 95 115 1 (POTENTIAL).
CC TRANSSEM 116 128 2 (POTENTIAL).
CC TRANSSEM 129 149 3 (POTENTIAL).
CC TRANSSEM 150 167 4 (POTENTIAL).
CC TRANSSEM 168 188 5 (POTENTIAL).
CC TRANSSEM 189 210 6 (POTENTIAL).
CC TRANSSEM 211 231 7 (POTENTIAL).
CC TRANSSEM 232 253 8 (POTENTIAL).
CC DOMAIN 232 253 EXTRACELLULAR (POTENTIAL).

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FT TRANSMEM 254 274 5 (POTENTIAL).
FT DOMAIN 275 305 6 (POTENTIAL).
FT TRANSMEM 306 326 6 (POTENTIAL).
FT DOMAIN 327 343 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 344 364 7 (POTENTIAL).
FT DOMAIN 365 402 CYTOPLASMIC (POTENTIAL).
SO SEQUENCE 402 AA; 44454 MW; 5D24B72E76CFAF82 CRC64;

Query Match 76.7%: Score 1696; DB 1; Length 402;
Best Local Similarity 83.2%: Pred. No. 1.2e-87;
Matches 341; Conservative 7; Mismatches 14; Indels 48; Gaps 4;

QY 50 PAVWEGS--SARLWEQATGTGMADLEASLLPTGPNASNTSDGPDN----- 92
D 4 PSKIDSGSGHRIHQETHGEKRD-----KISN-SEGRENCGRGFOMNGSLAE 52
QY 93 -----LTSAGSPRTGSIYINIIIMPVEGTCILGIGNSTVIF 132
D 53 HASRKSIVLRAPKMSNSORLLSLSPGSPRTGSIYINIIIMPVEGTCILGIGNSTVIF 112
QY 133 AVVKKSKLHMCNVPDIFIIINL SVYDLPFLGPFMIHQMGVWHFGEKCTLTITAMD 192
D 113 AVVKKSKLHMCNVPDIFIIINL SVYDLPFLGPFMIHQMGVWHFGEKCTLTITAMD 172
QY 193 ANSQSTYIITAMADRYLATVPISTFKRPSVATLVICLLMALSISTIPVWLAR 252
D 173 ANSQSTYIITAMADRYLATVPISTFKRPSVATLVICLLMALSISTIPVWLAR 232
QY 253 LIPEPGAVGGGIRLPNDPDLVFTLYQFPLAFVAVITAAVRIQMTSSVAPAS 312
D 233 LIPEPGAVGGGIRLPNDPDLVFTLYQFPLAFVAVITAAVRIQMTSSVAPAS 292
QY 313 QRSIRLRKRYTRAIACLVFVCMAPYYVLTOLISRPILTFYVLYNAISIGYAN 372
D 293 QRSIRLRKRYTRAIACLVFVCMAPYYVLTOLISRPILTFYVLYNAISIGYAN 352
QY 373 SCLEPFYIVLCETFRKRLVSVKPAQOGOLRAVSNQOTADERTESKGT 422
D 353 SCLEPFYIVLCETFRKRLVSVKPAQOGOLRAVSNQOTADERTESKGT 402

RESULT 3
SSR2_MOUSE STANDARD; PRT; 369 AA.
AC P30875; P30875; Created
DT 01-JUL-1993 (Rel. 26, last sequence update)
DT 01-JUL-1993 (Rel. 26, last sequence update)
DT 15-JUN-2002 (Rel. 41, last annotation update)
DE Somatostatin receptor type 2 (SS2R) (SRIF-1) (SS2RA and SS2RB).
GN SS2R OR SMS2R.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=92108031; Pubmed=1346068;
RA Yamada Y., Post S.R., Wang K., Tager H.S., Bell G.I., Seino S.;
RT "Cloning and functional characterization of a family of human and
RT mouse somatostatin receptors expressed in brain, gastrointestinal
RT tract, and kidney.";
RT Proc. Natl. Acad. Sci. U.S.A. 89:251-255(1992).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=93012001; Pubmed=1397330;
RA Vanetti M., Kouba M., Wang X., Vogt G., Hoell V.;
RT "Cloning and expression of a novel mouse somatostatin receptor
RT (SS2RB)";
RT FEBS Lett. 311:290-294(1992).
RN [3]
RP SEQUENCE OF 99-309 FROM N.A.
RA MEDLINE=94300079; Pubmed=7913111;
RA Elliott D.E., Metwalli A., Blum A.M., Sandor M., Lynch R.,

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RA Weinstein J.V.;
RT "Lymphocytes isolated from the hepatic granulomas of schistosome-
RT infected mice express somatostatin receptor subtype II (SS2R2)
RT messenger RNA.";
RL J. Immunol. 153:1180-1186(1994).
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=93387480; Pubmed=8104154;
RA Vanetti M., Hoell V.;
RT "The two isoforms of the mouse somatostatin receptor (MS2RB2 and
RT MS2RB) differ in coupling efficiency to adenylyl cyclase and in
RT agonist-induced receptor desensitization.";
RL FEBS Lett. 331:260-266(1993).
QY -1- FUNCTION: RECEPTOR FOR SOMATOSTATINS-14 AND -28. THIS RECEPTOR IS
CC COUPLED VIA PERTUSSIS TOXIN SENSITIVE G PROTEINS TO INHIBITION OF
CC ADENYLYL CYCLASE. IN ADDITION IT STIMULATES PHOSPHOTYROSINE
CC PHOSPHATASE AND PLC VIA PERTUSSIS TOXIN INSENSITIVE AS WELL AS
CC SENSITIVE G PROTEINS. IN RIN 5F CELLS, THIS RECEPTOR INHIBITS
CC CALCIUM ENTRY BY SUPPRESSING VOLTAGE DEPENDENT CALCIUM CHANNELS.
CC -1- SUBUNIT: BELONGS TO THE C-TERMINUS INTERACTS WITH SHANK1 PDZ DOMAIN (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: SS2RA (SHOWN HERE) AND SS2RB;
CC ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: CEREBRUM AND KIDNEY.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC MODIFIED AND THIS STATEMENT IS NOT REMOVED. USAGE BY AND FOR COMMERCIAL
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CC -----
DR EMBL; M81832; AAA58256.1; -;
DR EMBL; X68951; CAA48766.1; -;
DR EMBL; S71756; -; NOT_ANNOTATED_CDS.
DR PIR; D41795; D41795.
DR PIR; S29248; S29248.
DR HSSP; P02699; IBOJ.
DR MGD; MGI:98328; Smtsr2.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G-PROTEIN_RECEP_F1_2; 1.
KM G-protein coupled receptor; Transmembrane; Glycoprotein;
KM Multigene family; Lipoprotein; Palmitate; Alternative splicing.
FT DOMAIN 1 43
FT TRANSMEM 44 67
FT DOMAIN 68 78
FT TRANSMEM 79 103
FT DOMAIN 104 118
FT TRANSMEM 119 138
FT DOMAIN 139 161
FT TRANSMEM 162 181
FT DOMAIN 182 207
FT TRANSMEM 208 229
FT TRANSMEM 230 253
FT TRANSMEM 254 278
FT DOMAIN 279 288
FT TRANSMEM 289 303
FT DOMAIN 304 369
FT CARBOHYD 9
FT CARBOHYD 9
FT CARBOHYD 22
FT CARBOHYD 29
FT CARBOHYD 32
FT CARBOHYD 32
FT DIGLYCID 115
FT LIPID 328
FT VARSPLIC 332
FT CONFLICT 179 179

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CC	CONFIDENCE	305	305	S -> T (IN REF. 2)	
SC	SEQUENCE	369 AA,	41221 MW;	A78845AF4823039 CRC64;	
OY	Query Match	24.1%;	Score 532;	DB 1;	Length 369;
	Best Local Similarity	31.7%;	Pred. No. 3,4e-23;		
	Matches 118;	Conservative	76;	Mismatches 132;	Indels 46;
				Gaps	10
Db	62 EONATNG-WA----	DEASILPLPGPNAWNTSDGPONTLSAGSPPTGSGISYITIMPVSF	116		
	:::	:::	:::	:::	:::
Db	6 EQLNQSVVWVSSPDLDNGLGPS--	NGSNQTEPPYDIMS-----	NAVLLFFIY	50	
OY	117 GTICLIGIIINSTVIYAIVKRSKLHMCNNVPDIFINLSVDLFLGMFP----	MIH	170		
	:::::	:::	:::	:::	:::
Db	51 FVVCVGVLGCNTLVIVYLRYAKM---	KRTTNIYILTALADELFMLGTPLAQVALVH	107		
OY	171 QLMGNVWHGEFTMTCLITAMDANSQFTSTYLLTMALADRYLATVHPRLSSPKRKPESVAT	230			
	:::	:::	:::	:::	:::
Db	108 -----WPFGKACIRVMVTVDGINQFTSIFCLYWMSIDRYLAHVHPISKAMRRPRYAK	160			
OY	231 LVICILNALFSITTPFWLARLPPIPCGAVCGIRLPNDTDLY-WETLLYQFIAPALP	289			
	:::	:::	:::	:::	:::
Db	161 MINVAWCYSLLVLRPMIAYLAGLRSMQWRSSCTINMPESGAWTGTHIYAFILGLEVP	220			
OY	290 FVVITAAYVRILQRMTSSVAPASORSIRLTRKRVTRTAIALGVFYVCWMAHYVLTQLTOL	349			
	:::	:::	:::	:::	:::
Db	221 LTIIICLCFLIIIKVKSSGIRVGSKRKKSEKKVTRMWSIYAAVFPEWLFFYTFNVSSV	280			
OY	350 SIS-RPILLTFYLYENNAISLGVANSCINPFVYIVLCETFRKRLTVSLVPAQOGILRAVSN	408			
	:::	:::	:::	:::	:::
Db	281 SVALSPPALKGMDPEVYIILTYANSCANPLIAFLSLDNKK-----SQNWLCIVKV	332			
OY	409 AQTADERTESK	420			
	:::	:::			
Db	333 SCTEDGERDSK	344			
RESULT 4					
ID	SSR2_HUMAN	STANDARD;	PRT;	369 AA.	
AC	P30874;				
DT	01-JUL-1993 (Rel. 26, Created)				
DT	01-JUL-1993 (Rel. 26, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	Somatostatin receptor type 2 (SS2R) (SRIF-1).				
GN	STR2.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=92108031; PubMed=1346066;				
RA	Yamada Y., Post S.R., Wang K., Tager H.S., Bell G.I., Seino S.;				
RT	"Cloning and functional characterization of a family of human and mouse somatostatin receptors expressed in brain, gastrointestinal tract, and kidney."				
RL	Proc. Natl. Acad. Sci. U.S.A. 89:251-255(1992).				
RN	[2]				
RP	ALTERNATIVE SPLICING.				
RX	MEDLINE=93236586; PubMed=8386508;				
RA	Patel Y.C., Greenwood M., Kent G., Panetta R., Srikanth C.B.;				
RT	"Multiple gene transcripts of the somatostatin receptor SST2r: tissue selective distribution and cAMP regulation"				
RL	Biochem. Biophys. Res. Commun. 192:288-294(1993).				
RN	[3]				
RP	INTERACTION WITH SHANK1.				
RX	MEDLINE=20020275; PubMed=10551867;				
RA	Zitler H., Hoehnck H.-H., Baechner D., Richter D., Krelenkamp H.-J.;				
RT	"Somatostatin receptor interacting protein defines a novel family of multidomain proteins present in human and rodent brain."				
RL	J. Biol. Chem. 274:32997-33001(1999).				
CC	-1- FUNCTION: RECEPTOR FOR SOMATOSTATINS-14 AND -28. THIS RECEPTOR IS COUPLED VIA PERRUSSIS TOXIN SENSITIVE G PROTEINS TO INHIBITION OF				

[illegible]

DB	Query Match	Best Local Similarity	Matches	Conservative	Score	DB 1	Length	DB 2	Score	DB 3	Length	DB 4	Score	DB 5	Length	DB 6	Score	DB 7	Length	DB 8	Score	DB 9	Length	DB 10	Score	DB 11	Length	DB 12	Score	DB 13	Length	DB 14	Score	DB 15	Length	DB 16	Score	DB 17	Length	DB 18	Score	DB 19	Length	DB 20	Score	DB 21	Length	DB 22	Score	DB 23	Length	DB 24	Score	DB 25	Length	DB 26	Score	DB 27	Length	DB 28	Score	DB 29	Length	DB 30	Score	DB 31	Length	DB 32	Score	DB 33	Length	DB 34	Score	DB 35	Length	DB 36	Score	DB 37	Length	DB 38	Score	DB 39	Length	DB 40	Score	DB 41	Length	DB 42	Score	DB 43	Length	DB 44	Score	DB 45	Length	DB 46	Score	DB 47	Length	DB 48	Score	DB 49	Length	DB 50	Score	DB 51	Length	DB 52	Score	DB 53	Length	DB 54	Score	DB 55	Length	DB 56	Score	DB 57	Length	DB 58	Score	DB 59	Length	DB 60	Score	DB 61	Length	DB 62	Score	DB 63	Length	DB 64	Score	DB 65	Length	DB 66	Score	DB 67	Length	DB 68	Score	DB 69	Length	DB 70	Score	DB 71	Length	DB 72	Score	DB 73	Length	DB 74	Score	DB 75	Length	DB 76	Score	DB 77	Length	DB 78	Score	DB 79	Length	DB 80	Score	DB 81	Length	DB 82	Score	DB 83	Length	DB 84	Score	DB 85	Length	DB 86	Score	DB 87	Length	DB 88	Score	DB 89	Length	DB 90	Score	DB 91	Length	DB 92	Score	DB 93	Length	DB 94	Score	DB 95	Length	DB 96	Score	DB 97	Length	DB 98	Score	DB 99	Length	DB 100	Score	DB 101	Length	DB 102	Score	DB 103	Length	DB 104	Score	DB 105	Length	DB 106	Score	DB 107	Length	DB 108	Score	DB 109	Length	DB 110	Score	DB 111	Length	DB 112	Score	DB 113	Length	DB 114	Score	DB 115	Length	DB 116	Score	DB 117	Length	DB 118	Score	DB 119	Length	DB 120	Score	DB 121	Length	DB 122	Score	DB 123	Length	DB 124	Score	DB 125	Length	DB 126	Score	DB 127	Length	DB 128	Score	DB 129	Length	DB 130	Score	DB 131	Length	DB 132	Score	DB 133	Length	DB 134	Score	DB 135	Length	DB 136	Score	DB 137	Length	DB 138	Score	DB 139	Length	DB 140	Score	DB 141	Length	DB 142	Score	DB 143	Length	DB 144	Score	DB 145	Length	DB 146	Score	DB 147	Length	DB 148	Score	DB 149	Length	DB 150	Score	DB 151	Length	DB 152	Score	DB 153	Length	DB 154	Score	DB 155	Length	DB 156	Score	DB 157	Length	DB 158	Score	DB 159	Length	DB 160	Score	DB 161	Length	DB 162	Score	DB 163	Length	DB 164	Score	DB 165	Length	DB 166	Score	DB 167	Length	DB 168	Score	DB 169	Length	DB 170	Score	DB 171	Length	DB 172	Score	DB 173	Length	DB 174	Score	DB 175	Length	DB 176	Score	DB 177	Length	DB 178	Score	DB 179	Length	DB 180	Score	DB 181	Length	DB 182	Score	DB 183	Length	DB 184	Score	DB 185	Length	DB 186	Score	DB 187	Length	DB 188	Score	DB 189	Length	DB 190	Score	DB 191	Length	DB 192	Score	DB 193	Length	DB 194	Score	DB 195	Length	DB 196	Score	DB 197	Length	DB 198	Score	DB 199	Length	DB 200	Score	DB 201	Length	DB 202	Score	DB 203	Length	DB 204	Score	DB 205	Length	DB 206	Score	DB 207	Length	DB 208	Score	DB 209	Length	DB 210	Score	DB 211	Length	DB 212	Score	DB 213	Length	DB 214	Score	DB 215	Length	DB 216	Score	DB 217	Length	DB 218	Score	DB 219	Length	DB 220	Score	DB 221	Length	DB 222	Score	DB 223	Length	DB 224	Score	DB 225	Length	DB 226	Score	DB 227	Length	DB 228	Score	DB 229	Length	DB 230	Score	DB 231	Length	DB 232	Score	DB 233	Length	DB 234	Score	DB 235	Length	DB 236	Score	DB 237	Length	DB 238	Score	DB 239	Length	DB 240	Score	DB 241	Length	DB 242	Score	DB 243	Length	DB 244	Score	DB 245	Length	DB 246	Score	DB 247	Length	DB 248	Score	DB 249	Length	DB 250	Score	DB 251	Length	DB 252	Score	DB 253	Length	DB 254	Score	DB 255	Length	DB 256	Score	DB 257	Length	DB 258	Score	DB 259	Length	DB 260
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OY		131	IFAAVVKSKLHMCNNVPDIFILNLSVVDLLFLGMP-----MTHDMNGVHHBEETM	164
Dd		65	IYLIRLVAK---KTIINYYILNLALIDELEFMGLPIFLAMQVALVVH-----WPEFKAI	114
OY		185	CTLTADANANOQFSTYTITFTMAIDRYATIAVHPISSTPKRKPSPAVTIVICLMLALPSISI	244
Dd		115	GRVMTVDGNIOFPTSIICLVWASIDRLAYVAHPITKSARKMRPRRAKMINAANGVSILLVI	174
OY		245	TPWMVLARLIFFPGAGVGCGIRLPNPDTDLX-WFTLYOFELAFALPFPVITAAVRIILOR	303
Dd		175	LPMIYIACLRBNONGRRSSCTINMGEGESAWTGFIYAFLIGLIVPLIIICLCYCLFITLIK	234
OY		304	MTSVAPASQSRSIRLKRTVTRIALAICLVFVCWAPRYVQLTQLSIS-RPTLFYVLY	362
Dd		235	VKSSSIGRVSSKKRKSEKKVTIRMYSIVAVFPCWLPPIPNVSSVASISPITALKGMF	294
OY		363	NAAISLGVANSCLNPFYIVICEFRKKVLTVSVPAAGOLRAVSNMOTADEERTESK	420
Dd		295	DFVAVLTANSKANPFIYAFLISDNFK-----SRQNVLICYKVSGSTDGERSDSK	344
 RESULT 7 SSR2_BOVIN				
ID	SSR2_BOVIN	STANDARD:	PRT:	368 AA.
AC	P349933			
DT	01-FEB-1994 (Rel. 28, Created)			
DT	01-FEB-1994 (Rel. 28, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Somatostatin receptor type 2 (SS2R) (SRIF-1).			
GN	SSR2.			
OS	Bos taurus (bovine).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC	Bovidae; Bovinae; Bos.			
OX	NCBI_TaxID=9913;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-Brain:			
RA	Xin W.W., Wong M.-L., Rimland J., Nestler E.J., Duman R.S.;			
RL	Submitted (XX-1992) to the EMBL/Genbank/DBD databases.			
CC	-1- FUNCTION: RECEPTOR FOR SOMATOSTATINS-14 AND -28. THIS RECEPTOR IS COUPLED VIA PERUSSIS TOXIN SENSITIVE G PROTEINS TO INHIBITION OF ADENYLYL CYCLASE. IN ADDITION IT STIMULATES PHOSPHORYLASE PHOSPHATASE AND PLC VIA PERTUSSIS TOXIN INSENSITIVE AS WELL AS SENSITIVE G PROTEINS. IN RIN 5F CELLS, THIS RECEPTOR INHIBITS CALCIUM ENTRY BY SUPPRESSING VOLTAGE DEPENDENT CALCIUM-CHANNELS.			
CC	-1- SUBUNIT: THE C-terminus interacts with SHAK1 PDZ domain (by similarity).			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).			
CC	or send an email to license@isb-sib.ch).			
DR	EMBL: L06613; AAA30764.1; -.			
DR	HSSP: P02699; IBOI.			
DR	InterPro: IPR000276; GPCR_Rhodpsn.			
DR	pfam: PF00001; 7tm_1.1.			
DR	PRINTS: PR00237; GPCR_RHO_DPSN.			
DR	PROSITE: PS00237; G_PROTEIN_REC_P1_1; 1.			
DR	PROSITE: PS00262; G_PROTEIN_REC_P2_1; 1.			
KW	G-protein coupled receptor; Transmembrane; Glycoprotein;			
KW	MultiGene family; Lipoprotein; Palmitate			
FT	DOMAIN 1 42 EXTRACELLULAR (POTENTIAL).			
FT	TRANSMEM 43 66 1 (POTENTIAL).			
FT	DOMAIN 67 77 CYTOPLASMIC (POTENTIAL).			
FT	TRANSMEM 78 102 2 (POTENTIAL).			

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FT DOMAIN 103 117 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 118 137 3 (POTENTIAL).
FT DOMAIN 138 160 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 161 180 4 (POTENTIAL).
FT DOMAIN 181 206 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 207 228 5 (POTENTIAL).
FT DOMAIN 229 252 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 253 277 6 (POTENTIAL).
FT DOMAIN 278 287 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 288 302 7 (POTENTIAL).
FT DOMAIN 303 368 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 8 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 21 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 28 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 31 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 114 192 BY SIMILARITY.
FT LIPID 327 PALMITATE (POTENTIAL).
SQ SEQUENCE 368 AA; 41133 MW; B5852262A6B808B CRC64;

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Query Match 23.78; Score 523.5; DB 1; Length 368;
Best Local Similarity 31.68; Pred. No. 1e-22;
Matches 112; Conservative 74; Mismatches 131; Indels 37; Gaps 8;

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OY 79 TGPNAINTSDGPDNLTSGSPRTGTSYI---NITMPVFGICLIGTIGNSTVIFAV 134
DB 15 TTPEDLNSVGAANISNTER-----YDDLASNVLTITIVYVCLIGCTIVIIYI 67
OY 135 VKSKLHCNVPDIFITINSVDLFLGNPF-----MIDLMGNGVHGETMCTLI 188
DB 68 LRYAKM--KITITNYILNLAIDELFMGLGFLAMOVALLVH-----WPFKAICRVV 117
OY 189 TAMDANSQFTSTYLLTAMADRYLATVHPISSTFKRSVATVLCILMAISFISTIPW 248
DB 118 MTVGGINQFTISFICTLWASIDRIYLVHPKSAKMRPRAKMINAVMGVSLVILPIM 177
OY 249 IYARLIPPGAGVCGIRLPNPDIDLY-WFTLYOFLAFALPFVITAAVRILOQMTSS 307
DB 178 IYAGIRSNQMGRRSCTIIMWPGESGAWYTGFIYAFILGFLVPLIICLCYLFITIKVKS 237
OY 308 VAPASQSRIRLTRKRVPTALAIICLVFCVCAPIYVQLTOLSLIS-REPTLTFYVILNAI 366
DB 238 GIRGSSRRKRSKRVIMSVIVAVFLFCWLPPIYINVSVAISVPTALGMEDFVY 297
OY 367 SLGVANSCLNPFYVIVLCETFRKRLVLSVYKPAAGQLRAVSNQTADEERTESK 420
DB 298 VLTVANSCLNPIYAFILASDNFK-----SPQNVLCIVKVGSTDGEHSDSK 343

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RESULT 8
SSRL_HUMAN STANDARD; PRT; 391 AA.
ID SSRL_HUMAN
AC P30872;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Somatostatin receptor type 1 (SSIR) (SRIF-2).
GN SSRL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92108031; PubMed=1346068;
RA Yamada Y., Post S.R., Wang K., Tager H.S., Bell G.I., Sello S.;
RT "Cloning and functional characterization of a family of human and
RT mouse somatostatin receptors expressed in brain, gastrointestinal
RT tract, and kidney."
RL Proc. Natl. Acad. Sci. U.S.A. 89:251-255(1992).
CC -1- FUNCTION: RECEPTOR FOR SOMATOSTATIN WITH HIGHER AFFINITY FOR
CC SOMATOSTATIN-14 THAN -28. THIS RECEPTOR IS COUPLED VIA PERTUSSIS
CC TOXIN SENSITIVE G PROTEINS TO INHIBITION OF ADENYLATE CYCLASE. IN
CC ADDITION IT STIMULATES PHOSPHORYROSINE PHOSPHATASE AND NA+/H+

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CC EXCHANGER VIA PERTUSSIS TOXIN INSENSITIVE G PROTEINS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: FETAL KIDNEY, FETAL LIVER, AND ADULT PANCREAS,
CC BRAIN, LUNG, JEJUNUM, AND STOMACH.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sdb.ch/announce/
CC or send an email to license@isb-sdb.ch).
CC
CC EMBL; M81829; AAA58247.1; .
CC PIR; A41795; A41795.
CC GeneW: HGNC:11330; SSRL.
CC MIM: 182451; .

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DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_Rhodopsn.
DR PROSITE: PS00237; G-PROTEIN_RECP_F1_1; 1.
DR PROSITE: PS00262; G-PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Lipoprotein; Palmitate.
FT DOMAIN 1 56 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 57 84 1 (POTENTIAL).
FT DOMAIN 85 94 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 95 120 2 (POTENTIAL).
FT DOMAIN 121 131 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 132 153 3 (POTENTIAL).
FT DOMAIN 154 175 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 176 196 4 (POTENTIAL).
FT DOMAIN 197 219 5 (POTENTIAL).
FT TRANSMEM 220 244 6 (POTENTIAL).
FT DOMAIN 245 270 7 (POTENTIAL).
FT TRANSMEM 271 296 8 (POTENTIAL).
FT DOMAIN 297 303 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 304 327 7 (POTENTIAL).
FT DOMAIN 328 391 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 4 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 44 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 48 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 130 208 BY SIMILARITY.
FT LIPID 339 PALMITATE (POTENTIAL).
SQ SEQUENCE 391 AA; 42686 MW; 85C99A9FF39AA3D CRC64;

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Query Match 23.58; Score 519; DB 1; Length 391;
Best Local Similarity 30.98; Pred. No. 1.9e-22;
Matches 112; Conservative 70; Mismatches 136; Indels 44; Gaps 7;

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OY 29 PLPDGACAPGGRRRMLPQPAWVEGSSARLWEOATGTGMADEASLPTGPNAINTSD 88
DB 14 PPSFGSGGEGGSR-----GAGAGAAD---GMEPRGNASQNGT 50
OY 89 GPDNLTSGASPPRTGTSYIINIMPVFGICLIGTIGNSTVIFAVYKSKLHCNVPD 148
DB 51 LSEGSGSA-----ILISFYVCLVGLGSGNSMVIVILIRYAKMTATN--- 94
OY 149 IFINILSVVDLFLGMPFMTHOLMGNGVHGETMCTLTAMDANSQFTSTYLLTAMAI 208
DB 95 IYILNLAIDELMLSVFELVSTLLRH-WFGALDLRLVLSDAVAMFSTICYCLVLSY 153
OY 209 DRYLATVHPISSTFKRSVATVLCILMAISFISTIPWLYARLIPFGAGVCGIRLP 268
DB 154 DRYVAVHPHKAARYRRTYAKVNLGVWVLSLIVIPYVFSRTAANSQTVACNMAMP 213
OY 269 NP-DTDLKWTFLXOFLFALPFVITAAVRILOQMTSSVAPASQSRIRLTRKRTTA 327
DB 214 EAQRMVLGVFVYFLKMFLLVCAICLCYLLIAKRMVALRAGWQORRSRKTLLAV 273
OY 328 IAIQVFEVCAPIYVQLTOLSLISRPLTFVLYNNAISLGANSCLNPFYVIVLCET 387

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DB 274 MAMVWVVICMMPFYVOLVWVFAEQDQATVSQL---SVILGYANSCANPIIYGLSDNF 330
 OY 388 RX 389
 DB 331 KR 332

RESULT 9
 SSRL HUMAN
 ID SSRL HUMAN STANDARD; PRT; 388 AA.
 AC P1391; OSUUY1.
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Somatostatin receptor type 4 (SS4R).
 GN SS4R.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=93290656; PubMed=8512564;
 RA Xu Y., Song J., Bruno J.F., Berelowitz M.;
 RT "Molecular cloning and sequencing of a human somatostatin receptor,
 hsstr4".
 RL Biochem. Biophys. Res. Commun. 193:648-652(1993).
 [2]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=93248256; PubMed=8483934;
 RA Rohrer R., Raulf F., Bruns C., Buettner R., Hofstaedter F.,
 RT Schuele R.;
 RT "Cloning and characterization of a fourth human somatostatin
 receptor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:4196-4200(1993).
 [3]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=93384611; PubMed=8373420;
 RA Yamada Y., Kagimoto S., Kubota A., Yasuda K., Masuda K., Someya Y.,
 RT Ihara Y., Li Q., Imura H., Saito S., Saito Y.;
 RT "Cloning, functional expression and pharmacological characterization
 of a fourth (hsstr4) and a fifth (hsstr5) human somatostatin receptor
 subtype.";
 RL Biochem. Biophys. Res. Commun. 195:844-852(1993).
 [4]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=93302729; PubMed=8100352;
 RA Demchyshyn L.L., Srikanta C.B., Sunahara R.K., Kent G., Seeman P.,
 RT van Tol H.H.M., Panetta R., Patel Y.C., Niznik H.B.;
 RT "Cloning and expression of a human somatostatin-14-selective receptor
 variant (somatostatin receptor 4) located on chromosome 20.";
 RL Mol. Pharmacol. 43:894-901(1993).
 [5]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=21638749; PubMed=11780052;
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavrakas G., Almeida J.P., Babbage A.R., Bagguley C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 RA Buck D., Burrill W.D., Butler A.P., Garder C., Carter S.Y., Clee C.M.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosich K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights K., Laird G.R., Lawlor S.,
 RA Leharvalho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConnell L.J., McLeay K., McMurray A.A.,
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,

RA Rice C.M., Ross M.T., Scott C.E., Sehara H.K., Showkeen R., Sims S.,
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sultson J.E.,
 RA Swann R.M., Symamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:865-871(2001).
 CC -I- FUNCTION: RECEPTOR FOR SOMATOSTATIN-14. THE ACTIVITY OF THIS
 CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH INHIBITS ADENYLYL
 CC CYCLASE. IT IS FUNCTIONALLY COUPLED NOT ONLY TO INHIBITION OF
 CC ADENYLYL CYCLASE, BUT ALSO TO ACTIVATION OF BOTH ARACHIDONATE
 CC RELEASE AND MITOGEN-ACTIVATED PROTEIN (MAP) KINASE CASCADE.
 CC MEDIATES ANTIPLASMODIAL ACTION OF SOMATOSTATIN IN TUMOR CELLS.
 CC SUBCELLULAR LOCATION: Integral membrane protein.
 CC -I- TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED IN FETAL AND ADULT
 CC BRAIN, LONG TISSUE, STOMACH, AND IN LESSER QUANTITIES IN THE
 CC KIDNEY, PITUITARY, AND ADRENALS.
 CC -I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 CC EMBL: D16826; BA004106.1; -;
 CC EMBL: L14856; AA36623.1; -;
 CC EMBL: L07833; AA60565.1; -;
 CC EMBL: L07061; -; NOT ANNOTATED_CDS.
 CC EMBL: AL049651; CAB51953.1; -;
 CC PIR: JN0605; JN0605.
 CC PIR: JN0762; JN0762.
 CC HSP: P02699; IBOU.
 CC GeneW: HGNC:11333; SS4R.
 CC MIM: 182454; -;
 CC InterPro: IPR000276; GPCR_Rhodpsn.
 CC Pfam: PF00001; 7tm1.1; 1.
 CC PRINTS: PR00237; GPCR_Rhodpsn.
 CC PROSITE: PS00237; G_PROTEIN_RECPT_FL1; 1.
 CC DR PROSITE: PS50262; G_PROTEIN_RECPT_FL2; 1.
 CC KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 CC Multigene family; Lipoprotein; Palmitate; Phosphorylation;
 CC Polymorphism.
 CC KW DOMAIN 1 46
 CC TRANSMEM 47 73
 CC DOMAIN 74 83
 CC TRANSMEM 84 104
 CC DOMAIN 105 120
 CC TRANSMEM 121 142
 CC DOMAIN 143 161
 CC TRANSMEM 162 185
 CC DOMAIN 186 208
 CC TRANSMEM 209 232
 CC DOMAIN 233 260
 CC TRANSMEM 261 280
 CC DOMAIN 281 291
 CC TRANSMEM 292 314
 CC DOMAIN 315 388
 CC CARBOHYD 24 24
 CC DISULFID 119 198
 CC LIPID 327 327
 CC VARIANT 83 83
 CC FT CONFLICT 284 284
 CC FT CONFLICT 321 321
 CC FT CONFLICT 365 365
 CC SEQUENCE 388 AA; 41894 MW; 8BCDD69B5F3BC2F5 CRC64;
 Query Match 23.2%; Score 513.5; DB 1; Length 388;

RA MEDLINE=93149123; PubMed=1337145; Ihara Y., Kubota A., Kagitani S.,
 RA Yamada Y., Reisine T., Law S.F., Saito S.,
 RA Saito M., Saito Y., Bell G.I., Saito S.,
 RT "Somatostatin receptors, an expanding gene family: cloning and
 RT functional characterization of human SST3R, a protein coupled to
 RT adenylyl cyclase." Mol. Endocrinol. 6:2136-2142(1992).
 [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=93238970; PubMed=8097479; Seeman P., van Tol H.H.M.,
 RA Cornes J.D., Demchyshyn L.L., Seeman P., van Tol H.H.M.,
 RA Stikart C.B., Kent G., Patel Y.C., Niznik H.B.,
 RT "A human somatostatin receptor (SSTR3), located on chromosome 22,
 RT displays preferential affinity for somatostatin-14 like peptides." J.
 RT Febs Lett. 321:279-284(1993).
 [3]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=20057165; PubMed=10591208; Bruskewich R., Beare D.M.,
 RA Dunham I., Hunt A.R., Collins J.E., Almeida J.P., Babbage A.K.,
 RA Clapp M., Smink L.J., Almscough R., Bates K.N., Beasley O.P.,
 RA Baguley C., Bailey J., Barlow K.F., Buck D., Burgess J.,
 RA Bird C.P., Blakey S.E., Bridgeman A.M., Carter N.P., Chen Y., Clark G.,
 RA Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
 RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
 RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
 RA Dhami P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
 RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,
 RA Gilbert J.G.R., Goward M.E., Graham D.V., Griffiths M.N.D., Hall C.,
 RA Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,
 RA Hunt S.E., Jones M.C., Kersey J., Kimberley A.M., King A.,
 RA Laird G.K., Langford C.F., Leverash M.A., Lloyd C., Lloyd D.M.,
 RA Martin I.D., Mashreghy-Mohammadi M., Matthews L.H., Mccann O.T.,
 RA Mcclay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.,
 RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,
 RA Phillips S.H., Plumb R.W., Ramsey H., Ramsey Y., Rogers L., Ross M.T.,
 RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,
 RA Soederlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,
 RA Vandin M., Wall M., Wallis J.M., Whitley M.N., Willey D.L.,
 RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
 RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
 RA Mimosha S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,
 RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyama S.,
 RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
 RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
 RA Lewis J., Lewis S., Lin S.-P., Loh P., Mala J.E., Nguyen T., Pan H.,
 RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shauli S., Sloan D., Song L.,
 RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
 RA Zhan M., Zhang G., Chissos S., Murray J., Miller N., Minx P.,
 RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
 RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
 RA Hinds K., Kemp K., Latreille P., Layman D., Ozerky P., Rohlfing T.,
 RA Scheet P., Walker C., Wamsley A., Wohlmann P., Pepin K., Nelson J.,
 RA Korf I., Bedell J.A., Hillier L., Mardis E., Waterston R., Wilson R.,
 RA Emanuel B.S., Shaikh T., Kurahashi H., Saita S., Budarf M.L.,
 RA McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E., Edelman L.,
 RA Kim U.J., Shizuya H., Simon M.I., Dumanski J.P., Peyrard M., Kedra D.,
 RA Seroussi E., Fransson I., Tapia I., Bruder C.E., O'Brien K.P.,
 RA Wilkinson P., Bodenteich A., Hartman K., Hu X., Khan A.S., Lane L.,
 RA Tilihan Y., Wright H.,
 RT "The DNA sequence of human chromosome 22." Nature 402:489-495(1999).
 RT FUNCTION: RECEPTOR FOR SOMATOSTATIN-14 AND -28. THIS RECEPTOR IS
 CC COUPLED VIA PERTUSSIS TOXIN SENSITIVE G PROTEINS TO INHIBITION OF
 CC ADENYLYL CYCLASE.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: BRAIN, PITUITARY AND PANCREAS.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 CC EMBL: M96738; AAA60592.1; -
 CC EMBL: 282188; CAB45263.1; -
 CC PIR: S32501; S32501.
 CC PIR: A46226; A46226.
 CC HSP: P34996; 1DDP.
 CC Genew: HGNC:11332; SSTR3.
 CC MIM: 182453; -
 CC InterPro: IPR00276; GPCR_Rhodopsn.
 CC Pfam: PF00001; 7tm_1; 1.
 CC PRINTS: PR00237; GPCR_Rhodopsn.
 CC PROSITE: PS00237; G-PROTEIN_RECPT_FL1; 1.
 CC PROSITE: PS00262; G-PROTEIN_RECPT_FL2; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family; Polymorphism.
 FT DOMAIN 1 43
 FT TRANSMEM 44 69
 FT DOMAIN 70 79
 FT TRANSMEM 80 101
 FT DOMAIN 102 116
 FT TRANSMEM 117 138
 FT DOMAIN 139 161
 FT TRANSMEM 162 181
 FT DOMAIN 182 205
 FT TRANSMEM 206 231
 FT DOMAIN 232 257
 FT TRANSMEM 258 279
 FT DOMAIN 280 293
 FT TRANSMEM 294 316
 FT DOMAIN 317 348
 FT CARBOHYD 17 17
 FT CARBOHYD 30 30
 FT DISULFID 116 191
 FT DOMAIN 346 360
 FT VARIANT 411
 FT SEQUENCE 418 AA; 45847 MW; 1227095F801190C4 CRC64;
 SO
 Query Match 22.8%; Score 504.5; DB 1; Length 418;
 Best Local Similarity 32.5%; Pred. No. 1.3e-21;
 Matches 118; Conservative 76; Mismatches 134; Indels 35; Gaps 11;
 QY 81 PNASNTSDGPDNLTSGSP-----PRGSIYINIMPSVFTGLIGTGNSTV 130
 DB 6 PSSVSTTSEPNASNSAMPDPTATGNVSAGSPAGLVLPVLYVVCVGLGNSLY 65
 QY 131 IPAVYKSKLHCNNVPDFTITLVSVDLFLGPFMHLQMGNGV--WHGEMCTLI 188
 DB 66 IYVLRHTA---SPSVYNYVILMALDELFMGLPFLAAQ--NALSYWPGSLMCRVL 119
 QY 189 TAMDANSQFSTYILRAMADRYLATVHPISFKFKPSVAULTVILMALSFISTPYW 248
 DB 120 MVDGILQFSTICLYMSVDRLLAYVHPRSRKMTAPARKVSAVWVAVVLPV 179
 QY 249 LYALTIFFPGAVGCGITLPNPDTLYW---FTLYOFFLAFLPFTVITAAYRIIQRMF 305
 DB 180 VFSGV---PRGMSCHQMGPEPA--AWRAGFIITAAALGFEPPLVICLYLIVKVR 234
 QY 306 SS---VAPASQSRIRLRTVTRTAITGLVFPVCAPPIYQLTQLSIRP-TITFYV 360
 DB 235 SAGRVRVAPSCQRR-RRSERRTVMVAVALFVLGMPEYVYINIVYVCPLEEDPAFG 293
 QY 361 LYNAISLIGANGSLNPFYVIVCEFR---KRLVSYKRAAGGOLRAVNAQTADERT 417
 DB 294 LYELVVALPFRANSCANILXGLFSYKQGRVRLVPSRRVRSQEPYGPPEKTEEDE 353
 QY 418 ESK 420
 DB 354 EEE 356

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RESULT 12
SSRL_RAT STANDARD: PRT: 391 AA.
ID SSRL_RAT
AC P28646:
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Somatostatin receptor type 1 (SS1R) (SRIF-2).
GN SSRL.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Missar; TISSUE=Brain;
RX MEDLINE=92096119; PubMed=1661599;
RA Meyerhof W., Paust H.J., Schoenrock C., Richter D.;
RT "Cloning of a cDNA encoding a novel putative G-protein-coupled
RL receptor expressed in specific rat brain regions.";
RL DNA Cell Biol. 10:689-694(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=93016064; PubMed=1400442;
RA Li X.-Y., Forte M., North R.A., Ross C.A., Snyder S.H.;
RT "Cloning and expression of a rat somatostatin receptor enriched in
RL brain.";
RL J. Biol. Chem. 267:21307-21312(1992).
CC -1- FUNCTION: RECEPTOR FOR SOMATOSTATIN WITH HIGHER AFFINITY FOR
CC SOMATOSTATIN-14 THAN -28. THIS RECEPTOR IS COUPLED TO
CC PHOSPHOTYROSINE PHOSPHATASE AND NA+/H+ EXCHANGER VIA PERTUSSIS
CC TOXIN INSENSITIVE G PROTEINS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: BRAIN, PITUITARY, ISLET, JEJUNUM, STOMACH,
CC HEART, SPLEEN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL: X62314; CAA4193.1; -.
DR EMBL: M97656; -. NOT_ANNOTATED_CDS.
DR PIR: A39297; A39297.
DR PIR: A43102; A43102.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G-PROTEIN_RECEP_FL1; 1.
DR PROSITE: PS50262; G-PROTEIN_RECEP_FL2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Lipoprotein; Palmitate.
FT DOMAIN 1 56 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 57 84 1 (POTENTIAL).
FT DOMAIN 85 94 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 95 120 2 (POTENTIAL).
FT DOMAIN 121 131 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 132 153 3 (POTENTIAL).
FT DOMAIN 154 175 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 176 196 4 (POTENTIAL).
FT DOMAIN 197 219 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 220 244 5 (POTENTIAL).
FT DOMAIN 245 270 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 271 296 6 (POTENTIAL).
FT DOMAIN 297 303 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 304 327 7 (POTENTIAL).
FT DOMAIN 328 391 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 4 4 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 44 44 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 48 48 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 130 208 BY SIMILARITY.
FT LIPID 339 339 PALMITATE (POTENTIAL).
SQ SEQUENCE 391 AA; 42746 MW; 28ED6894B72FBH7 CRC64;

Query Match 22.6%; Score 500; DB 1; Length 391;
Best local similarity 31.2%; Pred. No. 2,1e-21;
Matches 105; Conservative 73; Mismatches 134; Indels 24; Gaps 6;

OY 55 GSSARLMEQATGTGMADLEASLLPTGPNASNTSGDPNLTISAGSPPTGISTITNIMPS 114
DB 20 GCGEGVCSRGPSGSAAD--GMEBGRNSONGTSLSGOGSA-----LLISP 63
OY 115 VGTICILIGITGNSVYFAVVKSKSLKHCNVPDIFINISYVDLFLGLPMPHIOHMG 174
DB 64 IISVYCLVGLGNSMVIYIIRYAKMKATN---IYLNLAIDELMLSVPLVSTLL 120
OY 175 NGVWHPGETMCTLTAMDANSQFTSTYLLTMAIDRYLATVHPISSTPKPSVALVYC 234
DB 121 RH-WFPGALCLRLVLSVDVAVNMFTSICYLTLSVDRYVAVVHPKARYRRPTVAKVNL 179
OY 235 LTMALSFISTPVMYLARLIPFGAVCGIRLPNP-DTDLWPTLYQFLAFALPVPV 293
DB 180 GWNVLSLVILPIVFSSTANSDGTACNNLMPEAPQRNLVGVLTFLMGLFPLPGAI 239
OY 294 TAAVYRIIQRTSSVAPASQSRISRLRTKRTVTRTAICLVFVCGADYVYLQTLQISR 353
DB 240 CLCYLLIILAKMVMVAKKAGMOQRKSEKRTILAMVMVVFVLCMPFVYVQLVNFAEQ 299
OY 354 PLTFEVLVYNAISIGVANSQCNPEVYIVLCETPRK 389
DB 300 DATVSQ---SVILGANSKANPLIYGLFSDNFKR 332

RESULT 13
SSRL_RAT STANDARD: PRT: 384 AA.
ID SSRL_RAT
AC P30937:
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Somatostatin receptor type 4 (SS4R).
GN SSRL4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=93087484; PubMed=1360663;
RA Bruno J.F., Xu Y., Song J., Berelowitz M.;
RT "Molecular cloning and functional expression of a brain-specific
RL somatostatin receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:11151-11155(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Hippocampus;
RX MEDLINE=94230347; PubMed=8175684;
RA Bito H., Mori M., Sakana C., Takano T., Honda Z., Gotoh Y.,
RA Nishida E., Shimizu T.;
RT "Functional coupling of SSRL4, a major hippocampal somatostatin
RT receptor, to adenylate cyclase inhibition, archadonate release and
RT activation of the mitogen-activated protein kinase cascade.";
RL J. Biol. Chem. 269:12722-12730(1994).
CC -1- FUNCTION: RECEPTOR FOR SOMATOSTATIN-14. THE ACTIVITY OF THIS
CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH INHIBITS ADENYLATE
CC CYCLASE. IT IS FUNCTIONALLY COUPLED NOT ONLY TO INHIBITION OF
CC ADENYLATE CYCLASE, BUT ALSO TO ACTIVATION OF BOTH ARACHIDONATE
CC RELEASE AND MITOGEN-ACTIVATED PROTEIN (MAP) KINASE CASCADE.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: BRAIN, LUNGS, HEART AND ISLETS. MODERATE

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CC LEVELS IN THE HIPPOCAMPUS, CORTEX, AND OLFACTORY BULB.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC
 DR EMBL: M6544; AAA42180.1; -;
 DR EMBL: U04738; AAA17519.1; -;
 DR PIR: A47249; A47249.
 DR HSSP: P02699; IBOJ.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCRHHODOPS.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_1; 1.
 DR PROSITE: PS50262; G-PROTEIN_RECEP_FL_2; 1.
 DR G-protein coupled receptor; Transmembrane; Glycoprotein;
 DR Multigene family; Lipoprotein; Palmitate.
 FT DOMAIN 1 41
 FT TRANSMEM 42 69
 FT TRANSMEM 70 79
 FT TRANSMEM 80 105
 FT TRANSMEM 106 116
 FT TRANSMEM 117 138
 FT TRANSMEM 139 160
 FT TRANSMEM 161 181
 FT TRANSMEM 182 203
 FT TRANSMEM 204 228
 FT TRANSMEM 229 234
 FT TRANSMEM 235 280
 FT TRANSMEM 281 287
 FT TRANSMEM 288 311
 FT DOMAIN 312 384
 FT CARBOHYD 21 21
 FT DISULFID 115 194
 FT LIPID 323 323
 SQ SEQUENCE 384 AA; 42087 MW; 044542B4922411B5 CRC64;
 Query Match 22.4%; Score 494.5; DB 1; Length 384;
 Best Local Similarity 33.0%; Pred. No. 4.2e-21;
 Matches 104; Conservative 66; Mismatches 116; Indels 29; Gaps 8;
 OY 85 NTSDEPDLTSAGSPPTGSIYINIMPSVFGITCLIGTIGNSTVIFPAVKKSKLHCN 144
 DB 21 NASMAPDEEDAVRSDGTAGMTI--QCIYALVCLGLVGNALVIVILRYAKMKTAT 78
 OY 145 NVPDIFITNLAVVDLFLIGMPENI-----HQLMGNGVMHGETMCTLTAMANSOFT 198
 DB 79 N---YLLNLAVADELFMLSVFVASAALRH-----WFFGAVLCNAVLSVDGLNFT 128
 OY 199 STYITLMAIDRYLATVHPISSTKFRKPSVATLVICLMAFSISITPWTVARLIPPG 258
 DB 129 SVFCLVLSVDYVAVHPLRATYRPSVAKLINLGLWLSLAVTLPLIAVFADRRPARG 188
 OY 259 G-AVGGCIRLPNPDLDLY---FTIXQFLALPFPVITAAVYVILDRMTSSVAPASOR 314
 DB 189 GAVVACNLMFHP---AASAVFVITFLGLFLPVLAIIGCYLLIVKMRVALRAQMO 244
 OY 315 STRLRTKRYTFAIAICLFECVMAFYVLOLTQTSISRPFLTFYVLYNMAISLGANSC 374
 DB 245 QRRRSKKTITRLVLMVYVFCVCMPEFYVQVLNLFVSLDAT---VHVSLLISYANSC 301
 OY 375 LNFVYIVLCETFRK 389
 DB 302 ANPIIYGLSDNFR 316
 RESULT 14
 SSR4_MOUSE

ID SSR4_MOUSE STANDARD: PRT; 384 AA.
 AC P49660:
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Somatostatin receptor type 4 (SS4R).
 GN SSR4 OR SMSR4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxId=10090;
 RP [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SVJ; TISSUE=Liver;
 RC MEDLINE=96194903; PubMed=8654950;
 RA Schwabe W., Brennan M.B., Hochgeschwender U.;
 RT Isolation and characterization of the mouse (Mus musculus)
 RT somatostatin receptor type-4-encoding gene (SMSR4).
 RL Gene 168:233-235(1996).
 CC -1- FUNCTION: RECEPTOR FOR SOMATOSTATIN-14. THE ACTIVITY OF THIS
 CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH INHIBITS ADENYLATE
 CC CYCLASE. IT IS FUNCTIONALLY COUPLED NOT ONLY TO INHIBITION OF
 CC ADENYLATE CYCLASE, BUT ALSO TO ACTIVATION OF BOTH ARACHIDONATE
 CC RELEASE AND MITOGEN-ACTIVATED PROTEIN (MAP) KINASE CASCADE.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC
 DR EMBL: U26176; AAA67561.1; -;
 DR HSSP: P02699; IBOJ.
 DR MGD: MGI:105372; Smstr4.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCRHHODOPS.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_1; 1.
 DR PROSITE: PS50262; G-PROTEIN_RECEP_FL_2; 1.
 DR G-protein coupled receptor; Transmembrane; Glycoprotein;
 DR Multigene family; Lipoprotein; Palmitate.
 FT DOMAIN 1 41
 FT TRANSMEM 42 69
 FT TRANSMEM 70 79
 FT TRANSMEM 80 105
 FT TRANSMEM 106 116
 FT TRANSMEM 117 138
 FT TRANSMEM 139 160
 FT TRANSMEM 161 181
 FT TRANSMEM 182 203
 FT TRANSMEM 204 228
 FT TRANSMEM 229 234
 FT TRANSMEM 235 280
 FT TRANSMEM 281 287
 FT TRANSMEM 288 311
 FT DOMAIN 312 384
 FT CARBOHYD 21 21
 FT DISULFID 115 194
 FT LIPID 323 323
 SQ SEQUENCE 384 AA; 42089 MW; 04DB07514B1C6FB CRC64;
 Query Match 21.9%; Score 485; DB 1; Length 384;
 Best Local Similarity 29.9%; Pred. No. 1.4e-20;
 Matches 102; Conservative 69; Mismatches 134; Indels 36; Gaps 8;
 OY 53 VEGSSARKLWQAGTGTGNADLEASILPTGPNASNTSDGPDNLTSAGSPPTGSIYINIM 112
 DB 8 LRGEVDFTWTPGINASWA-----PQEDDAMGSDGTAGM-----VVI 46

QY 113 PSVFGTICLLIGNSTVIFAVVKKSLHMCNVDIFITNLVVDLLFLGHPMHIQL 172
 Db 47 OCTVALCVGLVGNALVIFILYIRAKKATFN---ITLLNLAVADELFMLSPF-VRSA 102
 QY 173 MGNVWHEGEMCTLITAMANSOFTSTYITLITAMADRYLATVHPISSTKFRKPSVATLV 232
 Db 103 AALRIHMPGAVLCRAVLSDGLNMTSVFCLTVLSDRYAVAVHPRTATYRRSPVAKLI 162
 QY 233 ICLLWALFISITPWLVARLILPPGG-AVCGGIRLPNPDLDLW---FTLYQEFLLAFAL 288
 Db 163 NIGVWLASLITLPIAVADTRPARGEAVACNLHMDHP-----AMSAVFYITFLGLFEP 218
 QY 289 PNVVITAAVYRILQRTSSVAPASORSIRLTKRVTATACICVFVCAAPYVYIQLTQ 348
 Db 219 PVALGICLYLLIVGKRAVALRGWGQRRSEKRTIRLVIMVAVFVLCMMPEYVQLLN 278
 QY 349 LISRPFLFVYLYNAISLGVANSCLNPFYIYICENFRK 389
 Db 279 LEVTSIDLT---VNHVSILISYANSCANPILYGLSDNFR 316

RESULT 15

SSR3_RAT STANDARD; PRT; 428 AA.

ID SSR3_RAT
 AC P30936:
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE Somatostatin receptor type 3 (SS3R) (SSR-28).
 GN SSTR3.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_Taxid=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar; TISSUE=Brain;
 RA MEDLINE=93066220; PubMed=1279674;
 RX Meyerhof W., Wulfsen I., Schoenrock C., Fehr S., Richter D.;
 RT "Molecular cloning of a somatostatin-28 receptor and comparison of
 its expression pattern with that of a somatostatin-14 receptor in rat
 brain.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:10267-10271(1992).
 CC -1- FUNCTION: RECEPTOR FOR SOMATOSTATINS-14 AND -28. THIS RECEPTOR IS
 COUPLED VIA PERTUSSIS TOXIN SENSITIVE G PROTEINS TO INHIBITION OF
 ADENYLYL CYCLASE.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: DENSELY EXPRESSED IN CEREBELLUM AND IN MODERATE
 LEVELS IN THE AMYGDALA, CORTEX, STRIATUM, SPLEEN, LIVER.
 CC PITUITARY.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 DR EMBL: X63574; CAA45130.1; -.
 DR PIR: S30508; S30508.
 DR HSSP: P34996; 1DDP.
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7cm_1; 1.
 DR PRINTS: PR00237; GPCR_RHODOPSN.
 DR PROSITE: PS00237; G_PROTEIN_RECEPTOR_1; 1.
 DR PROSITE: PS00262; G_PROTEIN_RECEPTOR_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family.
 FT DOMAIN 1 45 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 46 71 1 (POTENTIAL).
 FT DOMAIN 72 81 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 82 103 2 (POTENTIAL).
 FT DOMAIN 104 118 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 119 140 3 (POTENTIAL).
 FT DOMAIN 141 162 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 163 182 4 (POTENTIAL).
 FT DOMAIN 183 206 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 207 232 5 (POTENTIAL).
 FT DOMAIN 233 266 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 267 288 6 (POTENTIAL).
 FT DOMAIN 289 302 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 303 325 7 (POTENTIAL).
 FT DOMAIN 326 428 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 18 18 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 31 31 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT DISULFID 117 192 BY SIMILARITY.
 FT DOMAIN 358 373 POLY-GLU.
 SQ SEQUENCE 428 AA; 47151 MW; BE0AA94804A9E9D CRC64;

Query Match 21.7%; Score 480.5; DB 1; Length 428;
 Best Local Similarity 31.3%; Pred. No. 2.ee-20;
 Matches 118; Conservative 73; Mismatches 143; Indels 43; Gaps 11;

QY 75 SLLEPTGPNASNTSDG---PDNLTSAGSPPTSGISYINIIMPVYFTICLLIGNSTVY 131
 Db 8 SSVPTTLDPGNASSAWPLDTSLGNASAGTSLAGVAGILISLYLVVGVGLNSLYI 67
 QY 132 PAVVKKSKLHMCNVDIFITNLVVDLLFLGHPMHIQLMNGV--WHFGETKCLIT 189
 Db 68 YVVLHRTS---SPSVTYIINLALADELFMLGLPFLAQ---NALSYWFGSLMCRLYV 121
 QY 190 AMDANSOFTSTYITLITAMADRYLATVHPISSTKFRKPSVATLVICLLMALSFTITPWL 249
 Db 122 AVDGINQFTSIFCLTVMSVDRIYLAHVHTRBSARRKTPVARMYSAANVAVVLPVY 181
 QY 250 VARLIHPEGAVGCGIRLPNPDLDLW---FTLYQEFLLAFALPVVITAAVYRILQRTMS 306
 Db 182 FSGV---PRGMSTCHMOPBEPAA--AMRTAFIITYALGFGGPLLICLYLIVVYKRS 236
 QY 307 SY-----APASORSIRLTKRVTATACICVFVCAAPYVYIQLTQSLISRP 354
 Db 237 TTRRRRAASCCWQVAPACQRR-RSESRVTRMVAVVAVLFLCMMPYLLNINVCPLP 295
 QY 355 -TLTVVLYNAISLGVANSCLNPFYIYICENFRK-----RLVSYKPAAGQL 403
 Db 296 EEPAFEGLYFLVALVPYANSCANPILYGLFSYRFGKGFRRILLRPSRRVRSQERGSGPPE 355
 QY 404 RAVSNAQTADERTESK 420
 Db 356 KTEEEDEDEBERREE 372

Search completed: February 13, 2003, 13:58:47
 Job time : 15.7494 secs


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Query Match          99.5%; Score 2200; DB 4; Length 422;
Best Local Similarity 99.5%; Pred.No. 2e-179;
Matches 420; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

0y      1 MSVGAKKKIVGRAVYIGGSSCGAATEEDPLDCCAGCAGGCGGRWRRLPGQAWTEGSSARL 60
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

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Db      1 MSVGAKKGVRAVGLGGGSCQATEEDPLPDGCACAPGGGRRWRLLPQPAVVEGSSARL 60
QY      61 WEQATGTGMADLEASLLPTGPNASNTSDGPDNLTSGSPPTGTSIYINIMPSVFGTIC 120
Db      61 WEQATGTGMADLEASLLPTGPNASNTSDGPDNLTSGSPPTGTSIYINIMPSVFGTIC 120
QY      121 LGGIIGNSTVIFAAYVKKSKLHMCNNVPDIFIINLSVVDLFLGMPFMIHQLMGNGVWHF 180
Db      121 LGGIIGNSTVIFAAYVKKSKLHMCNNVPDIFIINLSVVDLFLGMPFMIHQLMGNGVWHF 180
QY      181 GETMCTLTITAMANDANSQFSTYILITAMADRYLATVHPISSTFKRPSVATLVICLLMALS 240
Db      181 GETMCTLTITAMANDANSQFSTYILITAMADRYLATVHPISSTFKRPSVATLVICLLMALS 240
QY      241 FISITPVMYLARLIPFGAGVCGIRLPNPDITLWFTLYQFELAFALPEVYITAAYVRI 300
Db      241 FISITPVMYLARLIPFGAGVCGIRLPNPDITLWFTLYQFELAFALPEVYITAAYVRI 300
QY      301 LQRMSSVAPASORSIRLRTKRYRTAIAICLVFVCAPYVYLQTLQSLSPRTLTFVY 360
Db      301 LQRMSSVAPASORSIRLRTKRYRTAIAICLVFVCAPYVYLQTLQSLSPRTLTFVY 360
QY      361 LYNAISLGYANSCINLPFYIYLCETFRKRLVLSVKPAAGQLRAVSNAGTADERTESK 420
Db      361 LYNAISLGYANSCINLPFYIYLCETFRKRLVLSVKPAAGQLRAVSNAGTADERTESK 420
QY      421 GT 422
Db      421 GT 422

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RESULT 2

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ID      096S47      PRELIMINARY:      PRT:      422 AA.
AC      096S47;
DT      01-DEC-2001 (TREMBLrel. 19, Created)
DT      01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT      01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE      Somatostatin receptor-like protein.
GN      SLC1.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RL      Supo T., Mori M.;
      Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RX      MEDLINE=99373129; PubMed=10441476;
RA      Shimomura Y., Mori M., Supo T., Ishibashi Y., Abe M., Kurokawa T.,
      Ono H., Nishimura O., Sumino Y., Fujino M.;
      "Isolation and identification of melanin-concentrating hormone as the
      RT      endogenous ligand of the SLC-1 receptor.";
      Biochem. Biophys. Res. Commun. 261:622-626(1999).
RL      EMBL: AB063174; BAB60890.1; -.
DR      InterPro: IPR000276; GPCR_Rhodpsn.
DR      Pfam: PF00001; 7tm_1; 1.
DR      PRINTS: PRO1559; DUFFYANTIGEN.
DR      PROSITE: PS50262; G_PROTEIN_RECPEP_FL_2; 1.
KW      Receptor.
SQ      SEQUENCE 422 AA; 45962 MW; 3986919A18183818 CRC64;

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Query Match      99.3%; Score 2195; DB 4; Length 422;
Best Local Similarity 99.3%; Pred. No. 5.4e-179;
Matches 419; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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QY      1 MSVGAKKGVRAVGLGGGSCQATEEDPLPDGCACAPGGGRRWRLLPQPAVVEGSSARL 60
Db      1 MSVGAKKGVRAVGLGGGSCQATEEDPLPDGCACAPGGGRRWRLLPQPAVVEGSSARL 60
QY      61 WEQATGTGMADLEASLLPTGPNASNTSDGPDNLTSGSPPTGTSIYINIMPSVFGTIC 120

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Db      61 WEQATGTGMADLEASLLPTGPNASNTSDGPDNLTSGSPPTGTSIYINIMPSVFGTIC 120
QY      121 LGGIIGNSTVIFAAYVKKSKLHMCNNVPDIFIINLSVVDLFLGMPFMIHQLMGNGVWHF 180
Db      121 LGGIIGNSTVIFAAYVKKSKLHMCNNVPDIFIINLSVVDLFLGMPFMIHQLMGNGVWHF 180
QY      181 GETMCTLTITAMANDANSQFSTYILITAMADRYLATVHPISSTFKRPSVATLVICLLMALS 240
Db      181 GETMCTLTITAMANDANSQFSTYILITAMADRYLATVHPISSTFKRPSVATLVICLLMALS 240
QY      241 FISITPVMYLARLIPFGAGVCGIRLPNPDITLWFTLYQFELAFALPEVYITAAYVRI 300
Db      241 FISITPVMYLARLIPFGAGVCGIRLPNPDITLWFTLYQFELAFALPEVYITAAYVRI 300
QY      301 LQRMSSVAPASORSIRLRTKRYRTAIAICLVFVCAPYVYLQTLQSLSPRTLTFVY 360
Db      301 LQRMSSVAPASORSIRLRTKRYRTAIAICLVFVCAPYVYLQTLQSLSPRTLTFVY 360
QY      361 LYNAISLGYANSCINLPFYIYLCETFRKRLVLSVKPAAGQLRAVSNAGTADERTESK 420
Db      361 LYNAISLGYANSCINLPFYIYLCETFRKRLVLSVKPAAGQLRAVSNAGTADERTESK 420
QY      421 GT 422
Db      421 GT 422

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RESULT 3

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ID      09M201      PRELIMINARY:      PRT:      121 AA.
AC      09M201;
DT      01-OCT-2000 (TREMBLrel. 15, Created)
DT      01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT      01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE      Melanin-concentrating hormone receptor (Fragment).
OS      Sus scrofa (Pig).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
OX      NCBI_TaxID=9823;
RN      [1]
RP      SEQUENCE FROM N.A.
RL      Tissue=Brain; Hypothalamus;
      Materi R.L.;
      "Sus scrofa melanin-concentrating hormone (MCH) receptor.";
      RT      Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR      EMBL: AF273611; AAF81827.1; -.
DR      InterPro: IPR000276; GPCR_Rhodpsn.
DR      Pfam: PF00001; 7tm_1; 1.
DR      PRINTS: PRO0237; GPCR_HODOPSIN.
DR      PROSITE: PS50262; G_PROTEIN_RECPEP_FL_2; 1.
KW      Receptor.
FT      NON_TER 1 1
FT      NON_TER 121 121
SQ      SEQUENCE 121 AA; 13583 MW; 884D8268B6F9F010 CRC64;

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Query Match      27.2%; Score 601; DB 6; Length 121;
Best Local Similarity 99.2%; Pred. No. 9.7e-44;
Matches 120; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY      294 TAAVYRLQRMSSVAPASORSIRLRTKRYRTAIAICLVFVCAPYVYLQTLQSLSP 353
Db      1 TAAVYRLQRMSSVAPASORSIRLRTKRYRTAIAICLVFVCAPYVYLQTLQSLSP 60
QY      354 PTLTFVLYNAISLGYANSCINLPFYIYLCETFRKRLVLSVKPAAGQLRAVSNAGTAD 413
Db      61 PTLTFVLYNAISLGYANSCINLPFYIYLCETFRKRLVLSVKPAAGQLRAVSNAGTAD 120
QY      414 E 414
Db      121 E 121

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Query Match	25.6%; Score 565.5; DB 4; Length 340;
Best local similarity	37.0%; Pred. No. 3.6e-40;
Matches 113; Conservative 62; Mismatches 119; Indels 11; Gaps 4;	
110	110MSVFTGTLIGITGTVFAVYKRSKILHMCNNVDPDITLTVSDLLFLGDEMI 169
35	35VLPSTMGITCSGLVGNLILVFTILRSK-----KYVDITCLNLAADVHYHGVFEL 90
170	170HQLMGNVHPEGTCTLTAMDANSQFTSYIITLAMAIDRYLATVHPISISFRKRPVA 229
91	91HQAARGEWVFEGGPRITCTIITSDTNOFACSAIMTVMSVDYVFLVDPFLRTWRRYKT 150

[illegible]

RESULT	5
09BXAB	
ID	09BXAB
AC	09BXAB;
DT	01-JUN-2001 (TREMBLrel, 17, Created)
DT	01-JUN-2001 (TREMBLrel, 17, Last sequence update)
DT	01-DEC-2001 (TREMBLrel, 19, Last annotation update)
DE	G protein-coupled receptor MCH2.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxId=9606;
RP	[1]
RN	SEQUENCE FROM N.A.
RX	MEDLINE-21282939; PubMed-11274220;
RA	Hilli J., Duckworth M., Murdoch P., Rennie G., Sabido-David C.,
RA	Ames R.S., Szekeres P., Wilson S., Bergsma D.J., Gloger I.S.,
RA	Lavy D.S., Chambers J.K., Muir A.I.;
RT	"Molecular Cloning and Functional Characterization of MCH2, a Novel
RL	Human MCH Receptor";
RL	J. Biol. Chem. 276:20125-20129(2001).
DR	EMBL; AF347063; AAK32193.1; -
DR	InterPro; IPR000276; GPCR_Rhodopsn.
DR	Pfam; PF00001; 7tm_1; 1.
DR	PRINTS; PR00237; GPCRHHODOPS.
DR	PROSITE; PS00237; G_PROTEIN_RECP_F1.1; UNKNOWN_1.
DR	PROSITE; PS50262; G_PROTEIN_RECP_F1.2; 1.
FM	Receptor.
WQ	SEQUENCE. 340 AA; 38803 MW; 95A43ECB57511ACC CRC64;

[illegible]

Db	330	NNMGN	334
RESULT 6			
Q8SQ54	PRELIMINARY;	PRT;	340 AA.
AC Q8SQ54			
DT 01-JUN-2002 (TREMBLrel. 21, Created)			
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)			
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DE GPRV17.			
GN Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).			
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;			
OC Cercopithecinae; Macaca.			
OC NCBI_TaxID=9541;			
OX (1)			
RN SEQUENCE FROM N.A.			
RP Kurama T., Matsunoto S., Takasaki J., Terai K., Matsunoto M.,			
RA Kamohara M., Saito T., Soga T., Saito Y., Oda T., Masuko Y.,			
RA Furukishi K.;			
RT "Molecular characterization of a novel melanin-concentrating hormone			
RT receptor: Evidence of its expression in lateral hypothalamus.";			
RL Submitted (MAR-2001) to the EMBL/Genbank/DBJ databases.			
DR EMBL; AB058850; BAB8/843.1; -- BD22CF1972332439 CRC64;			
SQ SEQUENCE 340 AA; 38769 MW; BD22CF1972332439 CRC64;			
Query Match 25.3%; Score 559.5; DB 6; Length 340;			
Best Local Similarity 36.7%; Pred. No. 1.2e-39;			
Matches 112; Conservative 60; Mismatches 122; Indels 11; Gaps			
QY 110 IMPSVFETICLGITGNSVTYFAVKKSKLHMCNNVPDIFINLSVVDLLPLIGRPFI 169			
DB 35 VILPSMIGTIGSGIGLGNLIVFTIIRSKR---KTVPICTGNLAADLVHIGMPELI 90			
QY 170 HOLGSGVWHFGFTGTCVLTITAMDNSQFSTVLTITMAIDRYLATVHPISSTFKRPSVA 229			
DB 91 HGMARCGEWFEGPCLTIITISLDTQCFACSAIMTYMSVDRYALVQPRITISWRIRYKT 150			
QY 230 TLVICTLMLSFISTIPVWLVARLIPPGGAVCGGIRLPNDTDLWYFLYQFFLPAIP 289			
DB 151 IRLNLGLMAASFILALPWVIYSKVIKFKGVESCAEDLSPD-DVLMYLYLTITTFEPP 209			
QY 290 FVYITAYVRII-----QRTSSVAPASQDSI-RLRTRKYTRPAIACLVFEVCMAPIYV 343			
DB 210 LPLILVCYLITLITLWEMTQONKDARCNSFVKORVMKLTIKVYLVAVFILISAAPHYH 269			
QY 344 LQTLQISHPITLTFYLYNAAISLGYSANCLNPFYIVLCETFERKRLVLSVPAAGOL 403			
DB 270 IQLVNLQMEGPILAFYGYGLSLCLSYASSINPFIYIILSGNFKRLPQIGRRVIDKEI 329			
QY 404 RAVSN 408			
DB 330 KMMGN 334			
RESULT 7			
Q8QWU5	PRELIMINARY;	PRT;	370 AA.
ID Q8QWU5			
AC Q8QWU5			
DT 01-MAR-2002 (TREMBLrel. 20, Created)			
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)			
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DE Somatostatin receptor 2.			
GN SSTR2.			
OS Fugu rubripes (Japanese pufferfish) ('Takifugu rubripes').			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;			
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;			
OC Tetraodontidae; Takifugu.			
OX NCBI_TaxID=31033;			
RN [1]			

Query Match	Best Local Similarity	Score	DB	Length	370;
Matches 128; Conservative	74;	Mismatches 131;	Indels 56;	Gaps 13;	
23.7%;	32.9%;	Pred. No. 1.7e-36;			
SEQUENCE FROM N.A.					
MEMLINE=21564205; PubMed=11707075;					
Bagheri-Pan S., Ferraz C., Demaille J., Scherer G., Pfeiffer D.;					
"Comparative Genomics of the SOX Region in Human and Fugu Ruidipes:					
Conservation of Short Regulatory Sequence Elements within Large					
Intergenic Regions."					
Genomics 78:73-82(2001).					
EMBL; AF32945; AAL32173.1;					
InterPro: IPR000276; GPCR_Rhodpsn.					
Pfam: PF00001; 7tm.1; 1.					
PRINTS: PR00237; GPCR_RHODPSN.					
PROSITE; PS00237; G_PROTEIN_RECPE_FL1; UNKNOWN.1.					
PROSITE; PS50262; G_PROTEIN_RECPE_FL2; 1.					
Receptor.					
SEQUENCE 370 AA; 41364 MW; 420BB12F204946B6 CRC64;					
Query Match	23.7%;	Score 523;	DB 13;	Length 370;	
Best Local Similarity	32.9%;	Pred. No. 1.7e-36;			
Matches 128; Conservative	74;	Mismatches 131;	Indels 56;	Gaps 13;	
45 WRLPOPANVESSARLV---EQATGTGMADEASLPLTPGNASNTSDGPDNLTSAGSPR 101					
4 WILP-PSPINLSDHLIDYDFEQANG---SDLA-----NRTDHLNRTS----- 43					
102 TGSISVNTIMPSVECTLLGLIGNSYIFPAWKKSKLHMGNVPDITFINLSVDLFL 161					
44 -----YVITCMYLVACVAGLGNALTYILRRAK---KTVINITYILNLAVADYLE 93					
162 LIGMPFMIHQLMGNGVHFGFTMCTLITAMDANSQTSYIILTAADIDRYLATVHRISST 221					
94 MGLPFIATQL-ALVAMPGPVLCRVMMVDSLNQTSIFCLMVMISIDRLAVVHPKST 152					
222 KKKKPSVATLVICLLMALFESITPWLVARLIFPGGAVGCGIRLPNPDTLYW-FTLY 280					
153 KKKKPSVATLVINAVMGASLVNLPVITYISGITKDDGF-CITYPEPEEATYTAFTMY 211					
281 OFELAPALPFVVITAAVYVRLIORTSSVAPASQSRIRLTKRYRTALAICTVFCVQAP 340					
212 TELFGFLPLVLIVSLCYFIIYKVKSGIVGSSKKRRSEKRYTRMWSIYVAFFVLCWLP 271					
341 YYVLQITOLS-----ISPTLTFFYVILNNAISLGYANSCLEPFYIVLCEFFRRKL- 391					
272 EYVENVTYVIGSISATVHLKSTPAF-----VVLGIANSCLNPILYAFLENFKKSFOV 325					
392 VLSVKKPAOGQLRAVSNAGTADERTESK 420					
326 VLCLQ-----KVGGLDEAKERSDRQDKSR 349					
RESULT 8					
Q96GEO PRELIMINARY; PRT; 346 AA.					
Q96GEO; Q96GEO;					
DT 01-DEC-2001 (TREMblrel. 19, Created)					
DT 01-DEC-2001 (TREMblrel. 19, last sequence update)					
DT 01-MAR-2002 (TREMblrel. 20, last annotation update)					
DE Unknown (Protein for IMAGE:3354783) (Fragment).					
OS Homo sapiens (Human).					
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.					
OX NBL_TaxID=9606;					
OX [1]					
RP SEQUENCE FROM N.A.					
RC RISSUE=EYE;					
RA Strausberg R.;					
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.					
EMBL: BC009522; AA09522.1; -					
InterPro: IPR000276; GPCR_Rhodpsn.					
PFam: PF00001; 7tm.1; 1.					
DR PROSITE; PS00237; G_PROTEIN_RECPE_FL1; UNKNOWN.1.					
DR PROSITE; PS50262; G_PROTEIN_RECPE_FL2; 1.					
FT NON_TER 1					
SEQUENCE 346 AA; 38790 MW; EA073A6CC05FEB72 CRC64;					

Query Match 23.6%; Score 521.5; DB 4; Length 346;
Best Local Similarity 31.7%; Pred. No. 2.1e-36;
Matches 110; Conservative 73; Mismatches 123; Indels 39; Gaps 7;

QY 82 NASNTSDGPNMLTSGSPPTGTSISYINIMPSVEGTLICLGIGNSTVIFAVKSKLH 141
D 6 NTSNOTEPYDLS-----NAVLTFFYFVVCIIIGCGMTLVYLLRYAKM- 51
QY 142 MCNNPDIFFINLSVVDLFLGMPF-----MIHOLMGNGVWHFEGTCTLTADANS 195
D 52 --KTTNIIYILNLAIDLEMLGLPFLAMOVAVH-----WPFKALCRVVMFTDGIN 102
QY 196 QETSTYILTAMADRYLATVHPISSTKRRPSVATLYCLMLASFISTPWLVARLIP 255
D 103 QETSTFCLTVMSIDRYLATVHPKSAKWRPRPKMTMAVMSLVLPIIMYAGLS 162
QY 256 FPGGAVGGCIRLPNPDLDY-WFTLYOFLAFALPFPVITAAVRIILORNTSSVAPASQR 314
D 163 NQMGSSCTIWPBESGAWYGFITVFLGFLVPLTICLCYLFITIKKSSGIVGSS 222
QY 315 SIRLTKRVTRTAIAICLVFVCWAPYVQLTQLSIS-RPTLFVLYNAAISLGYANS 373
D 223 KRKSEKKEVTRMWSIVAVFIFCMLPFIYFNVSVMASIPFALKMGDFVVLVYANS 282
QY 374 CLNPFYIVLCETFRKRRLVSVKPAAGQLRANSNAOTADEERTSK 420
D 283 CANPLTYAFISDNFRK-----SFQNVLCVYKVSQTDGERSDSK 321

RESULT 9
096TF2 PRELIMINARY; PRT; 356 AA.

AC Q96TF2
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Somatostatin receptor 2B.
GN SSTR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20084417; PubMed=10619399;
RA Petersen S., Rasch A.C., Presch S., Bell F.U., Schulte H.M.;
RT "Genomic structure and transcriptional regulation of the human
RT somatostatin receptor type 2."
RL MOL. Cell. Endocrinol. 157:75-85(1999).
DR Interpro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PROSITE: PS00237; G_PROTEIN_RECPE_FL_1; UNKNOWN_1.
DR PROSITE: PS0262; G_PROTEIN_RECPE_FL_2; 1.
SQ SEQUENCE 356 AA; 40006 MW; D10FA237FAED61F3 CRC64;

Query Match 23.3%; Score 515.5; DB 4; Length 356;
Best Local Similarity 31.0%; Pred. No. 7e-36;
Matches 110; Conservative 77; Mismatches 123; Indels 45; Gaps 9;

QY 71 DLEASLPTGPNASNTSDGPNLTSAGSPPTGTSISYINIMPSVEGTLICLGIGNSTV 130
D 20 DLNGSVST--NTSNQTEPYDLS-----NAVLTFFYFVVCIIIGCGMTLV 64
QY 131 IFVAVKSKLHMCNNPDIFFINLSVVDLFLGMPF-----MIHOLMGNGVWHFEGTM 194
D 65 IYVILRYAKM--KTTNIIYILNLAIDLEMLGLPFLAMOVAVH-----WPFKAL 114
QY 185 CCLITLAMDANSQETSTYILTAMADRYLATVHPISSTKRRPSVATLYCLMLASFISI 244
D 115 CRYVMTVDGINSQETSTYILTAMADRYLATVHPISSTKRRPSVATLYCLMLASFISI 174

QY 245 TPWLVARLIPFGAVGCGIRLPNPDLDY-WFTLYOFLAFALPFPVITAAVRIILOR 303
D 175 LPIMYAGLSRNMONGRSSCTINMPGEGAMTYGFIITFLGVLVLTICLCYLFITIK 234
QY 304 MTSSVAPASQSRIRLTKRVRTAIAICLVFVCWAPYVQLTQLSIS-RPTLFVLY 362
D 235 VKSSGIRVSSKRRKSKRYTRMWSIVAVFIFCMLPFIYFNVSVMASIPFALKMGF 294
QY 363 NAAISLGYANCLNPFYIVLCETFRK--RVLVSYPKPAAGQLRANSNAOTADE 414
D 295 DFPVYLYTANSCANPIIYAFISDNFRKSFQNVLCVK-----YDNKSGEE 340

RESULT 10
091Y73 PRELIMINARY; PRT; 346 AA.

AC 091Y73
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Somatostatin receptor type 2.
GN SSTR2 OR SSTR2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129; TISSUE=LIVER;
RX MEDLINE=21201198; PubMed=11278805;
RA Puente E., Saint-Laurent N., Torrisani J., Furet C., Schally A.V.,
RA Vayssie N., Buscail L., Susini C.;
RT "Transcriptional Activation of Mouse sstr2 Somatostatin Receptor
RT Promoter by Transforming Growth Factor-beta. Involvement of Smad4."
RL J. Biol. Chem. 276:13461-13468(2001).
DR EMBL: AF008914; AAD01420.1; -.
DR MGD: MGI:98328; SSTR2.
DR Interpro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PROSITE: PS00237; G_PROTEIN_RECPE_FL_1; UNKNOWN_1.
DR PROSITE: PS0262; G_PROTEIN_RECPE_FL_2; 1.
KW Receptor.
SQ SEQUENCE 346 AA; 38586 MW; D7A20AEC1371C400 CRC64;

Query Match 23.3%; Score 515; DB 11; Length 346;
Best Local Similarity 31.2%; Pred. No. 7.5e-36;
Matches 115; Conservative 76; Mismatches 130; Indels 48; Gaps 11;

QY 62 EQATGTG-WA----DLEASLPTGPNASNTSDGPNLTSAGSPPTGTSISYINIMPSVF 116
D 6 EQLNGSQVWSSPPDLNGLSPS--NCSNOTEPYDLS-----NAVLTFFY 50
QY 117 GTICLLIGNSTVYIFAVKSKLHMCNNPDIFFINLSVVDLFLGMPF-----MIH 170
D 51 FVYCVGCGMTLVYILRYAKM--KTTNIIYILNLAIDLEMLGLPFLAMOVAVH 107
QY 171 QLMGNGVWHFEGTCTLTADANSQETSTYILTAMADRYLATVHPISSTKRRSVAT 230
D 108 -----WPFKALCRVVMFTDGINQETSTYILTAMADRYLATVHPISSTKRRSVAT 160
QY 231 IYICLMLASFISTPWLVARLIPFGAVGCGIRLPNPDLDY-WFTLYOFLAFALP 289
D 161 MIVNAVWCVSLVILPIIMYAGLSRNMONGRSSCTINMPGEGAMTYGFIITFLV 220
QY 290 FVYITAAVRIILORNTSSVAPASQSRIRLTKRVRTAIAICLVFVCWAPYVQLTQL 349
D 221 IITICLCYLFITIKKSSGIVGSSKRRKSKRYTRMWSIVAVFIFCMLPFIYFNVS 280
QY 350 SIS-RPTLFVLYNAAISLGYANCLNPFYIVLCETFRKR--VLSYPKPAAGQLRAV 406
D 281 SVAISPTALKMGDFVYLYTANSCANPIIYAFISDNFRKSFQNVLCYKA----- 332
QY 407 SNAOTADEE 415


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QY 121 LLAGTNSVYIFAVKSKLHMCNVPDIFIIINLSVVDLFLGMPFMIHOLMGVWHF 180
Db 63 AVGLCGNALVYVILRYAKM---KTYINIIYILNLAVADVLCMLSLPEIAQL-SLHWPF 118
QY 181 GETWCTLIITAMDANSOFTSTYIILTAIDAIDRYLATVHPISSTKFRKPSVATLVICLMAIS 240
Db 119 GSAICRYVLLTADSNMCFTSIFFLTVMSFDRLAVVHPHKSTKWRKPRMAKSISLAMVYIS 178
QY 241 FISTPYWLARLIPFPGAVGGIRLPNPDLDLW-FTLYOFELAPALPEVVITAAVVR 299
Db 179 LLVNLPMTISGVVKKNEARTCTMLMPEPONTYYTVFIFYTFMGFFLPLIYICMCIYL 238
QY 300 ILQRMSSVAPASQRSIRLRTKRYRTAIAICLVFVCNAPYYVLOLTQISIRPTLTFV 359
Db 239 IVIKVSSGMRYCCKRRKRSERKVTSMVSIWVVVEVLWCLPFYVENVTSTGTVPPTPVL 298
QY 360 -LYNMAISLGYANSCINPFYIVLCETFRKL--VLVSK 396
Db 299 KSTFDFVYVVLGYANSCANPILYAFLLSDNFKRSFQNVLCCK 338
```

Search completed: February 13, 2003, 14:00:16
Job time : 30.2615 secs


```
OY 361 LYNAISLGYANCLNPFYIVLCEFRKRLVSVKPAAGQLRAVSNQTADEERTESK 420
|||
Db 361 LYNAISLGYANCLNPFYIVLCEFRKRLVSVKPAAGQLRAVSNQTADEERTESK 420

OY 421 GT 422
||
Db 421 GT 422

RESULT 2
US-09-478-601-2
; Sequence 2, Application US/09478601
; Patent No. 6221616
; GENERAL INFORMATION:
; APPLICANT: Salton, John A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Nagorny, Raisa
; APPLICANT: Wilson, Amy E.
; TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
; FILE REFERENCE: 574532/JPM
; CURRENT APPLICATION NUMBER: US/09/478,601
; EARLIER FILING DATE: 2000-01-06
; EARLIER APPLICATION NUMBER: 09/224,426
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 2
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-478-601-2

Query Match 99.5%; Score 2200; DB 4; Length 422;
Best Local Similarity 99.5%; Pred. No. 2,1e-172;
Matches 420; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 MSYGAARKGVGRAVGLGGSGCQATEEDPLPDCGACAPGQGRWRRLPOPAMVEGSSARL 60
|||
Db 1 MSYGAARKGVGRAVGLGGSGCQATEEDPLPDCGACAPGQGRWRRLPOPAMVEGSSARL 60

OY 61 WEQATGTGMADLEASLLPTGPNASNTSDGPNLTSAGSPRTGTSISYINIMPSVFGTTC 120
|||
Db 61 WEQATGTGMADLEASLLPTGPNASNTSDGPNLTSAGSPRTGTSISYINIMPSVFGTTC 120

OY 121 LGIIGNSTVIRAVYKSKSLHMCNNVPDIFIINLSVVDLLFLGPMFMIHQLMGVWHF 180
|||
Db 121 LGIIGNSTVIRAVYKSKSLHMCNNVPDIFIINLSVVDLLFLGPMFMIHQLMGVWHF 180

OY 181 GETMCTLTITAMANDSOFTSTYILITAMAIDRYLATVHPISSTKFRKPSVATLVICLMAIS 240
|||
Db 181 GETMCTLTITAMANDSOFTSTYILITAMAIDRYLATVHPISSTKFRKPSVATLVICLMAIS 240

OY 241 FTSITPVMYLARLIPFGGAVGCGIRLPNDTDLTWFTLYOFLFALPFFVITAAVRI 300
|||
Db 241 FTSITPVMYLARLIPFGGAVGCGIRLPNDTDLTWFTLYOFLFALPFFVITAAVRI 300

OY 301 LQRMSSVAPASQSRIRLRTKRYTRTAIAICLVFVCMAPIYVLOLTQLSISRPILTFEY 360
|||
Db 301 LQRMSSVAPASQSRIRLRTKRYTRTAIAICLVFVCMAPIYVLOLTQLSISRPILTFEY 360

OY 361 LYNAISLGYANCLNPFYIVLCEFRKRLVSVKPAAGQLRAVSNQTADEERTESK 420
|||
Db 361 LYNAISLGYANCLNPFYIVLCEFRKRLVSVKPAAGQLRAVSNQTADEERTESK 420

OY 421 GT 422
||
Db 421 GT 422

RESULT 3
US-09-478-602-2
; Sequence 2, Application US/09478602
```

```
; Patent No. 6291195
; GENERAL INFORMATION:
; APPLICANT: Salton, John A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Nagorny, Raisa
; APPLICANT: Wilson, Amy E.
; TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
; FILE REFERENCE: 574532/JPM
; CURRENT APPLICATION NUMBER: US/09/478,602
; EARLIER FILING DATE: 2000-01-06
; EARLIER APPLICATION NUMBER: 09/224,426
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 2
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-478-602-2

Query Match 99.5%; Score 2200; DB 4; Length 422;
Best Local Similarity 99.5%; Pred. No. 2,1e-172;
Matches 420; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 MSYGAARKGVGRAVGLGGSGCQATEEDPLPDCGACAPGQGRWRRLPOPAMVEGSSARL 60
|||
Db 1 MSYGAARKGVGRAVGLGGSGCQATEEDPLPDCGACAPGQGRWRRLPOPAMVEGSSARL 60

OY 61 WEQATGTGMADLEASLLPTGPNASNTSDGPNLTSAGSPRTGTSISYINIMPSVFGTTC 120
|||
Db 61 WEQATGTGMADLEASLLPTGPNASNTSDGPNLTSAGSPRTGTSISYINIMPSVFGTTC 120

OY 121 LGIIGNSTVIRAVYKSKSLHMCNNVPDIFIINLSVVDLLFLGPMFMIHQLMGVWHF 180
|||
Db 121 LGIIGNSTVIRAVYKSKSLHMCNNVPDIFIINLSVVDLLFLGPMFMIHQLMGVWHF 180

OY 181 GETMCTLTITAMANDSOFTSTYILITAMAIDRYLATVHPISSTKFRKPSVATLVICLMAIS 240
|||
Db 181 GETMCTLTITAMANDSOFTSTYILITAMAIDRYLATVHPISSTKFRKPSVATLVICLMAIS 240

OY 241 FTSITPVMYLARLIPFGGAVGCGIRLPNDTDLTWFTLYOFLFALPFFVITAAVRI 300
|||
Db 241 FTSITPVMYLARLIPFGGAVGCGIRLPNDTDLTWFTLYOFLFALPFFVITAAVRI 300

OY 301 LQRMSSVAPASQSRIRLRTKRYTRTAIAICLVFVCMAPIYVLOLTQLSISRPILTFEY 360
|||
Db 301 LQRMSSVAPASQSRIRLRTKRYTRTAIAICLVFVCMAPIYVLOLTQLSISRPILTFEY 360

OY 361 LYNAISLGYANCLNPFYIVLCEFRKRLVSVKPAAGQLRAVSNQTADEERTESK 420
|||
Db 361 LYNAISLGYANCLNPFYIVLCEFRKRLVSVKPAAGQLRAVSNQTADEERTESK 420

OY 421 GT 422
||
Db 421 GT 422

RESULT 4
US-08-984-288-2
; Sequence 2, Application US/08984288
; Patent No. 603872
; GENERAL INFORMATION:
; APPLICANT: BERGSM, DEK
; APPLICANT: ELIS, CATHERINE
; TITLE OF INVENTION: NOVEL HUMAN 11CB SPLICE V
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
```



```

; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION NUMBER: US/08/984,288
; APPLICATION NUMBER: 23,031
; FILING DATE: 03-DEC-1997
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 60/032,763
; FILING DATE: 11-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET INFORMATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-984-288-2

Query Match      82.3%; Score 1819; DB 3; Length 353;
Best Local Similarity 100.0%; Pred. No. 2.5e-141;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 71 DLEASLPTGPNASNTSDGPDNLTSAGSPRTGSIYINIIIMPVSFGTICLLGIIGNSTV 130
DB 2 DLEASLPTGPNASNTSDGPDNLTSAGSPRTGSIYINIIIMPVSFGTICLLGIIGNSTV 61
QY 131 IFAYVAKSKLHMCNNVPDIFIINLSVVDLLFLGMPFMIHOLMGVWHFGEYTCILITA 190
DB 62 IFAYVAKSKLHMCNNVPDIFIINLSVVDLLFLGMPFMIHOLMGVWHFGEYTCILITA 121
QY 191 MDANSOFTSTYLLTAMADRYLATVHPISSTFKRPSVATLVICLLMALSFISTPWLX 250
DB 122 MDANSOFTSTYLLTAMADRYLATVHPISSTFKRPSVATLVICLLMALSFISTPWLX 181
QY 251 ARLIPEPGGAVCGIRLPNPDLDLWFTLYQFPLAFALPFVYITAAVYRIIQRTSSVAP 310
DB 182 ARLIPEPGGAVCGIRLPNPDLDLWFTLYQFPLAFALPFVYITAAVYRIIQRTSSVAP 241
QY 311 ASORSIRLRTKRTKRTAIAICLVFFVCNAPYYVQLTQLSISRPITLVYLYNNAISLGY 370
DB 242 ASORSIRLRTKRTKRTAIAICLVFFVCNAPYYVQLTQLSISRPITLVYLYNNAISLGY 301
QY 371 ANSCLMPFYIYLCETFRKRLVLSYKPAAGOLRAVSNAGTADERTESKGT 422
DB 302 ANSCLMPFYIYLCETFRKRLVLSYKPAAGOLRAVSNAGTADERTESKGT 353

RESULT 5
US-09-218-467B-2
; Sequence 2, Application US/09218467B
; Patent No. 6362326
; GENERAL INFORMATION:
; APPLICANT: SATHE, GANESH
; APPLICANT: ELLIS, CATHERINE
; APPLICANT: HALSEY, WENDY
; APPLICANT: BERGMA, DEREK
; TITLE OF INVENTION: 11cby Genomic Sequence
; FILE REFERENCE: GP-50010
; CURRENT APPLICATION NUMBER: US/09/218,467B
; CURRENT FILING DATE: 2001-06-22
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; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 353
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; US-09-218-467B-2

Query Match      82.3%; Score 1819; DB 4; Length 353;
Best Local Similarity 100.0%; Pred. No. 2.5e-141;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 71 DLEASLPTGPNASNTSDGPDNLTSAGSPRTGSIYINIIIMPVSFGTICLLGIIGNSTV 130
DB 2 DLEASLPTGPNASNTSDGPDNLTSAGSPRTGSIYINIIIMPVSFGTICLLGIIGNSTV 61
QY 131 IFAYVAKSKLHMCNNVPDIFIINLSVVDLLFLGMPFMIHOLMGVWHFGEYTCILITA 190
DB 62 IFAYVAKSKLHMCNNVPDIFIINLSVVDLLFLGMPFMIHOLMGVWHFGEYTCILITA 121
QY 191 MDANSOFTSTYLLTAMADRYLATVHPISSTFKRPSVATLVICLLMALSFISTPWLX 250
DB 122 MDANSOFTSTYLLTAMADRYLATVHPISSTFKRPSVATLVICLLMALSFISTPWLX 181
QY 251 ARLIPEPGGAVCGIRLPNPDLDLWFTLYQFPLAFALPFVYITAAVYRIIQRTSSVAP 310
DB 182 ARLIPEPGGAVCGIRLPNPDLDLWFTLYQFPLAFALPFVYITAAVYRIIQRTSSVAP 241
QY 311 ASORSIRLRTKRTKRTAIAICLVFFVCNAPYYVQLTQLSISRPITLVYLYNNAISLGY 370
DB 242 ASORSIRLRTKRTKRTAIAICLVFFVCNAPYYVQLTQLSISRPITLVYLYNNAISLGY 301
QY 371 ANSCLMPFYIYLCETFRKRLVLSYKPAAGOLRAVSNAGTADERTESKGT 422
DB 302 ANSCLMPFYIYLCETFRKRLVLSYKPAAGOLRAVSNAGTADERTESKGT 353

RESULT 6
US-09-224-426-4
; Sequence 4, Application US/09224426
; Patent No. 6221613
; GENERAL INFORMATION:
; APPLICANT: Salton, John A
; APPLICANT: Laz, Thomas M
; APPLICANT: Nagorny, Raisa
; APPLICANT: Wilson, Amy E
; TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
; FILE REFERENCE: 57453/CPW/CJB
; CURRENT APPLICATION NUMBER: US/09/224,426
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 4
; LENGTH: 353
; TYPE: PRT
; ORGANISM: rat
; US-09-224-426-4

Query Match      79.5%; Score 1758; DB 4; Length 353;
Best Local Similarity 96.0%; Pred. No. 2.4e-136;
Matches 338; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 71 DLEASLPTGPNASNTSDGPDNLTSAGSPRTGSIYINIIIMPVSFGTICLLGIIGNSTV 130
DB 2 DLEASLPTGPNASNTSDGPDNLTSAGSPRTGSIYINIIIMPVSFGTICLLGIIGNSTV 61
QY 131 IFAYVAKSKLHMCNNVPDIFIINLSVVDLLFLGMPFMIHOLMGVWHFGEYTCILITA 190
DB 62 IFAYVAKSKLHMCNNVPDIFIINLSVVDLLFLGMPFMIHOLMGVWHFGEYTCILITA 121
QY 191 MDANSOFTSTYLLTAMADRYLATVHPISSTFKRPSVATLVICLLMALSFISTPWLX 250
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Db	122	MDANSQFTSYIILTAMTIDRYLATVHPISSTKRRKBSMATVILCLMALNSFISITFWLX	181
Oy	251	ARLPEFGAGVCGCIRLPNPBDLWPEFTLYQFLAFALPEVVTAAVRILQBMSTSVAP	310
Db	182	ARLPEFGAGVCGCIRLPNPBDLWPEFTLYQFLAFALPEVVTAAVYKILQBMSTSVAP	241
Oy	311	ASQSRIRLRTKRVTRTAIAICLVEFCWAPYYVQLTQLSISRPRTLFEVLYLYNAISLGY	370
Db	242	ASQSRIRLRTKRVTRTAIAICLVEFCWAPYYVQLTQLSISRPRTLFEVLYLYNAISLGY	301
Oy	371	ANSCINPEVYIVLCETPRKRLYLSVKRAAQQLRAVSNAGTADDERPESKGT	422
Db	302	ANSCINPEVYIVLCETPRKRLYLSVKRAAQQLTVAASNAGTADDERPESKGT	353

```

RESULT 7
US-09-478-601-4
; Sequence 4, Application US/09478601
; Patent No. 62216
; GENERAL INFORMATION:
; APPLICANT: Salon, John A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Nagorny, Ralsa
; APPLICANT: Wilson, Amy E.
; TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
; TITLE OF INVENTION: Receptor (Mcl1) And Uses Thereof
; FILE REFERENCE: 574532.NPW
; CURRENT APPLICATION NUMBER: US/09/478,601
; CURRENT FILING DATE: 2000-01-06
; EARLIER APPLICATION NUMBER: 09/224,426
; EARLIER FILING DATE: 1998-12-31
; NUMBER OF SEQ. ID NOS.: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ. ID NO. 4
;
; LENGTH: 353
;
; TYPE: PR1
; ORGANISM: Rattus norvegicus
US-09-478-601-4

```

Query Match	79.5%;	Score 1758;	DB 4;	Length 353;
Best Local Similarity	96.0%;	Pred. No. 2.4e-136;		
Matches 338: Conservative	6;	Mismatches 8;	Indels 0;	Gaps 0.

[illegible]

RESULT 8
US-09-478-602-4
; Sequence 4, Application US/09478602
; Patent No. 6291195
; GENERAL INFORMATION:

APPLICANT: Salom, John A.
 APPLICANT: Iaz, Thomas M.
 APPLICANT: Nagorny, Raisa
 APPLICANT: Wilson, Amy E.
 TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
 TITLE OF INVENTION: Receptor (MC1R) And Uses Thereof
 FILE REFERENCE: 57453Y/JPM
 CURRENT APPLICATION NUMBER: US/09/478,602
 CURRENT FILING DATE: 2000-01-06
 EARLIER APPLICATION NUMBER: 09/224,426
 EARLIER FILING DATE: 1998-12-31
 NUMBER OF SEQ. ID NOS: 15
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 4
 LENGTH: 353
 TYPE: PRT
 ORGANISM: Rattus norvegicus
 US-09-478-602-4

Query Match 79.5%; Score 1758; DB 4; Length 353;

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Best Local Similarity 50.00%; FREQ. NO: 270 (25%)
Matches 338; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

```

[illegible]

RESULT 9
US-08-602-809-2
: Sequence 2, Application US/08602809

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1 / GENERAL INFORMATION:
2 /
3 / APPLICANT: BERGSMÄ, DEREK
4 /
5 / APPLICANT: ELLIS, CATHERINE
6 /
7 / TITLE OF INVENTION: HUMAN SOMATOSTATIN-LIKE R
8 /
9 / TITLE OF INVENTION: RECEPTOR
10 /
11 / NUMBER OF SEQUENCES: 3
12 /
13 / CORRESPONDENCE ADDRESS:
14 /
15 / ADDRESSEE: Ratner & Prestia
16 /
17 / STREET: P.O. Box 980
18 /
19 / CITY: Valley Forge
20 /
21 / STATE: PA
22 /
23 / COUNTRY: US
24 /
25 / ZIP: 19482-0980
26 /
27 / COMPUTER READABLE FORM:
28 /
29 / MEDIUM TYPE: Diskette
30 /
31 / COMPUTER: IBM Compatible
32 /
33 / OPERATING SYSTEM: DOS
34 /
35 / SOFTWARE: FASTSEQ for Windows Version 2.0
36 /
37 / CURRENT APPLICATION DATA:
38 /
39 / APPLICATION NUMBER: US/08/602,809
40 /
41 / FILING DATE: 13-JUN-1997

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1 MEDIUM TYPE: floppy disk
2
3 COMPUTER: IBM PC compatible
4
5 OPERATING SYSTEM: PC-DOS/MS-DOS
6
7 SOFTWARE: PatentIn Release #1.0, Version #1.25
8
9 CURRENT APPLICATION DATA:
10
11 APPLICATION NUMBER: PCT/US95/16472
12
13 FILING DATE:
14
15 CLASSIFICATION:
16
17 ATTORNEY/AGENT INFORMATION:
18
19 NAME: Sutton, Jeffrey A
20
21 REGISTRATION NUMBER: 34,028
22
23 REFERENCE/DOCKET NUMBER: P50277
24
25 TELECOMMUNICATION INFORMATION:
26
27 TELEPHONE: 610 270 5024
28
29 TELEFAX: 610 270 5090
30
31 INFORMATION FOR SEQ ID NO: 2:
32
33 SEQUENCE CHARACTERISTICS:
34
35 LENGTH: 400 amino acids
36
37 TYPE: amino acid
38
39 STRANDEDNESS: single
40
41 TOPOLOGY: linear
42
43 MOLECULE TYPE: protein
44
45 PCT-US95-16472-2

```

[illegible]

RESULT 11
US-08-120-601B-9
Sequence 9, Application US/08120601B
Patent No. 6235496
GENERAL INFORMATION:
APPLICANT: Yu, Lei
TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND
METHODS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210

```

1 COMPUTER READABLE FORM:
2 MEDIUM TYPE: Floppy disk
3 COMPUTER: IBM PC compatible
4 OPERATING SYSTEM: PC-DOS/MS-DOS
5 SOFTWARE: PatentIn Release #1.0, Version #1.30
6
7 CURRENT APPLICATION DATA:
8 APPLICATION NUMBER: US/08/120,601B
9 FILING DATE: 13-SEP-1993
10 CLASSIFICATION: 435
11 ATTORNEY/AGENT INFORMATION:
12 NAME: Wilson, Mark B.
13 REGISTRATION NUMBER: 37,259
14 REFERENCE/DOCKET NUMBER: INDA.002
15 TELECOMMUNICATION INFORMATION:
16 TELEPHONE: 512/418-5000
17 TELEFAX: 512/474-7577
18 INFORMATION FOR SEQ ID NO: 9:
19 SEQUENCE CHARACTERISTICS:
20 LENGTH: 369 amino acids
21 TYPE: amino acid
22 STRANDEDNESS:
23 TOPOLOGY: linear
24
25 US-08-120-601B-9

```

ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,103
FILING DATE: 05-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/816,283
FILING DATE: 01-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: ARCD:144
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 369 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-417-103-8

Query Match 24.1%; Score 532; DB 1; Length 369;
Best Local Similarity 31.7%; Pred. No. 4,9e-36;
Matches 118; Conservative 76; Mismatches 132; Indels 46; Gaps 10;

QY 62 EQATGQ-WA-----DEASLPTGPNASNTSDGPNLTSAGSPPTGSIYINIMPSVFI 116
DB 6 EQANGSVWVSPDLNGLSGPS--NGSNQTEPYIDLT-----NAVLFTFYVCIIGLGTLY 50
QY 117 GTICLLGIIONSTVIFAVVKKSLHMCNNVDPFIILNSVVDLFLGMPF-----MIH 170
DB 51 FVVCVGLCGNTLVIVILRYAKM--KITNNIYLINLAIDELFMLGFLPMQVALVH 107
QY 171 QLMNGVWHFGEIMCTILITAMDANSQFTSTYIITAMIDRYLATVPISTFRKPSVAT 230
DB 108 -----WPGKAIQCRVMTVDISINQFTSIFCLTVMSIDRYLAIVHPIKSAKWRPRPAK 160
QY 231 LVICLWALSIFISITPVMLYARLIPPGAVGCGIRLPNPDLDL-WFTLYOFFLAFLP 289
DB 161 MINVAVMCVSLVILPIMYAGLRSNQWGRSSCTIMWPGSGAWYTGFIYAFILGLVLP 220
QY 290 FVYTATAYVRILOMTSSVAPASQBSIRLRTKRVFTALAIQVFFVCNAPYVYLQTL 349
DB 221 LTIICLCYLFITIKVSSGIRVSSKRRKSEKVTMVSIVAVFIFCWLPEYIFNVSSV 280
QY 350 SIS-RPTLTFVLYLNAISIGVANSCLNPFVYIVLCETFRKRLVLSVKPAAGOLRAVSN 408
DB 281 SVASIPPALKGMDFEVLITVANSCLNPFVYIVLCETFRKRLVLSVKPAAGOLRAVSN 408
QY 409 AQTADERTESK 420
DB 333 SGTEGERSDSK 344

RESULT 14
US-07-816-283-6
; Sequence 6, Application US/07816283
; Patent No. 5436155
; GENERAL INFORMATION:
; APPLICANT: Bell, Graeme I.
; APPLICANT: Yamada, Yuichiro
; APPLICANT: Saino, Susumu
; TITLE OF INVENTION: SOMATOSTATIN RECEPTORS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee

STREET: PO Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/816,283
FILING DATE: 19911231
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McDaniel, C. Steven
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-787-1400
TELEFAX: 713-789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 369 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-816-283-6

Query Match 24.0%; Score 530.5; DB 1; Length 369;
Best Local Similarity 31.8%; Pred. No. 6,5e-36;
Matches 114; Conservative 75; Mismatches 128; Indels 41; Gaps 8;

QY 71 DEASLPTGPNASNTSDGPNLTSAGSPPTGSIYINIMPSVFI 130
DB 20 DLNGSVVST--MNSNTEPYIDLT-----NAVLFTFYVCIIGLGTLY 64
QY 131 IFVAVKSKLHMCNNVDPFIILNSVVDLFLGMPF-----MIHOLMNGVWHFGETM 184
DB 65 IYVILRYAKM--KITNNIYLINLAIDELFMLGFLPMQVALVH-----WPGKAI 114
QY 185 CITITAMDANSQFTSTYIITAMIDRYLATVPISTFRKPSVATLYCLMALSFISI 244
DB 115 CRVAVMTVDISINQFTSIFCLTVMSIDRYLAIVHPIKSAKWRPRPAKMTMAWCVSLVI 174
QY 245 TPVMLYARLIPPGAVGCGIRLPNPDLDL-WFTLYOFFLAFLP 303
DB 175 LPIMTYAGLRSNQWGRSSCTIMWPGSGAWYTGFIYAFILGLVLP 234
QY 304 MTSVAPASQBSIRLRTKRVFTALAIQVFFVCNAPYVYLQTL 362
DB 235 VKSSGIRVSSKRRKSEKVTMVSIVAVFIFCWLPEYIFNVSSVMAISIPALKGMF 294
QY 363 NAISIGVANSCLNPFVYIVLCETFRKRLVLSVKPAAGOLRAVSN 420
DB 295 DFVYVLTVANSCLNPFVYIVLCETFRKRLVLSVKPAAGOLRAVSN 420

RESULT 15
US-08-417-103-6
; Sequence 6, Application US/08417103
; Patent No. 5732299
; GENERAL INFORMATION:
; APPLICANT: Bell, Graeme I.
; APPLICANT: Yamada, Yuichiro
; APPLICANT: Saino, Susumu
; TITLE OF INVENTION: SOMATOSTATIN RECEPTORS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America

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OM protein - protein search, using sw model

Run on: February 13, 2003, 13:55:16 : Search time 29.2615 Seconds
(without alignments)
2971.547 Million cell updates/sec

Title: US-09-885-478-2

Perfect score: 2212
Sequence: 1 MSVGMKKKGVGRAVIGGGS.....LRVSNAGTADERTESKGT 422

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SP:REMBL_21:*
2: SP:archaea:*
3: SP:bacteria:*
4: SP:fungi:*
5: SP:human:*
6: SP:invertebrate:*
7: SP:mammal:*
8: SP:mhc:*
9: SP:organelle:*
10: SP:phage:*
11: SP:plant:*
12: SP:rodent:*
13: SP:virus:*
14: SP:vertebrate:*
15: SP:unclassified:*
16: SP:viirus:*
17: SP:bacteriap:*
17: SP:archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2212	100.0	422	4	Q9BV08
2	2207	99.8	422	4	Q96S47
3	601	27.2	121	6	Q9M201
4	565.5	25.6	340	4	Q969V1
5	559.5	25.3	340	4	Q9BAX8
6	559.5	25.3	340	6	Q8S054
7	523	23.6	370	13	Q8UWU5
8	521.3	23.6	346	4	Q96GE0
9	516.5	23.3	356	4	Q96TF2
10	516	22.3	346	11	Q91V73
11	502.5	22.7	367	13	Q9PVG0
12	499.5	22.6	367	13	Q9PVP9
13	497	22.5	315	6	Q9GKP7
14	494.5	22.4	346	6	Q9SKS6
15	487	22.0	380	13	Q9DG06
16	469	21.2	390	13	Q8GQ04

17	457	20.7	385	11	Q9UK40	Q9JK40 mus musculus
18	453.5	20.5	390	11	Q8V171	Q8V171 mus musculus
19	453.5	20.5	391	11	Q8V170	Q8V170 mus musculus
20	453.5	20.5	393	11	Q9R1M0	Q9R1M0 mus musculus
21	453.5	20.5	401	11	Q9R1L9	Q9R1L9 mus musculus
22	453.5	20.5	409	11	Q8V169	Q8V169 mus musculus
23	453.5	20.5	438	11	Q9R0D1	Q9R0D1 mus musculus
24	453.5	20.5	444	11	Q9J1Y1	Q9J1Y1 mus musculus
25	448	20.3	454	4	Q9H573	Q9H573 homo sapien
26	443	20.0	400	6	Q9SM54	Q9SM54 macaca fasc
27	435	19.7	383	13	Q42324	Q42324 catostomus
28	422.5	19.1	377	13	Q98U14	Q98U14 brachydanio
29	422	19.1	384	13	Q98U11	Q98U11 brachydanio
30	412	18.6	451	5	Q9V0V1	Q9V0V1 drosophila
31	407	18.4	373	13	Q57585	Q57585 brachydanio
32	402.5	18.2	272	4	Q9BWH1	Q9BWH1 homo sapien
33	393	17.8	362	11	Q8V174	Q8V174 mus musculus
34	392	17.7	362	11	Q9J1N4	Q9J1N4 ratu mus norv
35	373	16.9	380	5	Q9NPF2	Q9NPF2 lymnaea sta
36	370.5	16.7	393	5	Q9V0D0	Q9V0D0 drosophila
37	367	16.6	291	11	Q91Z24	Q91Z24 mus musculus
38	367	16.6	325	11	Q8V1N4	Q8V1N4 mus musculus
39	367	16.6	330	11	Q8V1P1	Q8V1P1 mus musculus
40	367	16.6	370	11	Q8V1P0	Q8V1P0 mus musculus
41	366	16.5	380	5	Q9NPF1	Q9NPF1 lymnaea sta
42	364.5	16.5	380	5	Q9NPF3	Q9NPF3 lymnaea sta
43	363	16.4	380	5	Q9NEV0	Q9NEV0 lymnaea sta
44	361.5	16.3	359	13	Q9PVY7	Q9PVY7 anguilla an
45	361	16.3	423	5	Q964D4	Q964D4 periplaneta

ALIGNMENTS

RESULT 1
ID Q9BV08 PRELIMINARY; PRT: 422 AA.

AC Q9BV08:
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Similar to G protein-coupled receptor 24 (Hypothetical 46.0 kDa protein).
DE OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI-TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC001736; AAH01736.1; -;
DR EMBL: BC021146; AAH21146.1; -;
DR InterPro: IPR00276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PRO1559; DUFFYANTIGEN.
DR PRINTS: PRO0237; GPCRHOPOPSN.
DR PROSITE: PSS0262; G-PROTEIN_RECPT_FL_2; 1.
KW Receptor. Hypothetical protein.
SQ SEQUENCE 422 AA; 45963 MW; 86A9F398B5D5F397 CRC64;

Query Match 100.0%; Score 2212; DB 4; Length 422;

Best Local Similarity 100.0%; Pred. No. 4, 3e-183;

Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSVGMKKKGVGRAVIGGSGCATIEDPLPDGACAPGGGRRRLPQPAWEGSSARL 60
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Db      1 MSYGAMKKGAVGAVGLGGSGCAATEEDPLPDGCACAPGGGGRWRRLPQPAWEGSSARL 60
QY      61 WEQATGTGMDLEASLLPTGPNASNTSDGPDNLTSAGSPPRGTSISTYINIMPSVFGTIC 120
        |||
Db      61 WEQATGTGMDLEASLLPTGPNASNTSDGPDNLTSAGSPPRGTSISTYINIMPSVFGTIC 120
QY      121 LGGTIGNSTVFAVAVKSKLHMKNVDPDIFINLSYVDLLFLGMPFMHQLMGNGVMHF 180
        |||
Db      121 LGGTIGNSTVFAVAVKSKLHMKNVDPDIFINLSYVDLLFLGMPFMHQLMGNGVMHF 180
QY      181 GETMCTLTAMDANSOFTSTYILITAMADRYLATVHPISSTFKRPSVATLVICLLMALS 240
        |||
Db      181 GETMCTLTAMDANSOFTSTYILITAMADRYLATVHPISSTFKRPSVATLVICLLMALS 240
QY      241 FISTPFWLVARLIPPEGAVGCGIRLPNPDLDLYMFTLYQFLAFLPFWVITAAYVRI 300
        |||
Db      241 FISTPFWLVARLIPPEGAVGCGIRLPNPDLDLYMFTLYQFLAFLPFWVITAAYVRI 300
QY      301 LQRMSSVAPASORSIRLRTKRVTRTAIAICLVFVCMAPIYYQLTOLISRPDLTFVY 360
        |||
Db      301 LQRMSSVAPASORSIRLRTKRVTRTAIAICLVFVCMAPIYYQLTOLISRPDLTFVY 360
QY      361 LYNAAISLGYANSCINPFIYIVLCETFRKRLVLSVKPAAGQLRAVSNAGTADERTESK 420
        |||
Db      361 LYNAAISLGYANSCINPFIYIVLCETFRKRLVLSVKPAAGQLRAVSNAGTADERTESK 420
QY      421 GT 422
        ||
Db      421 GT 422

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RESULT 2

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ID      096S47      PRELIMINARY;      PRT;      422 AA.
AC      096S47;
DT      01-DEC-2001 (TREMBLrel. 19, Created)
DT      01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT      01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE      Somatostatin receptor-like protein.
GN      SLC-1.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Sugo T., Mori M.;
RL      Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RP      SEQUENCE FROM N.A.
RA      MEDLINE=99373129; PubMed=10441476;
RA      Shimomura Y., Mori M., Sugo T., Ishibashi Y., Abe M., Kurokawa T.,
RA      Onda H., Nishimura O., Sumino Y., Fujino M.;
RT      "Isolation and identification of melanin-concentrating hormone as the
RT      endogenous ligand of the SLC-1 receptor.";
RL      Biochem. Biophys. Res. Commun. 261:622-626 (1999).
DR      EMBL: AB063174; BAB60890.1; -.
DR      InterPro: IPR000276; GPCR_Rhodopsn.
DR      Pfam: PF00001; 7tm_1; 1.
DR      PRINTS: PR01559; DDFEYATIGEN.
DR      PROSITE: PS50262; G_PROTEIN_RECPEP_F1_2; 1.
KW      Receptor.
SQ      SEQUENCE 422 AA; 45962 MW; 3986919A18183818 CRC64;

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Query Match 99.8%; Score 2207; DB 4; Length 422;
 Best Local Similarity 99.8%; Pred. No. 1.2e-182;
 Matches 421; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY      1 MSYGAMKKGAVGAVGLGGSGCAATEEDPLPDGCACAPGGGGRWRRLPQPAWEGSSARL 60
        |||
Db      1 MSYGAMKKGAVGAVGLGGSGCAATEEDPLPDGCACAPGGGGRWRRLPQPAWEGSSARL 60
QY      61 WEQATGTGMDLEASLLPTGPNASNTSDGPDNLTSAGSPPRGTSISTYINIMPSVFGTIC 120

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```

Db      61 WEQATGTGMDLEASLLPTGPNASNTSDGPDNLTSAGSPPRGTSISTYINIMPSVFGTIC 120
QY      121 LGGTIGNSTVFAVAVKSKLHMKNVDPDIFINLSYVDLLFLGMPFMHQLMGNGVMHF 180
        |||
Db      121 LGGTIGNSTVFAVAVKSKLHMKNVDPDIFINLSYVDLLFLGMPFMHQLMGNGVMHF 180
QY      181 GETMCTLTAMDANSOFTSTYILITAMADRYLATVHPISSTFKRPSVATLVICLLMALS 240
        |||
Db      181 GETMCTLTAMDANSOFTSTYILITAMADRYLATVHPISSTFKRPSVATLVICLLMALS 240
QY      241 FISTPFWLVARLIPPEGAVGCGIRLPNPDLDLYMFTLYQFLAFLPFWVITAAYVRI 300
        |||
Db      241 FISTPFWLVARLIPPEGAVGCGIRLPNPDLDLYMFTLYQFLAFLPFWVITAAYVRI 300
QY      301 LQRMSSVAPASORSIRLRTKRVTRTAIAICLVFVCMAPIYYQLTOLISRPDLTFVY 360
        |||
Db      301 LQRMSSVAPASORSIRLRTKRVTRTAIAICLVFVCMAPIYYQLTOLISRPDLTFVY 360
QY      361 LYNAAISLGYANSCINPFIYIVLCETFRKRLVLSVKPAAGQLRAVSNAGTADERTESK 420
        |||
Db      361 LYNAAISLGYANSCINPFIYIVLCETFRKRLVLSVKPAAGQLRAVSNAGTADERTESK 420
QY      421 GT 422
        ||
Db      421 GT 422

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RESULT 3

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ID      09M201      PRELIMINARY;      PRT;      121 AA.
AC      09M201;
DT      01-OCT-2000 (TREMBLrel. 15, Created)
DT      01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT      01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE      Melanin-concentrating hormone receptor (Fragment).
OS      Sus scrofa (Pig).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX      NCBI_TaxID=96823;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      TISSUE-BRAIN: HYPOTHALAMUS;
RA      Materil R.L.;
RT      "Sus scrofa melanin-concentrating hormone (MCH) receptor.";
RL      Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR      EMBL: AF273611; AAF81827.1; -.
DR      InterPro: IPR000276; GPCR_Rhodopsn.
DR      Pfam: PF00001; 7tm_1; 1.
DR      PRINTS: PR00237; GPCR_RHODOPSN.
DR      PROSITE: PS50262; G_PROTEIN_RECPEP_F1_2; 1.
KW      Receptor.
FT      NON_TER 1
FT      NON_TER 1
SQ      SEQUENCE 121 AA; 13583 MW; 884D8268B6F9F010 CRC64;

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Query Match 27.2%; Score 601; DB 6; Length 121;
 Best Local Similarity 99.2%; Pred. No. 1.9e-44;
 Matches 120; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY      294 TAAVYRIIDRMWSSVAPASORSIRLRTKRVTRTAIAICLVFVCMAPIYYQLTOLISR 353
        |||
Db      1 TAAVYRIIDRMWSSVAPASORSIRLRTKRVTRTAIAICLVFVCMAPIYYQLTOLISR 60
QY      354 PRTTFYLYNNAISLGYANSCINPFIYIVLCETFRKRLVLSVKPAAGQLRAVSNAGTAD 413
        |||
Db      61 PRTTFYLYNNAISLGYANSCINPFIYIVLCETFRKRLVLSVKPAAGQLRAVSNAGTAD 120
QY      414 E 414
        |
Db      121 E 121

```



```

RESULT 4
0969YL ID Q969YL PRELIMINARY; PRT; 340 AA.
AC Q969YL;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE G protein-coupled receptor (Melanin-concentrating hormone 2 receptor)
DE (Melanin-concentrating hormone receptor MCH-R2) (GPRV17).
GN SLR OR GPRV17.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21255282; PubMed=11355873;
RA Mori M., Harada M., Terao Y., Sugo T., Watanabe T., Shimomura Y.,
RA Abe M., Shintani Y., Onda H., Nishimura O., Fujino M.;
RT "Cloning of a novel g protein-coupled receptor, slr, a subtype of the
RT melanin-concentrating hormone receptor."
RL Blochem. Biophys. Res. Commun. 283:1013-1018(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=21309932; PubMed=11404457;
RA Saller A.W., Sano H., Zeng Z., McDonald T.P., Pan J., Pong S.-S.,
RA Felgner S.D., Tan C.P., Fukami T., Iwasa H., Hrenluk D.L.,
RA Morin N.R., Sadowski S.J., Ito M., Ito M., Bansal A., Ky B.,
RA Figueroa D.J., Jiang Q., Austin C.P., MacNeill D.J., Ishihara A.,
RA Ihara M., Kanatani A., Van der Ploeg L.H.T., Howard A.D., Liu Q.;
RT "Identification and characterization of a second melanin-concentrating
RT hormone receptor, MCH-2R."
RL Proc. Natl. Acad. Sci. U.S.A. 98:7564-7569(2001).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21433976; PubMed=11459838;
RA Wang S., Behan J., O'Neill K., Weig B., Fried S., Iaz T., Bayne M.,
RA Gustafson E., Hawes B.E.;
RT "Identification and pharmacological characterization of a novel human
RT melanin-concentrating hormone receptor, MCH-R2."
RL J. Biol. Chem. 276:34604-34670(2001).
RN [4]
RP SEQUENCE FROM N.A.
RA Kurama T., Matsumoto S., Takasaki J., Terai K., Matsumoto M.,
RA Kanohara M., Saito T., Soga T., Saito Y., Oda T., Masuno Y.,
RA Furuichi K.;
RT "Molecular characterization of a novel melanin-concentrating hormone
RT receptor: Evidence of its expression in lateral hypothalamus."
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB060151; BAB5677.1; -
DR EMBL; AY029596; AAK38157.1; -
DR EMBL; AF399937; AAL05528.1; -
DR EMBL; AB058849; BAB87842.1; -
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1; 1
DR PROSITE; PS00237; G_PROTEIN_RECP_FL1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECP_FL2; 1.
DR KW Receptor.
SQ SEQUENCE 340 AA; 38849 MW; 754A302B951FAC6 CRC64;

Query Match 25.6%; Score 565.5; DB 4; Length 340;
Best Local Similarity 37.0%; Pred. No. 8e-41;
Matches 113; Conservative 62; Mismatches 119; Indels 11; Gaps 4;
QY 110 IIMPSVFTCLLIGNSVIFAIVKSKLHMCNNVPDIFINLSVVDLFLFLGMPFI 169
DB 35 VILPSEMIIGICSTGVNGLIVFTIIRSRK---KTVPDYICNLAVADLVHIVGPEFLI 90
QY 170 HQLMNGVYHNGEMTCLITAMDANSOFTSTYILTAMADRYLATVHPISSTFRKPSVA 229
DB 91 HQMARGGEVWFGPLCTITISLDTGONFACSAIMTVMSVDRYALVOPFRILTRMRYKT 150

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QY 230 TLVICLMAISFISIPVWLYARLIPPGAGVCGIRLNPDPDILKWTYQFLAFLP 289
DB 151 IRLNGILMAASFILALPFWYVSKYIKFKGVESGACADLISPD-DVMTYTLITLITFFFP 209
QY 290 FVITAAVYRL-----ORMTSVAAPASORSI-RLRTRVYRTAIALCLVEFVCAPYV 343
DB 210 LPLILVCYILICYTWEMYOQNKRCARCNSVPKQRMKTKMVLVLYVFTLSAPYHV 269
QY 344 LQTLQISRPETLFEVLYNAATSLGANSCLNPFYIYCEIFERRKLVSYPAAQGL 403
DB 270 IQLVNLQHEQPTLAFYGYITLSICLSTASSINPEFLITLSGNFQRLPQIORATEKEI 329
QY 404 RAVSN 408
DB 330 NNMGN 334

RESULT 5
Q9BXA8 ID Q9BXA8 PRELIMINARY; PRT; 340 AA.
AC Q9BXA8;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE G protein-coupled receptor MCH2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21282939; PubMed=11274220;
RA Hill J., Duckworth M., Murdoch P., Rennie G., Sabido-David C.,
RA Ames R.S., Stekeler P., Wilson S., Bergsma D.J., Gloger I.S.,
RA Levy D.S., Chambers J.K., Muir A.I.;
RT "Molecular Cloning and Functional Characterization of MCH2, a Novel
RT Human MCH Receptor."
RL J. Biol. Chem. 276:20125-20129(2001).
DR EMBL; AF347063; AAK32193.1; -
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECP_FL1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECP_FL2; 1.
DR KW Receptor.
SQ SEQUENCE 340 AA; 38803 MW; 95AA3ECB57511AAC CRC64;

Query Match 25.3%; Score 559.5; DB 4; Length 340;
Best Local Similarity 36.7%; Pred. No. 2.6e-40;
Matches 112; Conservative 62; Mismatches 120; Indels 11; Gaps 4;
QY 110 IIMPSVFTCLLIGNSVIFAIVKSKLHMCNNVPDIFINLSVVDLFLFLGMPFI 169
DB 35 VILPSEMIIGICSTGVNGLIVFTIIRSRK---KTVPDYICNLAVADLVHIVGPEFLI 90
QY 170 HQLMNGVYHNGEMTCLITAMDANSOFTSTYILTAMADRYLATVHPISSTFRKPSVA 229
DB 91 HQMARGGEVWFGPLCTITISLDTGONFACSAIMTVMSVDRYALVOPFRILTRMRYKT 150
QY 230 TLVICLMAISFISIPVWLYARLIPPGAGVCGIRLNPDPDILKWTYQFLAFLP 289
DB 151 IRLNGILMAASFILALPFWYVSKYIKFKGVESGACADLISPD-DVMTYTLITLITFFFP 209
QY 290 FVITAAVYRL-----ORMTSVAAPASORSI-RLRTRVYRTAIALCLVEFVCAPYV 343
DB 210 LPLILVCYILICYTWEMYOQNKRCARCNSVPKQYMKTKMVLVLYVFTLSAPYHV 269
QY 344 LQTLQISRPETLFEVLYNAATSLGANSCLNPFYIYCEIFERRKLVSYPAAQGL 403
DB 270 IQLVNLQHEQPTLAFYGYITLSICLSTASSINPEFLITLSGNFQRLPQIORATEKEI 329
QY 404 RAVSN 408

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Db 330 NNMGN 334

RESULT 6

08S054 PRELIMINARY; PRT; 340 AA.

AC 08S054; 01-JUN-2002 (Tremblrel, 21, Created)

DT 01-JUN-2002 (Tremblrel, 21, last sequence update)

DE 01-JUN-2002 (Tremblrel, 21, last annotation update)

GN GPR17.

OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).

OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

OC Cercopithecinae; Macaca.

OX NCBI_TaxID=9541;

RN [1]

RP SEQUENCE FROM N.A.

RA Kurama T., Matsumoto S., Takasaki J., Terai K., Matsumoto M.,

RA Kanohara M., Saito T., Saito Y., Oda T., Masuh Y.,

RA Fuyuchi K.;

RT "Molecular characterization of a novel melanin-concentrating hormone

RT receptor : Evidence of its expression in lateral hypothalamus.";

RU Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB058850; BAB87843.1; .

SQ SEQUENCE 340 AA; 38769 MW; BD22CF1972332439 CRC64;

Query Match 25.3%; Score 559.5; DB 6; Length 340;

Best Local Similarity 36.7%; Pred. No. 2.6e-40;

Matches 112; Conservative 60; Mismatches 122; Indels 11; Gaps 4;

QY 110 IIMSEVETICLLGIGNSTYIFAVYKSKLHMCNNPDIIFINLSVLDLFLGMPFI 169

Db 35 VILPMIGITSTGVNGILLVFIIRSRK---KIVPDIYICNLAVADLVHIGMPFI 90

QY 170 HOLMGVHMFGEWCTITITAMDANSOFTSYITLMAIDRYLATVPISSTKFRPSVA 229

Db 91 HOMAGGEMVFCGLCTITISLDCNQCACAIMTVASVDRIALVQFRLTSMKRRYKT 150

QY 230 TLVLCMLAISPSTIPVWLYARLIPPGAGVGGIRLPNDPDLWFTLYOFELALP 289

Db 151 IRIINGLMAASFILALPWYISKYIKFKDYGSCAFDLTSPD-DVLWFTLYLTITTFPP 209

QY 290 FVITAAAVRLI-----QRMSSVAPASORSI-RLTKRYTRRAICLVEFYCMAPYV 343

Db 210 LPLHVCITLICITWEMYQNKDARCONSPVPRQVMKLFKYLVAVFILSAAPYH 269

QY 344 IQLTQLSISRPFLTFVLYLNAISLGYANSCLPFVYIVLCETFRKRLVSVKPAQGL 403

Db 270 IQLVNLQWEOPTLAFVYGYLSICLSYASSINPFIYLLSGNQRKLPQIGRWVDKEI 329

QY 404 RAVSN 408

Db 330 NNMGN 334

RESULT 7

08UWL5 PRELIMINARY; PRT; 370 AA.

AC 08UWL5; 01-MAR-2002 (Tremblrel, 20, Created)

DT 01-MAR-2002 (Tremblrel, 20, last sequence update)

DE 01-JUN-2002 (Tremblrel, 21, last annotation update)

GN SSTR2.

OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).

OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neuteleostei;

OC Acanthomorphae; Acanthopterygii; Percomorphae; Tetraodontiformes;

OC Tetraodontidae; Takifugu.

OX NCBI_TaxID=31033;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21564205; PubMed=11707075;

RA Baderli-Fam S., Ferraz C., Demaille J., Scherer G., Pfeiler D.;

RT "Comparative Genomics of the SOX9 Region in Human and Fugu rubripes:

RT Conservation of Short Regulatory Sequence Elements within Large

RT Intergenic Regions.";

RL Genomics 78:73-82(2001).

DR EMBL; AF329945; AAL32173.1; .

DR InterPro; IPR000276; GPCR_Rhodopsin.

DR Pfam; PF00001; 7tm.1; 1.

DR PRINTS; PR00237; GPCR_RHODOPSIN.

DR PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_1; UNKNOWN_1.

DR PROSITE; PS0262; G_PROTEIN_RECEPTOR_F1_2; 1.

KW Receptor.

SQ SEQUENCE 370 AA; 41364 MW; 420BH12F204946B6 CRC64;

Query Match 23.6%; Score 523; DB 13; Length 370;

Best Local Similarity 32.9%; Pred. No. 4.2e-37;

Matches 128; Conservative 74; Mismatches 131; Indels 56; Gaps 13;

QY 45 WRLPQPAWVEGSSARLW---EQATGTGMDLEASLPTGPNASNTSGPDNLTSAQSPR 101

Db 4 WILP-PSPLNLSDDLXYDGEQANGS---DLHA-----NRDHSLNKTS----- 43

QY 102 TGSISYINIMPSVETICLLGIGNSTYIFAVYKSKLHMCNNPDIIFINLSVLDL 161

Db 44 -----TVYTTCMYFLVCAVGLCGNALVTVILRYAKM---KTVNITILNLAVADVL 93

QY 162 LIGMPFIHOLMGVHMFGEWCTITITAMDANSOFTSYITLMAIDRYLATVPISS 221

Db 94 MLGIPFLAIQV-ALVHMPFGVLCRVYMTVDLSNFTSIFCLMVSIDRYLAVHFKST 152

QY 222 KFRPSAATVITCLMALSPSTIPVWLYARLIPPGAGVGGIRLPNDPDLWFTLY 280

Db 153 KWRKPRRAKTIYNAVWQASLVMLPIYISGITTKDCCF-CTIVPEDEAVYAFAMLY 211

QY 281 QEFLAFLPFWITAAVRLIORTMSSVAPASORSIRLTKRYTRRAICLVEFYCMA 340

Db 212 TFIIGFLPLIVISLCLVFIIVKYSSGIRVSKRRKRYTRAVSIYAVFVLCWLP 271

QY 341 YVYLQTLQLS-----ISRPFLTFVLYLNAISLGYANSCLPFVYIVLCETFR 391

Db 272 FVFNVTISVTSISATVLTSTFAFV-----VLGYANSCAMPILYALSENFKKSFG 325

QY 392 VLSVKPAQGLRAVYNAQTADERTESK 420

Db 326 VLCLQ-----KVGGLDEERSDSRQDKSR 349

RESULT 8

09GGE0 PRELIMINARY; PRT; 346 AA.

AC 09GGE0; 01-DEC-2001 (Tremblrel, 19, Created)

DT 01-DEC-2001 (Tremblrel, 19, last sequence update)

DT 01-MAR-2002 (Tremblrel, 20, last annotation update)

DE Unknown (Protein for IMAGE:3354783) (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Strausberg R.;

RT TISSUE=EYE;

RU Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC009522; AA009522.1; .

DR InterPro; IPR000276; GPCR_Rhodopsin.

DR Pfam; PF00001; 7tm.1; 1.

DR PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_1; UNKNOWN_1.

DR PROSITE; PS0262; G_PROTEIN_RECEPTOR_F1_2; 1.

FT NON_TER 1

SQ SEQUENCE 346 AA; 38790 MW; EA073A6CC05FB72 CRC64;

Query Match 23.6%; Score 521.5; DB 4; Length 346;
 Best Local Similarity 31.7%; Pred. No. 5.2e-37;
 Matches 110; Conservative 73; Mismatches 125; Indels 39; Gaps 7;

QY 82 NASNTSDGPDNLTSAGSPRTGSIYINIMPSVFGTICLLIGTGNSTVIAVVKSKRLH 141
 DB 6 NTSNOTPEPYDLS-----NAVLFIFYEVVCIIGLGNLTIVILIRYAKM- 51
 QY 142 WCNVNPDIETINLSVVDLLFLIGMP-----MIHOLMGNGVMHGEMLTITAMANS 195
 DB 52 --KITINIIYILMAIADLDELFMGLPEFLAMQVALVH-----WFGAICRVAVTVGGIN 102
 QY 196 QFTSYIITLAMAIDRYLATVHPISSTFRKPSVATVLCILMALSFISTIPVWLARLP 235
 DB 103 QFTSIFCLTVMSIDRYLAVVHPIKSAKMRPRRTAKMITMAVGVSLVILIPIMYAGLRS 162
 QY 256 FPGAVGCGIRLPNPDLDL-WETLYQFLAPALPFWITAAVRIILOMTSSVAPASQR 314
 DB 163 NONGNSSCTINWPGESGAMTGFITITLGLVLPVLTICLCTYFLITIKASSGIRVSS 222
 QY 315 S1RLRTKRVTRTAICLVFEVCAPVYVLTOLSLIS-RPTLTFVYLYNNAISLIGYANS 373
 DB 223 KKKSKSKVTBWSIVAVFICMLPFYFNVSYSMAISPTPAKGMEDFVVVLTVANS 282
 QY 374 CLNPFIYVILCEFRKRLVLSYKPAAGQLRAVSNAGTADERTESK 420
 DB 283 CANPIIYAFSLDNFK-----SFQNVLCIVKVSCTDDESDSK 321

RESULT 9

Q96TF2 PRELIMINARY; PRT; 356 AA.
 AC 096TF2;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Somatostatin receptor 2B.
 GN SSTR2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 ON NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20084417; PubMed=10619399;
 RA Petersen S., Rasch A.C., Presch S., Bell F.U., Schulte H.M.;
 RT "Genomic structure and transcriptional regulation of the human
 RT somatostatin receptor type 2".
 RL Mol. Cell. Endocrinol. 157:75-85(1999).
 DR EMBL; AF184174; AAF42810.1; -.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PROSITE; PS00237; G_PROTEIN_RECPEP_FL1; UNKNOWN_1.
 DR PROSITE; PS00262; G_PROTEIN_RECPEP_FL2; 1.
 SQ SEQUENCE 356 AA; 40006 MW; D10FA237FAED6193 CRC64;

Query Match 23.3%; Score 516.5; DB 4; Length 356;
 Best Local Similarity 30.7%; Pred. No. 1.5e-36;
 Matches 111; Conservative 78; Mismatches 123; Indels 49; Gaps 10;

QY 69 WM-----DEASLLPTGNASNTSDGPDNLTSAGSPRTGSIYINIMPSVFGTICLLGI 124
 DB 14 WLSIPDLNGSVST--NTSNOTPEPYDLS-----NAVLFIFYEVVCIIGL 58
 QY 125 IGNSVIFAVVVKSKLHWCNNVPDIFITINLSVVDLLFLIGMP-----MIHOLMGNGVW 178
 DB 59 CGNTLVYIILRYAKM--KITINIIYILMAIADLDELFMGLPEFLAMQVALVH-----W 108
 QY 179 HGEHMTCTIITAMDANSOTSTYIITAMADRYLATVHPISSTFRKPSVATVLCILMA 238
 DB 109 PFKAICRVAVTVGGINQFTSIFCLTVMSIDRYLAVVHPIKSAKMRPRRTAKMITMAVWG 168

QY 239 LSFISTIPVWLARLPPEGAVGCGIRLPNPDLDL-WETLYQFLAPALPFWITAAV 297
 DB 169 VSLVILIPIMYAGLRSNOMGRSSCTINWPGESAMTGFITITLGLVLPVLTICLCT 228
 QY 298 VRILOMTSSVAPASQNSIRLRTKRVTRTAICLVFEVCAPVYVLTOLSLIS-RPTL 356
 DB 229 LFIILIKVSSGIRVSSKRRKSKKRVBWSIVAVFICMLPFYFNVSYSMAISPTP 288
 QY 357 FEVYLYNNAISLIGYANSCLNPFYVILCEFRK--RLVLSYKPAAGQLRAVSNAGTAD 413
 DB 289 ALKGHEDFVVVLTVANSANPIIYAFSLDNFKSFQNVLCIVK-----VDNKSNGE 339
 QY 414 E 414
 DB 340 E 340

RESULT 10

Q91Y73 PRELIMINARY; PRT; 346 AA.
 AC Q91Y73;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Somatostatin receptor type 2.
 GN SSTR2 OR SSTR2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129; TISSUE=LIVER;
 RX MEDLINE=21201198; PubMed=11278805;
 RA Puente E., Saint-Laurent N., Tortissani J., Furet C., Schally A.V.,
 RA Vayssé N., Bussac L., Susini C.;
 RT "Transcriptional Activation of Mouse sstr2 Somatostatin Receptor
 RT Promoter by Transforming Growth Factor-beta. Involvement of Smad4".
 RL J. Biol. Chem. 276:13461-13468(2001).
 DR EMBL; AF008914; AAD01420.1; -.
 DR MGD; MGI:98328; Ssstr2.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PROSITE; PS00237; G_PROTEIN_RECPEP_FL1; UNKNOWN_1.
 DR PROSITE; PS00262; G_PROTEIN_RECPEP_FL2; 1.
 KW Receptor.
 SQ SEQUENCE 346 AA; 38586 MW; D7A20AEC1371C400 CRC64;

Query Match 23.3%; Score 516; DB 11; Length 346;
 Best Local Similarity 31.2%; Pred. No. 1.6e-36;
 Matches 115; Conservative 77; Mismatches 129; Indels 48; Gaps 11;

QY 62 EQATGNG-WM-----DEASLLPTGNASNTSDGPDNLTSAGSPRTGSIYINIMPSV 116
 DB 6 EQLNGQVWVSPDPDLNLSLGS--NGSNOTPEPYDMS-----NAVLFIFY 50
 QY 117 GTICLLIGTGNSTVIAVVKSKLHWCNNVPDIFITINLSVVDLLFLIGMP-----MIH 170
 DB 51 FVVCVAGLGNLTIVILIRYAKM--KITINIIYILMAIADLDELFMGLPEFLAMQVALVH 107
 QY 171 QLMGNGVMHGEHMTCTIITAMDANSOTSTYIITAMADRYLATVHPISSTFRKPSVAT 230
 DB 108 -----WFGAICRVAVTVGGINQFTSIFCLTVMSIDRYLAVVHPIKSAKMRPRRTAK 160
 QY 231 LVICLLMALSFISTIPVWLARLPPEGAVGCGIRLPNPDLDL-WETLYQFLAPALP 289
 DB 161 MINVAVMCSVLIVIPIMYAGLRSNOMGRSSCTINWPGESGAMTGFITITLGLVLP 220
 QY 290 FVYITAAVYRILOMTSSVAPASQNSIRLRTKRVTRTAICLVFEVCAPVYVLTOL 349
 DB 221 LFTICLCTYFLITIKVSSGIRVSSKRRKSKKRVBWSIVAVFICMLPFYFNVS 280
 QY 350 SIS-RPTLTFVYLYNNAISLIGYANSCLNPFYVILCEFRKRL--VLSVPAAGQLRAV 406

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Db      281  SVALSPPTALGMFDEYVILTYANSCANPILYAFLLSDNFKKSPQNVYCLVKA----- 332
QY      407  SNAQTADDEE 415
Db      333  DNSQSGAED 341

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RESULT 11

Q9PVG0 PRELIMINARY; PRT; 367 AA.

DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Somatostatin receptor type 1 subtype A.
 GN SST1A.
 OS Carassius auratus (Goldfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Carassius.
 OX NCBI_TaxId=7937;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RC MEDLINE=20005543; PubMed=10537151;
 RA Lin X., Janowick J.A., Brothers S., Conn P.M., Peter R.E.;
 RT "Molecular cloning and expression of two type one somatostatin
 receptors in goldfish brain.";
 RL Endocrinology 140:5211-5219(1999).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL; AF097726; AAF08613.1; -
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PFO0001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCRHOOPSn.
 DR PROSITE: PS00237; G-PROTEIN_RECP_FL_1; 1.
 DR PROSITE: PS50262; G-PROTEIN_RECP_FL_2; 1.
 KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
 SQ SEQUENCE 367 AA; 41658 MW; BB85EC26C103614 CMC64;

Query Match	22.7%;	Score 502.5;	DB 13;	Length 367;
Best Local Similarity	30.1%;	Pred. No. 2.5e-35;		
Matches 97;	Conservative 80;	Mismatches 120;	Indels 25;	Gaps 6;

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QY      71  DEASLLEPTGPNASTSDGPDNLNLSAGSPRPTGSIYINIMESVEFOTLGLLIGNSY 130
Dh      9   NLEDGLYLINFSSNETHNDHGSSA-----IFISPIYSVWLVBGLGCSMW 55
QY      131 IFAYVAKSLHMCNNVPDLEIFINLSVDLLEFLGPFMIHGLMGNGVWHGEMTCLITRA 190
Dh      56 IYVIFRYAKMKATN---YYIINLIMAEGLMLSVPLVYSSLHH--WPGSLICRLVLS 111
QY      191 MDANSQFSTYIILTAMADIRYATVHPISSTFRKPSVATLVICLLMALSFISSITPWWY 250
Dh      112 VDAIMFETSYICLYTISIDRYISVYHPIKARYRRTIAKKVYNLGVMMFSLIVLPIIF 171
QY      251 ARLLPPGGAVSGGIRLPNDPTDLYW---FTLYOFLFALPEVYVITAAYVRILOKRTSS 307
Dh      172 STAPRNSDGSVCNMMPERERO--WMAVFVYIATMGFLPEVIAICMCTYLLIVKRVY 229
QY      308 VAPASQSRIRLKRKRYTKRAIACLVFVVCAPRYVVLVDLDSIRPLTFVYLYNNAIS 367
Dh      230 ALKAGMOQRKSRERKITTVMWVYVYVLCMPHFIMOLVSFVQOHNAT---LSQLAVI 286
QY      368 LGYANSGLNPEVYIVCFEFR 389
Dh      287 LGYANSCANPIYLGFLSDNFR 308

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RESULT 12	
Q9PVF9	
ID Q9PVF9	PRELIMINARY; PRT; 367 AA

AC Q9PVE9; 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, last annotation update)
DE Somatostatin receptor type I subtype B.

	Query Match	Score	499.5;	DB 13;	Length	367;
-1- SUBCELLULAR LOCATION: INTEGRAL	Similarity	30.1%	Pred. No.	4.5e-35		
-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.	Conservative	97;	Mismatches	120;	Indels	25;
EMBL: AF0097726; AA08613.1; -					Gaps	6

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QY 71 DEEASLEPPGPNASTSOGPDNLTASGSPRRTGSIYINIIMPSVEFOLLIGIGSTV 130
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 9 NLEDGGLYLLNFNSNETHNSGSSA-----IFISFYVCLVJGCGSNMV 55
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 131 IFVAVVKKSLHMCNNVPDIFINILSVDDLFELGPEMFIHOLMGNGVWHGETMCTLITA 190
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 56 IYVIFRYAKMKATN---IYIINLAIADDLMLSLVPLVTSLLAH-WPFGSLCRLVLS 111
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 191 MDANSQFSTYILITAMADIDRLATVHPISSTKFRKPSVATLVICLLMALSFITPWWLY 250
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 112 VDAINMFTSYICLYTSDIRYSVHPHKAARYRRTAKVWNGVMWFSILVPLPIIF 171
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 251 ARLEPPGAGVGCGIRLEPNPDLDLY--FTLYQETLAFLEPVYTAAYRIILQRTSS 307
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 172 STTAPNSDSVACNMMPERQ--WMAFVYIYALMGFLPVPVIAICMCIYLIIMKRVV 229
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 308 VAPASQSRITLRKRYTRAIAlAICLYEVCAPVYVLOLDLISRPLTFVYLYNNAIS 367
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 230 ALKAGMOQRKSERKITLVMWVYVYICMPEHIVQVLSVFOQHNS---LSQLAVI 286
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 368 LGYANSCINPEYVYICETFR 389
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 287 LGYANSCANPILIGTLDNFRK 308
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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RESULT 13	
09GKP7	
ID 09GKP7	PRELIMINARY; PRT; 315 AA.
AC 09GKP7;	
DT 01-MAR-2001 (TREMBLrel. 16, Created)	
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)	
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)	
DE Somatostatin receptor 1 (Fragment).	
GN SSTrl.	
OS Sus scrofa (Pig).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.	
OX NCBI_TaxID=9823;	
RN [1]	

RP SEQUENCE FROM N.A.
 RX MEDLINE-20556840; Pubmed-11105212;
 RA Marklund S., Tuggle C.K., Rothschild M.F.;
 RT "Mapping of the CYP1A1, SSTR1 and TTF1 genes to pig chromosome 7q
 RT refines the porcine-human comparative map.";
 CC Annu. Genet. 31:318-321(2000).
 RL -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL: AF148990; AAG40780.1; -;
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR00237; GPCR_RHODOPSIN.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_1; 1.
 DR PROSITE: PS50262; G-PROTEIN_RECEP_FL_2; 1.
 KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
 FT NON TER 1
 FT SEQUENCE 315 AA; 34355 MW; 0B973038C472A882 CRC64;

Query Match 22.5%; Score 497; DB 6; Length 315;
 Best Local Similarity 30.6%; Pred. No. 6.1e-35;
 Matches 108; Conservative 67; Mismatches 134; Indels 44; Gaps 7;

QY 29 PLPDGACAPGCGRRRLPQPAVEGSSARLMQATGTMQMLESLPTGPNASNTSD 88
 DB 2 PSCPSCGEGXGSR-----GGACTAD--GMEEPGRNNAQNGT 38
 QY 89 GPDNLTSAGSPRTGISISYINIMPSVETICLLIGTSTVIAVAVKSKSLMNCNVDP 148
 DB LSEGGSA-----ILISFYSVCLVGLCGNSMVIYILRAKMKTAIIN--- 82
 QY 149 IFITNLSTVVDLLFLGMPFMIHQMGNGVHFGTCTLTADANSQFTSTIILAMAI 208
 DB 83 IYIILALADELLMSVPELVTSTLRH-WFGALLCRVLSDAVNMFTSYCLTVLSV 141
 QY 209 DRYLATVPISTFKRSVATLVICLLMALSFISITPWLARLIPFGAGVCGIRLP 268
 DB 142 DRYAVVAPRIKARRRRTAKVNLGVLSLVLIPYVFSRTAANSQGYACNMAMP 201
 QY 269 NP-DTDLWFTPLQFFLAFEPVYITAAVYRILOKMTSSVAAPSORSIRLRKRYTRA 327
 DB 202 EPAGRMVLFVLYFLMFLPVGALICLVYLITAKRMVALKAGWQRRSRKITTLMV 261
 QY 348 IATCFVFCNAPYVYLQTLQSLISRPITLFEVLYLNAISIGYANSCINPFVY 380
 DB 262 MNVWVFYICMFPYVQLVNFAEQDQATVYSQL---SVILGYANSCANPILY 311

RESULT 14

Q95KS6 PRELIMINARY; PRT; 346 AA.
 AC Q95KS6:
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE Somatostatin receptor subtype 1 (Fragment).
 GN Sst1.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PIUTARY;
 RA Debus N., Dutour A., Vauroqueaux V., Oliver C., Ouafik L.;
 RT "The ovine somatostatin receptor subtype 1 (sst1): Partial cloning
 RT and tissue distribution.";
 RN Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 RP SEQUENCE FROM N.A.
 RC TISSUE=PIUTARY;
 RA Debus N.;

RL Thesis (1999),
 RL Department of Aix-Marseilles II, Marseilles, France.
 RL EMBL: AJ314853; CAC69545.1; -;
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_1; UNKNOWN_1.
 DR PROSITE: PS50262; G-PROTEIN_RECEP_FL_2; 1.
 KW Receptor.
 FT NON TER 1
 FT SEQUENCE 346 AA; 38479 MW; 65547713CF2CA5C6 CRC64;

Query Match 22.4%; Score 494.5; DB 6; Length 346;
 Best Local Similarity 33.3%; Pred. No. 1.1e-34;
 Matches 98; Conservative 69; Mismatches 116; Indels 11; Gaps 5;

QY 100 PRTGISY---INIMPSVETICLLIGTSTVIAVAVKSKSLMNCNVDPDIITNLSTV 156
 DB 1 PONGTISEGGSAIILISFYSVCLVGLCGNSMVIYILRAKMKTAIIN---IYIILNAI 57
 QY 157 VDLFLGMPFMIHQMGNGVHFGTCTLTADANSQFTSTIILAMAIIDRYLATVH 216
 DB 58 ADELMLMSVPELVTSTLRH-WFGALLCRVLSDAVNMFTSYCLTVLSYDRYAVVH 116
 QY 217 PISTFKRPSVATLVICLLMALSFISITPWLARLIPFGAGVCGIRLPN-DTDLX 275
 DB 117 PIKARYRPTVAVVNLGVWVLSLVLIPYVFSRTAANSQGYACNMAMPAGRWLV 176
 QY 276 WFTYQFELAFEPVYITAAVYRILOKMTSSVAAPSORSIRLRKRYTRAICLVPE 335
 DB 177 GFVLITFLMGFLPVGALICLVYLITAKRMVALKAGWQRRSRKITTLMVWVYV 236
 QY 336 VCMAPYVYLQTLQSLISRPITLFEVLYLNAISIGYANSCINPFVYVLCETPK 389
 DB 237 ICMPFVYVQLVNFAEQDQATVYSQL---SVILGYANSCANPILYGLSDNFKR 287

RESULT 15

Q9DQ06 PRELIMINARY; PRT; 380 AA.
 AC Q9DQ06:
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE Somatostatin receptor type two.
 GN SST2.
 OS Carassius auratus (Goldfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Carassius.
 OX NCBI_TaxID=7957;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RA Lin X., Janovick J.A., Cardenas R., Conn P.M., Peter R.E.;
 RT "Molecular cloning and expression of a type-two somatostatin receptor
 RT in goldfish brain and pituitary.";
 RT Mol. Cell. Endocrinol. 166:75-87(2000).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL: AF139597; AAF98367.1; -;
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR00237; GPCR_RHODOPSIN.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_1; 1.
 DR PROSITE: PS50262; G-PROTEIN_RECEP_FL_2; 1.
 KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
 FT SEQUENCE 380 AA; 43146 MW; CE897FF537CFF30 CRC64;

Query Match 22.0%; Score 487; DB 13; Length 380;
 Best Local Similarity 32.4%; Pred. No. 5.6e-34;
 Matches 112; Conservative 68; Mismatches 140; Indels 26; Gaps 8;

Thu Feb 20 11:32:28 2003

us-09-885-478-2.rspt

Page 8

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QY 67 TGM-----MDLEASLLPTGPNASNSD-----GPNLTASASPTGTSIYINIMPS 114
Db 3 TKRMFMPNSNSLSDRLDRLNDSFFPGNSDGLGEMYPINSHTHPGFDQTS-----SVITF 56
QY 115 VEGTICLIGTGNSTVFIAVVKRSKELMWCNNVDPDIFITLNSVDDLFLCLMPFMHOLMG 174
Db 57 YVFVCAAGTGCGLNLMVILIRYAKM--KVTMTYILNLAVDVLCSMLSPETALDLS 112
QY 175 NGVWHFGCTMTLTADANSOFSPTYILRPMALDRILATVHPISSTPKPKPSVATVIC 234
Db 113 LHMFGSALICRVVLTDASNQFISIFFLYMASDRILAVHPIKSKIKMKPKRPAKISL 172
QY 235 LLMALSFISTPVMVLYARLPEPGAVGCGIRLNPOTDLTW-FTLYQFLARLPPVVI 233
Db 173 AMWVISTLVNPIIMYISGVNKKNEARCTMLMPEBPONTYYTVEIFETFMGFLPLTVI 222
QY 294 TAAVYRILQMTSSVAPASORSIRLTKRVYRTAIAICLFEVGCMAVYVYLQTLTOLISR 353
Db 233 CMCYLLIYIKVKSOMRWCSKRRKSEKRVKRMYSIVVYVFLCMLPEFYFVNVTSGTV 292
QY 354 PTLTVT-ILYNNALISGYANCLNPFYIVICETFERKL--VLSYK 396
Db 293 PTPVPAKSTFDPVVVLGYANSCLNITLALISDNFKSFOVNYLCK 338

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Search completed: February 13, 2003, 14:00:15
Job time : 31.2615 secs
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 13, 2003, 13:56:01 ; Search time 15.1596 Seconds
(without alignments)
2676.114 Million cell updates/sec

Title: US-09-885-478-2

Perfect score: 2212
Sequence: 1 MSYGAMKKGVGRAVLGGSS.....LRVSNAGTADERTESKGT 422

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2207	99.8	422	2	JC7080 melanin-concentrat
2	565.5	25.6	340	2	JC7695 G protein-coupled
3	533	24.1	369	2	D41795 somatostatin recep
4	531.5	24.0	369	2	B41795 somatostatin recep
5	527	23.8	369	2	A45291 somatostatin recep
6	525.5	23.8	369	2	JC2083 somatostatin recep
7	515	23.3	346	2	S29248 somatostatin recep
8	514	23.2	391	2	A41795 somatostatin recep
9	513.5	23.2	388	2	JN0605 somatostatin recep
10	508	23.0	391	2	C41795 somatostatin recep
11	504.5	22.8	418	2	A46226 somatostatin recep
12	497.5	22.5	391	2	A39297 somatostatin recep
13	494.5	22.4	384	2	A47249 somatostatin recep
14	483	21.8	384	2	JC4629 brain-specific som
15	480.5	21.7	428	2	S30508 somatostatin recep
16	478.5	21.6	363	2	I57955 somatostatin recep
17	478.5	21.6	364	2	JN0763 somatostatin recep
18	472	21.3	428	2	A44021 somatostatin recep
19	470.5	21.3	363	2	I57940 somatostatin recep
20	453.5	20.5	398	2	A57510 mu oploid recep
21	453	20.5	372	2	I38532 mu oploid recep
22	452.5	20.5	398	2	I56517 mu oploid recep
23	448	20.3	400	2	I56553 mu opiate receptor
24	447	20.2	392	2	S65693 oploid receptor mu
25	446.5	20.2	392	2	S34592 delta oploid recep
26	445.5	20.1	398	2	I56504 mu oploid receptor
27	441	19.9	372	2	B48227 delta oploid recep
28	435.5	19.7	380	2	JC3338 kappa oploid recep
29	431.5	19.5	380	2	A55259 kappa oploid recep

30	421	19.0	328	2	I38973 G protein-coupled
31	420.5	19.0	380	2	A48227 kappa oploid recep
32	419	18.9	380	2	S36143 kappa oploid recep
33	413	18.7	370	2	S43087 orphan oploid rece
34	411.5	18.6	367	2	I49022 kappa oploid recep
35	411.5	18.6	367	2	JC2421 oploid receptor ho
36	410.5	18.5	367	2	I56520 G protein-coupled
37	409.5	18.5	333	2	I38974 kappa oploid recep
38	409.5	18.5	380	2	JC2434 G protein-coupled
39	407	18.4	373	2	JE0087 kappa oploid recep
40	372.5	16.8	359	2	I51372 angiotensin II rec
41	368	16.6	362	2	JN0694 angiotensin II rec
42	361	16.3	423	2	JC677 angiotensin II rec
43	347	15.7	371	2	JC5796 allatostatin recep
44	341	15.4	350	2	A42009 probable chemotatr
45	341	15.4	359	2	A42656 N-formyl peptide r
					angiotensin II rec

ALIGNMENTS

RESULT 1

JC7080

Melanin-concentrating hormone receptor [validated] - human

N:Alternate names: MCHR; orphan somatostatin-like receptor 1 (SLC-1)

C:Species: Homo sapiens (man)

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 11-May-2000

C:Accession: JC7080

R:Shimomura, Y.; Mori, M.; Sugo, T.; Ishibashi, Y.; Abe, M.; Kurokawa, T.; Onda, H.;

Biochem. Biophys. Res. Commun. 261, 622-626, 1999

A:Title: Isolation and identification of melanin-concentrating hormone as the endogen

A:Reference number: JC7080; MUID:99373129; PMID:10441476

A:Accession: JC7080

A:Molecule type: mRNA

A:Residues: 1-422 <SH1>

A>Note: It is uncertain whether Met-1, Met-6 or Met-70 is the initiation codon

C:Superfamily: neurokinin 1 receptor

C:Keywords: hormone receptor; transmembrane protein

Query Match	99.8%	Score 2207;	DB 2;	Length 422;
Best Local Similarity	99.8%	Pred. No. 6.3e-177;		
Matches 421;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MSYGAMKKGVGRAVLGGSSGQATEEDPLPDGACAPGGGRMRRLPQPAWVGSSARL	60	
DB	1	MSYGMKKGVGRAVGLGGSSGQATEEDPLPNCGACAPGGGRMRRLPQPAWVGSSARL	60	
QY	61	WEQATGTGMDLEASILPTGPNASNTSDGPNLTSAGSPRTGSIYINIMPSVFGTIC	120	
DB	61	WEQATGTGMDLEASILPTGPNASNTSDGPNLTSAGSPRTGSIYINIMPSVFGTIC	120	
QY	121	LLGTTGNTVIFAYVKKKLMHCNNVPDIFITINSVDLFLFLCAMPPIHQLMGVWHF	180	
DB	121	LLGTTGNTVIFAYVKKKLMHCNNVPDIFITINSVDLFLFLCAMPPIHQLMGVWHF	180	
QY	181	GETMCTLTAMDANSQFSTYITLAMAIDRYLAVVHPSRKERKPSVATVITCLMAL	240	
DB	181	GETMCTLTAMDANSQFSTYITLAMAIDRYLAVVHPSRKERKPSVATVITCLMAL	240	
QY	241	FISTPFWLVARLIPFGAVGCGIRLPNPDITLWFTLYQFLAFALPFVITAAVRI	300	
DB	241	FISTPFWLVARLIPFGAVGCGIRLPNPDITLWFTLYQFLAFALPFVITAAVRI	300	
QY	301	LQRMSSVAPASQSIKRTKRVRTAIAICLVFVCWAPYVYQLTOLISRPTEFVY	360	
DB	301	LQRMSSVAPASQSIKRTKRVRTAIAICLVFVCWAPYVYQLTOLISRPTEFVY	360	
QY	361	LYNAISLGYANSCINPFVYIVLCETFRKRLVLSVKPAAGOLRAVSNAGTADERTESK	420	
DB	361	LYNAISLGYANSCINPFVYIVLCETFRKRLVLSVKPAAGOLRAVSNAGTADERTESK	420	
QY	421	GT 422		

Db 421 GT 422

RESULT 2

JC7695

G protein-coupled receptor, SLT receptor - human

C:Species: Homo sapiens (man)

C>Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 22-Oct-2001

C:Accession: JC7695

R:Morl, M.; Harada, M.; Terao, Y.; Sugo, T.; Watanabe, T.; Shimomura, Y.; Abe, M.; Shint

Biochem. Biophys. Res. Commun. 283, 1013-1018, 2001

A:Title: Cloning of a novel G protein-coupled receptor, SLT, a subtype of the melanin-co

A:Reference number: JC7695; MUID:21255282; PMID:11355873

A:Contents: Hippocampus

A:Accession: JC7695

A:Molecule type: mRNA

A:Residues: 1-340 <MOR>

A:Cross-references: DDBJ:AB060151

C:Comment: This receptor, a second subtype of the melanin-concentrating hormone (MCH) re

memory

C:Genetics:

A:Gene: slt

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match

Best Local Similarity 37.0%; Pred. No. 1e-39; Mismatches 119; Indels 11; Gaps 4;

Matches 113; Conservative 62;

Db

110 IIMPEFGTICLGIIGSVIFAVKSKLHMCNNVPDIFIINLSVVDLFLGMPFI 169

35 VILPMGIITICSTGLVGNILVFTIRSRK-----KIVPDYICMLAVADLVHIGMFLI 90

170 HOLMGNGVHGEIMCTLITAMANDSOFTSTYIITAMADRYLATVHPISSTKFRKPSVA 229

91 HQMANGGEVWEGPLCTIITSIDTCNCFACSAIMTVMSVDVDFALVOPFLTRMRTYKKT 150

230 TLIVCLMALSFISTTPWLYARLIPFGAGVCGIRLPNDPDLVMTLYQFLALALP 289

151 IRINGLMAASFILALPWAYSKYIKFKDVGESCAFEDLTSPD-DVLAWTLTLTITTFPP 209

290 FVVTAAAYVRIL-----ORMTSSVAPASQRSI-RLRTKRVTRTAICLVFVCWAPYV 343

210 LPLILVCIILICTYWEMQNKDARCNPSVPRKQVKLKLMLVLVAVETLSAAPHV 269

344 LQTLDSISRPPLTFVYLYNAISLIGVANSCLNPFIYVLCETRRKRLVSVKPAAGQL 403

270 IQLVMIQMEQPLAFYVGYVSLICLSVASSSINPFLYTLISGNFQKRLPQIQRATEKEI 329

404 RAVSN 408

330 NNMGN 334

Db

Db

Db

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A:Accession: I56236

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 99-309 <RES>

A:Cross-references: GB:S71756; NID:9560631

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; hormone receptor; transmembrane protein

Query Match

Best Local Similarity 31.7%; Pred. No. 5.9e-37; Mismatches 131; Indels 46; Gaps 10;

Matches 118; Conservative 77;

Db

62 EOATGTG-WM-----DLEASILPTGNASNTSDGPNLTSAGSPPRGSIYINIMPSVF 116

6 EQMNSQVWVSSPFLNGSLGPS--NGSNQTEPYDNTS-----NAVLFPIY 50

117 GTICLIGTGNSTVIFAVKSKLHMCNNVPDIFIINLSVVDLFLGMPFI-----MIH 170

51 FVVCVGLGCMPLVYIVILRYAKM--KTIITVILNLAIDELMLGLPFLAMQVALVH 107

171 QLMGNGVHGEIMCTLITAMANDSOFTSTYIITAMADRYLATVHPISSTKFRKPSVAT 230

108 -----WFGKALICVYVMTVDGINQFTSIFCLTWSIDRYLAVVHPISAKWRPRAK 160

231 LVICLMAISFISTTPWLYARLIPFGAGVCGIRLPNDPDLVMTLYQFLALALP 289

161 MINVAVWCVSLVILPIMYAGLRSMQGRSSCTIIMWPEGAMVTFITVAFILGLFVP 220

290 FVVTAAAYVRILORMTSSVAPASQRSI-RLRTKRVTRTAICLVFVCWAPYVQQLQOL 349

221 LTIICCYFLIILIKVSSGIRVGSSKRRKSEKRVMSIVAVLFCWLPYIFNVSSV 280

350 SIS-REPLTFVYLYNAISLIGVANSCLNPFIYVLCETRRKRLVSVKPAAGQLRAVSN 408

281 SVASIPPLAIKGFEDVYVLTITANSCLNFIILAFSLDNFK-----SFQNVLCVKV 332

409 AQTAEDEETESK 420

333 SGTEDGERSDSK 344

Db

Db

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Proc. Natl. Acad. Sci. U.S.A. 90, 4196-4200, 1993
 A>Title: Cloning and characterization of a fourth human somatostatin receptor.
 A:Reference number: A47457; MUID:93248256; PMID:8483934
 A:Accession: A47457
 A:Molecule type: DNA
 A:Residues: 1-82, 'T', 84-364, 'K', 366-388 <ROR>
 A:Cross-references: GB:J07833; NID:9307429; PIDN:AAA60565.1; PID:9307430
 A>Note: sequence extracted from NCBI backbone (NCBIN:130856, NCBI:P.130858)
 C:Comment: This protein mediates the diverse actions of the tetradecaptide somatostatin.
 C:Genetics:
 A:Gene: GDB:SSTR4
 A:Cross-references: GDB:202662; OMIM:182454
 A:Map position: 20p11.2-20p11.2
 A:Introns: #status absent
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; glycoprotein; hormone receptor; lipoprotein; phc
 F:47-73/Domain: transmembrane #status predicted <TM1>
 F:84-109/Domain: transmembrane #status predicted <TM2>
 F:121-142/Domain: transmembrane #status predicted <TM3>
 F:162-184/Domain: transmembrane #status predicted <TM4>
 F:208-238/Domain: transmembrane #status predicted <TM5>
 F:257-284/Domain: transmembrane #status predicted <TM6>
 F:291-314/Domain: transmembrane #status predicted <TM7>
 F:24/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:119-198/Disulfide bonds: #status predicted
 F:161,253/Binding site: phosphate (Ser) (covalent) (by CAMP-dependent kinase) #status pr
 F:357/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match 23.2%; Score 513.5; DB 2; Length 388;
 Best Local Similarity 31.7%; Pred. No. 2,7e-35;
 Matches 107; Conservative 74; Mismatches 118; Indels 39; Gaps 9;

QY 62 EQATGTCGMDEASLLPTGPNASNTSDGPDNLTASGSPRTGISYINIMPSVETICL 121
 DB 12 EEGIGTAW-----PSAANASSAPAEAEAVAGGDAAAGM-VAIGCTIVATCL 59
 QY 122 LGIINGSTVFEAVVKKSKLHCNNVPDIFILINSYVDLLFLGLGPMPI-----HOLMGN 175
 DB 60 VGLVGNALVFEVLIRYAKKKTATN---IYLLNLAVALDELFMLSVPEVASSAALRH----- 111
 QY 176 GVWPFETMCTLTITAMDNSOFTSYILITAMADRILATLVHPSSEKPKPSAVATVLC 235
 DB 112 --WPFQSVLCRAVLSDGLMFTSVCLVLSDRVAVVHPRATVYRRSPVAKLTING 169
 QY 236 LMALESTISTPWLVARLIPFGG-AVGGGIRLPNPDITLVY---FTLYQFLAFLAPV 291
 DB 170 VMLASLVLPLAIFADTRPARGQAVACNLQMPHP---AMSAYVVYVTFLLGLFLPV 225
 QY 292 VINAAYVRLIORTSSVAASQSRSTLRKRTTAIAICLVFCWADYVYLQTLQSTI 351
 DB 226 AIGLCYLLVIGKRAVALRAGWQRRSEKITTRLVMVVVFLCMFPEVYVQLINLV 285
 QY 352 SREPTLFVLYNAAISLGYANSCINPFVYIVLCETPRK 389
 DB 286 TSLDAT---VNHVSLTSLANSCANPIIXGFLSDNFR 320

RESULT 10
 C41795
 somatostatin receptor 1 - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 30-Sep-1993 #sequence_revision 31-Dec-1993 #text_change 24-Nov-1999
 C:Accession: C41795
 R:Yamada, Y.; Post, S.R.; Wang, K.; Teger, H.S.; Bell, G.I.; Selino, S.
 Proc. Natl. Acad. Sci. U.S.A. 89, 251-255, 1992
 A>Title: Cloning and functional characterization of a family of human and mouse somatost
 A:Reference number: A41795; MUID:92108031; PMID:1346068
 A:Accession: C41795
 A>Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 1-391 <YAM>
 A:Cross-references: GB:M81831; NID:9201058; PIDN:AAA58255.1; PID:9201059
 C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; hormone receptor; transmembrane protein

Query Match 23.0%; Score 508; DB 2; Length 391;
 Best Local Similarity 30.7%; Pred. No. 7,8e-35;
 Matches 111; Conservative 73; Mismatches 134; Indels 44; Gaps 8;

QY 29 PLPDGACAPAGGGRWRRLPQAWEGSSARLMEQATGTGMDLASLLPTGPANASTSD 88
 DB 14 PPSRPSGCG-----EGACSR---GPSGAD---GMEEPGRNASSONGT 50
 QY 89 GPDNLTASGSPRTGISYINIMPSVETICLLIGISYVIFAVVKKSLHCNNVPD 148
 DB 51 LSEGGQSA-----ILISFISYVCLVGLCGNSMTYIYLAKKKTATN--- 94
 QY 149 ITILINSYVDLLFLGLGPMPIHQLMGNGVWHEGTMCTLTITAMDNSOFTSYILITAMAI 208
 DB 95 ITILNLAIDELIMLSVPLVSTILRH-WPEGALCLRLVSDVANNFTSYICLVLSV 153
 QY 209 DRYLATVHPISSTKRKPSVATVLCILMALSFISTPVMYLARLIPPGAVCGIRLP 268
 DB 154 DRYVAVVHPIKARRRPFAKVVNLGVVLSLVILPITVFSRTAANSDETACNMLMP 213
 QY 269 NP-DTDLVWFTLYQFLAFLAPFVITAAVYRILOKMTSSVAPASQSRIRLRTKRTTA 327
 DB 214 EPAQRWLVGFVLYTFILMGFLIPVGAICLYILIKMVMVALKMGQRRKSEKITTLMV 273
 QY 328 IALCLVFVCNAPRYVLOTLQSLRPLTFEYLYNAAISLGYANSCINPFVYIVLCETP 387
 DB 274 MNVAVVFWICWMPFVYVQLVNVFAEODATVTSQ---SVIIGYANSCANPIIXGFLSDNF 330
 QY 388 RK 389
 DB 331 KR 332

RESULT 11
 A46226
 somatostatin receptor 3 - human
 C:Species: Homo sapiens (man)
 C>Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999
 C:Accession: A46226; S32501
 R:Yamada, Y.; Reisine, T.; Law, S.F.; Ihara, Y.; Kubota, A.; Kagimoto, S.; Selino, M.;
 Mol. Endocrinol. 6, 2136-2142, 1992
 A>Title: Somatostatin receptors, an expanding gene family: cloning and functional cha
 A:Reference number: A46226; MUID:93149123; PMID:1337145
 A:Accession: A46226
 A:Molecule type: DNA
 A:Residues: 1-418 <YAM>
 A:Cross-references: GB:M96738; NID:9338498; PIDN:AAA60592.1; PID:9338499
 A>Note: sequence extracted from NCBI backbone (NCBIN:123685, NCBI:P.123690)
 R:Corneess, J.D.; Demchyshyn, L.L.; Seeman, P.; van Tol, H.H.M.; Strikant, C.B.; Kent,
 FEBS Lett. 321, 279-284, 1993
 A>Title: A human somatostatin receptor (SSTR3), located on chromosome 22, displays pr
 A:Reference number: S32501; MUID:93238970; PMID:8097479
 A:Accession: S32501
 A>Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-418 <COR>
 C:Genetics:
 A:Gene: GDB:SSTR3
 A:Cross-references: GDB:134187; OMIM:182453
 A:Map position: 22q13.1-22q13.1
 A:Introns: #status absent
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane p
 F:44-70/Domain: transmembrane #status predicted <TM1>
 F:81-106/Domain: transmembrane #status predicted <TM2>
 F:118-139/Domain: transmembrane #status predicted <TM3>
 F:159-181/Domain: transmembrane #status predicted <TM4>
 F:203-233/Domain: transmembrane #status predicted <TM5>
 F:255-282/Domain: transmembrane #status predicted <TM6>
 F:289-316/Domain: transmembrane #status predicted <TM7>
 F:17,30/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:116-191/Disulfide bonds: #status predicted
F:151,251,317,332/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status
F:251/Binding site: phosphate (Ser) (covalent) (by CAMP-dependent kinase) #status predic
F:256/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
F:412/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 22.8%; Score 504.5; DB 2; Length 416;

Best Local Similarity 32.5%; Pred. No. 1,7e-34;

Matches 118; Conservative 76; Mismatches 134; Indels 35; Gaps 11;

```
QY 81 PNASNTSDGPDNLTSAGSP-----PRGSIYINIMPSVFGTICLLIGNSTV 130
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 6 PSSVSTSEPNASSMPDPDAILGNVSAGPSAGLAVSGVLLPIYLVVCGVGLGNSLV 65
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 131 IFANVRSKSLHMCNNVPDIFIINLSVVDLLFLGMPFMIHOLMGNGV--WHFGEMTCTLI 188
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 66 IYVVALRHTA---SPSVTNVYLNLALADELFMLGLPEFLAAQ--NALSYWPGSLMCRILV 119
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 189 TAMDANSQFSTYITLTMADRYLATVHPISSTFKRSPVATLYICLLMAISFISTIPVW 248
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 120 MAVDGINQFISFLCTVMSVDRLAVHPRSARMTAPARTVSAANVAVASVAVVLPV 179
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 249 LYARLIFPGGAVGCGIRLPNPDLDLYW--FTLYQFLAFALPFVYITAAVYRILQRMF 305
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 180 VFGGV---PRGMSCTHMQNPEPA--AMRAGFIITTAALGFEGEPILLVICLCYLLIVKYR 234
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 306 SS---VAPASQSRILRTKRTVTAIAICLVFVCMAPIYVQLTQLSISR-ITTFYV 360
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 235 SAGRRVWAPSCQRR-RKSERRTVMYAVAVALLVLCWMPFYVNTINVAVCPLEEPAPFG 293
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 361 LYNAAISLIGVNSCLNPFYIVICETFR--KRLVLSVKRAAGOLRAVNAQTADAEPT 417
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 294 LYELVVALPYANSCANPILIGFLSYRKQGFRLVLRPSRRVNSQEPYTPGPKTEEDB 353
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 418 ESK 420
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 354 EEE 356
```

RESULT 12

A39297

somatostatin receptor - rat

N:Alternate names: probable G-protein-coupled receptor; SRIF receptor

C:Species: Rattus norvegicus (Norway rat)

C>Date: 03-Aug-1992 #sequence, revision 03-Aug-1992 #extl_change 24-Nov-1999

C:Accession: A39297; M45102; S20088

R:KeyWord: W.; Faust, H.J.; Schoenrock, C.; Richter, D.

DNA Cell Biol. 10, 689-694, 1991

A:Title: Cloning of a cDNA encoding a novel putative G-protein-coupled receptor expressed

A:Reference number: A39297; MUID:92096119; PMID:1661599

A:Accession: A39297

A:Molecule type: mRNA

A:Residues: 1-391 <MRY>

A:Cross-references: GB:X62114; GB:X61630; NID:956309; PIDN:CA44193.1; PID:956310

A:Experimental source: brain

A>Note: It is uncertain whether Met-1 is the initiator or whether translation is initiated

R:Lit. X.J.; Forte, M.; North, R.A.; Ross, C.A.; Snyder, S.H.

J. Biol. Chem. 267, 21307-21312, 1992

A:Title: Cloning and expression of a rat somatostatin receptor enriched in brain.

A:Accession: A45102

A:Reference number: A45102; MUID:93016064; PMID:1400442

A:Molecule type: nucleic acid

A:Status: preliminary; not compared with conceptual translation

A:Residues: 1-391 <LTI>

A:Experimental source: brain

A>Note: sequence extracted from NCBI backbone (NCBI:116692)

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; glycoprotein; receptor; transmembrane protein

```
QY 78 PTGNASNTSDG-----DNLISAG--SPRRTGISY---INIMPSVFGTICLLIGNS 128
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 18 PGCGGEGVCSGPGSGAADGKEEGRNSSQGLISBQSGAIIISFISVYVCLVGLGNS 77
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 129 TVIAVAVKSKSLHMCNNVPDIFIINLSVVDLLFLGMPFMIHOLMGNGVWHFGEMTCTLI 188
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 78 MVIYVILRYAMKATATN---IYILNLAIADLELMLSVPLVTSYLIRH--WFGALLCRIV 133
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 189 TAMDANSQFSTYITLTMADRYLATVHPISSTFKRSPVATLYICLLMAISFISTIPVW 248
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 134 LSVDAVNMFSTIYCLTVLSVDRYAVVHPKAAKRRPVAKVNNLGVWLSLILPIV 193
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 249 LYARLIFPGGAVGCGIRLPNPDLDLYW--FTLYQFLAFALPFVYITAAVYRILQRMF 307
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 194 VFSRIANSDDTVACNMLMEPEPAORMLVGFYLYTFMLGFLIPVCAICLCYLLIAKRMV 253
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 308 VAPASQSRILRTKRTVTAIAICLVFVCMAPIYVQLTQLSISRITLTFVYLYNAIS 367
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 254 ALKAGMOQRKSEKRIITLMVMVMVVFVLCWMPFYVQLVNVFAEQDADATVSQL--SVI 310
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 368 LGYANSCINPFYIVICETFRK 389
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 311 LGYANSCANPILYGLSDNFRK 332
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
```

RESULT 13

A47249

brain-specific somatostatin receptor SSTR-4 - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 21-Sep-1993 #sequence, revision 18-Nov-1994 #extl_change 24-Nov-1999

C:Accession: A47249

R:Bruno, J.F.; Xu, Y.; Song, J.; Berelowitz, M.

Proc. Natl. Acad. Sci. U.S.A. 89, 11151-11155, 1992

A:Title: Molecular cloning and functional expression of a brain-specific somatostatin

A:Reference number: A47249; MUID:93087484; PMID:1360663

A:Accession: A47249

A:Status: Preliminary

A:Molecule type: nucleic acid

A:Residues: 1-384 <BRU>

A:Cross-references: GB:M6544; NID:9207072; PIDN:AAA42180.1; PID:9207073

A>Note: sequence extracted from NCBI backbone (NCBI:119731; NCBI:P.119732)

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 22.4%; Score 494.5; DB 2; Length 384;
Best Local Similarity 33.0%; Pred. No. 1e-33;
Matches 104; Conservative 66; Mismatches 116; Indels 29; Gaps 8;

```
QY 85 NTSQDGPDLNLSGSPRRTGISYINIMPSVFGTICLLIGNSTVIFAVKSKSLHMCN 144
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 21 NASWAPDEDEEDVRSDDGTAGMVT--QCIYALVCLVGLGNALVIFVILRYAMKATAT 78
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 145 NVPDFIINLSVVDLLFLGMPFMI-----HQLMGNGVWHFGEMTCTLITAMDANSQFT 198
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 79 N---IYLLNLAIADLELFMLSVFVSAALNR-----WPGAVLCAVLSYDGLNMF 128
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 199 STYIITMAIDRYLATVHPDISSTFKRSPVATLYICLLMAISFISTIPVWLYARLIPPG 258
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 129 SEFCLTVLSVDRYAVVHPLRAATYRPSVAKLINLGWLSLITVLEIAFADTRPARG 188
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 259 G-AVGGGILPNPDLDLYW--FTLYQFLAFALPFVYITAAVYRILQRMSSVAPASOR 314
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 189 GEAVACNLMHPH---AMSAVFVITFLLGLPLLAIGLCYLLIVGKMRVVALRAGQ 244
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 315 SIRLRTKRTVTAIAICLVFVCMAPIYVQLTQLSISRITLTFVYLYNAISLIGYANSC 374
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 245 QRRRSKKTIRLVAMVYVFLCWMFPYVQLNLFVSLDNT---VNVVSLISYANSC 301
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 375 LNFYVYVLCETFRK 389
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 302 ANPILYGLSDNFRK 316
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
```

Query Match	21.8%;	Score 483;	DB 2;	Length 384;
Best Local Similarity	31.9%;	Pred. No. 9.5e-33;		
Matches 105;	Conservative 69;	Mismatches 133;	Indels 22;	Gaps 8;

RESULT 15

Query Match	21.7%;	Score 480.5;	DB 2;	Length 428;
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Matches 118; Conservative 73; Mismatches 143; Indels 43; Gaps 11;

Search completed: February 13, 2003, 14:01:05
Job time : 16.1596 secs

